

STIC-Biotech/ChemLib

78693

From: Zeman, Mary
Sent: Friday, October 25, 2002 8:12 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/970966

Please run a regular search **and** an oligo search of the following sequences from 09/970966

SEQ ID NO: 199, 210, 211 and 214

please make the minimum window in the oligo searches 10 nucleotides.

please include interference files

Paper printout please.

Thank you,

Mary K. Zeman

Examiner, 1631

305-7133

CM1 12A17

mailbox: CM1 12D01

199 - EFD 09/656,668
9/7/2000

Point of Contact:

Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

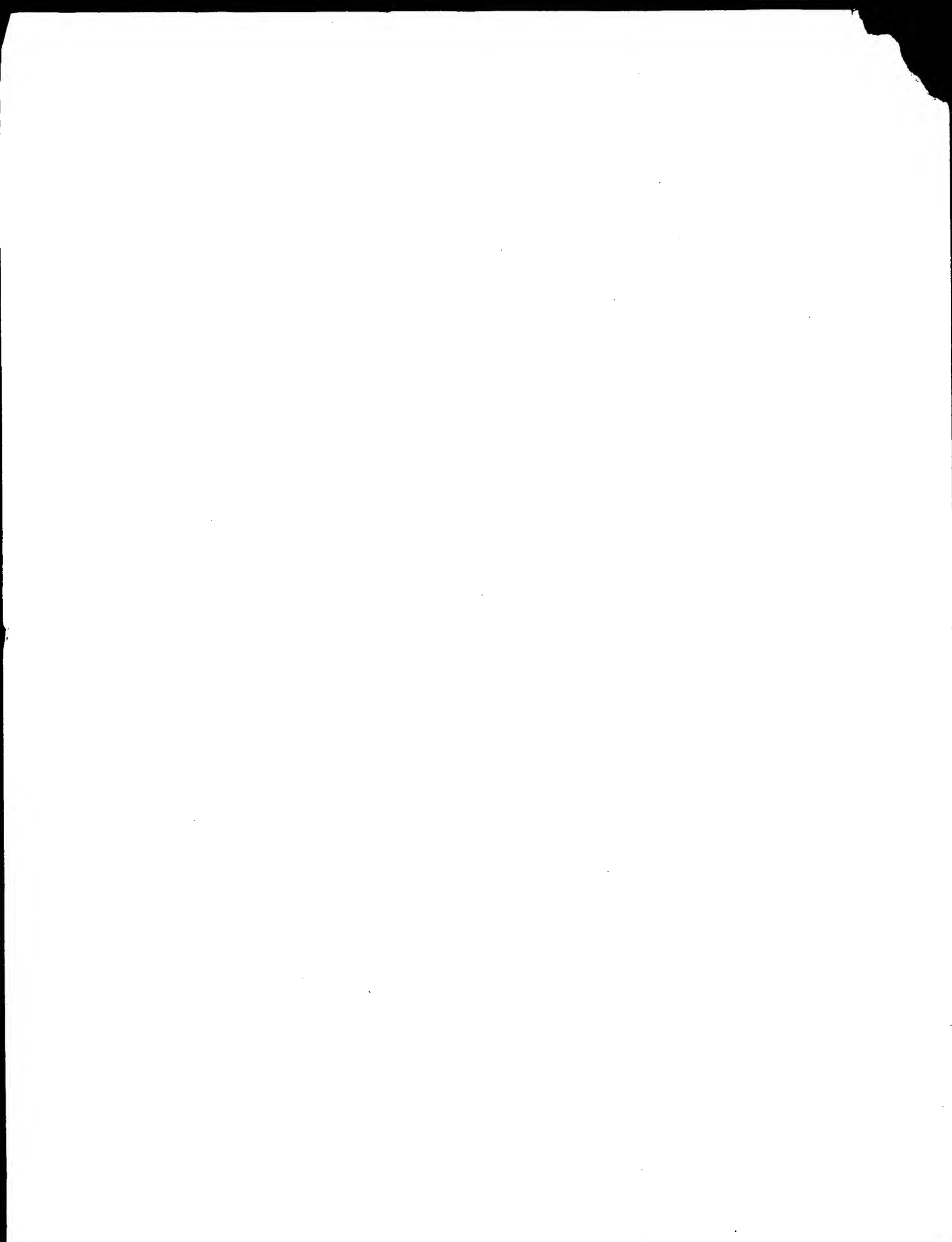
Searcher: Larson
Phone: _____
Location: _____
Date Picked Up: 11/08/02
Searcher Prep/Review: 40
Clerical: _____
Online time: 40

TYPE OF SEARCH:

NA Sequences: 4
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ABSS 03
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 938.618 Seconds
(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggcacacttttcgcgattgt.....tggctccgcacacacatcct 369

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 965615

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenDb1: *
1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
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21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_man: *
37: em_hlg_vrt: *
38: em_sy: *
39: em_hlg_hum: *
40: em_hlg_mus: *
41: em_hlg_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	6	AX093381
2	315	85.4	946	6	BC017318
3	315	85.4	1234	6	AX358762
4	315	85.4	1524	6	AX362255
5	315	85.4	1832	6	AK094501
6	315	85.4	1890	6	AX136281
7	314	85.1	2528	6	AX319944
8	281	76.2	396	6	AX093191
9	221	59.9	591	6	AX136556
10	175	47.4	129676	6	AC079773
11	142	38.5	147131	9	AC010974
12	47	12.7	209885	2	AC124493
13	38	10.3	1797	10	AB041649
14	22	6.0	113920	9	AL512284
15	22	6.0	161084	2	AC118794
16	20	5.4	157042	9	AC024061
17	20	5.4	171146	10	AC068808
18	20	5.4	180339	9	AC099049
19	20	5.4	190914	2	AC025029
20	20	5.4	205606	10	AL596204
21	19	5.1	2080	6	AX392969
22	19	5.1	2222	6	AX392971
23	19	5.1	2300	6	AX463719
24	19	5.1	2349	8	AF213399
25	19	5.1	2901	3	D49515
26	19	5.1	3914	10	AB017043
27	19	5.1	22752	9	AC104530
28	19	5.1	37635	9	AC004152
29	19	5.1	142329	2	AC128189
30	19	5.1	148571	9	AC105316
31	19	5.1	154693	9	AC084750
32	19	5.1	154772	2	AC106955
33	19	5.1	156128	2	AC113265
34	19	5.1	157533	9	AL354709
35	19	5.1	163041	2	AC116273
36	19	5.1	165873	9	AC066593
37	19	5.1	177070	2	AC018875
38	19	5.1	177426	2	AC021222
39	19	5.1	185551	2	AC112477
40	19	5.1	188172	9	AP003041
41	19	5.1	194769	2	AC113489
42	19	5.1	209418	2	AC122259
43	19	5.1	238472	9	AC010290
44	19	5.1	239904	2	AC096319
45	19	5.1	247865	2	AC097172

ALIGNMENTS

RESULT 1
LOCUS AX093381 369 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 199 from Patent WO0118046.
ACCESSION AX093381
VERSION AX093381.1 GI:13509829
KEYWORDS
SOURCE
ORANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 369)
Xu, J. and Stolk, J.A.
Ovarian tumor sequences and methods of use therefor
Patent: WO 0118046-A 199 15-MAR-2001;
JOURNAL

CORIMA CORPORATION (US)

FEATURES
Location/Qualifiers
source
1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature
1. .369
/note="n = A,T,C or G"

BASE COUNT 82 a 109 c 90 g 86 t 2 others
ORIGIN

Query Match 100.0%; Score 369; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 4,4e-211;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

Location/Qualifiers
1. .946

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastaglio, C., Mestrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantirip, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsourgon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 39 Row: D Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

CDS

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:29643 IMAGE:3641660"
/tissue_type="Pancreas, adenocarcinoma"
/clone_id="NIH_MGC_39"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
261..686
/product="Unknown (protein for MGC:29643)"
/protein_id="AA17318.1"
/db_xref="GI:16878240"
/translation="MW:16.8kDa; pI:5.5; N-terminal: NQIVNVDKMKQKVEKMSASIMIRKSSASSACILASIRGQSFQKLVNSVCLSCN TPINGRPRKRRSSASALRPGMLRTTLFLKLAIFSANC"

BASE COUNT

197 a 292 c 261 g 196 t

Query Match 85.4%; Score 315; DB 9; Length 946;
Best Local Similarity 100.0%; Pred. No. 1.9e-178;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 CAGGCTTTGGCGCTCAAAATCCAGTCTACCAAGTGAAGTTCAGTGAACAACGACT 89
Db 310 CAGGCTTTGGCGCTCAAAATCCAGTCTACCAAGTGAAGTTCAGTGAACAACGACT 369
Db 90 GCTCTCTCCCGAGTTCATTTGATTCGACGGTGAAGTTCAGTGAACAACGACT 149
Db 370 GCTCTCTCCCGAGTTCATTTGATTCGACGGTGAAGTTCAGTGAACAACGACT 429

LOCUS BC017318 946 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.
ACCESSION BC017318
VERSION BC017318.1 GI:16878239

KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 946)
Strausberg, R.
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

RESULT 3

AX358762

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AX358762 1524 bp DNA linear PAT 13-FEB-2002

Sequence 15 from Patent WO0193983.

AX358762

AX358762.1 GI:16875282

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godomski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 15 13-DEC-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. 1524
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 321 a 433 c 435 g 335 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.9e-178;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAATCATCAGTGTGAGAAATTCAGCTGAACACGACT 89
DB 170 CAGGCTTTGGCGTCAATCATCAGTGTGAGAAATTCAGCTGAACACGACT 229
QY 90 GCTCCTCCCCGAGTTCATTTGTAATTCAGGAGAAATTCAGCTGAACACGACT 149
DB 230 GCTCCTCCCCGAGTTCATTTGTAATTCAGGAGAAATTCAGCTGAACACGACT 289
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCT 209
DB 230 GCTCCTCCCCGAGTTCATTTGTAATTCAGGAGAAATTCAGCTGAACACGACT 349
QY 210 GTCATACGCTCTGCGGGGATCATGTGTAATTCAGGAGAAATTCAGCTGAACACGACT 269
DB 350 GTCATACGCTCTGCGGGGATCATGTGTAATTCAGGAGAAATTCAGCTGAACACGACT 409
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCAAGGCGCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCAAGGCGCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
DB 470 CTGCTCGGCGCTCA 484

RESULT 4
AX362255 1524 bp DNA linear PAT 15-FEB-2002
LOCUS AX362255
DEFINITION Sequence 15 from Patent WO0208288.
ACCESSION AX362255
VERSION AX362255.1 GI:18694585
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godomski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1. 1524
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 321 a 433 c 435 g 335 t
ORIGIN

Query Match 85.4%; Score 315; DB 6; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.9e-178;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAATCATCAGTGTGAGAAATTCAGCTGAACACGACT 89
DB 170 CAGGCTTTGGCGTCAATCATCAGTGTGAGAAATTCAGCTGAACACGACT 229
QY 90 GCTCCTCCCCGAGTTCATTTGTAATTCAGGAGAAATTCAGCTGAACACGACT 149
DB 230 GCTCCTCCCCGAGTTCATTTGTAATTCAGGAGAAATTCAGCTGAACACGACT 289
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCT 209
DB 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCT 349
QY 210 GTCATACGCTCTGCGGGGATCATGTGTAATTCAGGAGAAATTCAGCTGAACACGACT 269
DB 350 GTCATACGCTCTGCGGGGATCATGTGTAATTCAGGAGAAATTCAGCTGAACACGACT 409
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCAAGGCGCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCAAGGCGCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
DB 470 CTGCTCGGCGCTCA 484

RESULT 5
AK094501 1832 bp mRNA linear PRI 15-JUL-2002
LOCUS AK094501
DEFINITION Homo sapiens cDNA FLJ37182 fls, clone BRAZ2001350, weakly similar
to Homo sapiens Gz-selective GTPase-activating protein (RGS20)
mRNA.
ACCESSION AK094501
VERSION AK094501.1 GI:21753575
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone lib: BRAZ22
clone: BRAZ2001350.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hiro, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuna, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Suzuki, Y., Sugano, S., Negahari, K., Masuno, Y., Nagai, K.,
and Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1832)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan: cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="BRAZ2001350"
/tissue="alzheimer cortex"
/clone_lib="BRAZ22"
/note="Cloning vector: PME18SFJ3"
215..640

CDS

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/!note="unnamed protein product"
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BASE COUNT      411 a      501 c      513 g      407 t
ORIGIN

Query Match      85.4%; Score 315; DB 9; Length 1832;
Best Local Similarity 100.0%; Pred. No. 1.9e-178;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACT 89
D 264 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACT 323
QY 90 GCTCTCTCCCGGAGTTGTAATGTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 149
D 324 GCTCTCTCCCGGAGTTGTAATGTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 383
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
D 384 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 443
QY 210 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACTCAGTTT 269
D 444 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACTCAGTTT 503
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTT 329
D 504 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTT 563
QY 330 CTGCTCGGGCCCTCA 344
D 564 CTGCTCGGGCCCTCA 578

RESULT 6
AX136281      1890 bp      DNA      linear      PAT 30-MAY-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
FEATURES
source
CDS
CDS
BASE COUNT      419 a      528 c      533 g      410 t
ORIGIN

Query Match      85.4%; Score 315; DB 6; Length 1890;

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Best Local Similarity 100.0%; Pred. No. 1.9e-178;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACT 89
D 323 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACT 382
QY 90 GCTCTCTCCCGGAGTTGTAATGTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 149
D 383 GCTCTCTCCCGGAGTTGTAATGTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 442
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
D 443 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 502
QY 210 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACTCAGTTT 269
D 503 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACTCAGTTT 562
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTT 329
D 563 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTT 622
QY 330 CTGCTCGGGCCCTCA 344
D 623 CTGCTCGGGCCCTCA 637

RESULT 7
AX13944/c      2528 bp      DNA      linear      PAT 14-DEC-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
FEATURES
source
CDS
CDS
BASE COUNT      516 a      766 c      677 g      567 t      2 others
ORIGIN

Query Match      85.1%; Score 314; DB 6; Length 2528;
Best Local Similarity 100.0%; Pred. No. 7.8e-178;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACTG 90
D 2217 AGGCTTTGGCGTCAAAATCCAGTCTACAGTGGAAAGTAATCCAGTGAACAACGACTG 2158

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QY 91 CTCCTCCCCGAGTCATTTGTAATTTGCAGGGAACGTTCAAGACATGTCAGAAGA 150
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 Db 2157 CTCCTCCCCGAGTCATTTGTAATTTGCAGGGAACGTTCAAGACATGTCAGAAGA 2098
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 QY 151 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCTG 210
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 Db 2097 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCTG 2038
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 QY 211 TCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGACTCAGTTTG 270
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 Db 2037 TCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGACTCAGTTTG 1978
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 QY 271 CATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAGGCCCCAAGAAAGGGAAGTTTC 330
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 Db 1977 CATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAGGCCCCAAGAAAGGGAAGTTTC 1918
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 QY 331 TGCTTCGGGCTCA 344
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 Db 1917 TGCTTCGGGCTCA 1904
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RESULT 8
 AX093191 396 bp DNA linear PAT 30-MAR-2001
 LOCUS AX093191
 DEFINITION Sequence 9 from Patent WO0118046.
 ACCESSION AX093191
 VERSION AX093191.1 GI:13509640
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 396)
 Xu, J. and Stolk, J. A.
 TITLE Ovarian tumor sequences and methods of use therefor
 JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;
 CORIXA CORPORATION (US)

FEATURES
 source Location/Qualifiers
 1..396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 misc_feature 1..396
 /note="n = A,T,C or G"

BASE COUNT 90 a 117 c 95 g 92 t 2 others
 ORIGIN

Query Match 76.2%; Score 281; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 6.7e-158;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCGAATTCAGTGCATGCAAGTGAAGATTCACAGTGAACAAGCACT 89
 |||||||
 Db 40 CAGGCTTTGGCGTCGAATTCAGTGCATGCAAGTGAAGATTCACAGTGAACAAGCACT 99
 |||||||
 QY 90 GCCTCTCCCGGAGTTCATGTGAATTCAGCGTGAAGCAAGTTCAGACATGTGTAGAAG 149
 |||||||
 Db 100 GCCTCTCCCGGAGTTCATGTGAATTCAGCGTGAAGCAAGTTCAGACATGTGTAGAAG 159
 |||||||
 QY 150 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 209
 |||||||
 Db 160 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 219
 |||||||
 QY 210 GTCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 269
 |||||||
 Db 220 GTCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 279
 |||||||
 QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAAAG 310
 |||||||
 Db 280 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAAAG 320
 |||||||

RESULT 9

AX136556
 LOCUS AX136556 591 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 478 from Patent EP1067182.
 ACCESSION AX136556
 VERSION AX136556.1 GI:14272960
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 591)
 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
 Hayashi, K.

TITLE Secretory protein or membrane protein
 JOURNAL Patent: EP 1067182-A 478 10-JAN-2001;
 Helix Research Institute (JP)

FEATURES
 source Location/Qualifiers
 1..591
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 108 a 198 c 173 g 109 t 3 others
 ORIGIN

Query Match 59.9%; Score 221; DB 6; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.2e-121;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTCGAATTCAGTGCATGCAAGTGAAGATTCACAGTGAACAAGCACT 89
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 Db 323 CAGGCTTTGGCGTCGAATTCAGTGCATGCAAGTGAAGATTCACAGTGAACAAGCACT 382
 |||||||
 QY 90 GCTCTCCCGGAGTTCATGTGAATTCAGCGTGAAGCAAGTTCAGACATGTGTAGAAG 149
 |||||||
 Db 383 GCTCTCCCGGAGTTCATGTGAATTCAGCGTGAAGCAAGTTCAGACATGTGTAGAAG 442
 |||||||
 QY 150 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 209
 |||||||
 Db 443 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 502
 |||||||
 QY 210 GTCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 269
 |||||||
 Db 503 GTCTCATGCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 279
 |||||||

RESULT 10
 AC079773/c 129676 bp DNA linear PRI 09-JAN-2002
 LOCUS AC079773

DEFINITION Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.
 AC079773

AC079773.8 GI:15145561
 VERSION
 KEYWORDS
 SOURCE HTG.

ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 129676)
 Sulston, J. E. and Waterston, R.

TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792
 PUBMED 9847074

REFERENCE 2 (bases 1 to 129676)
 Shah, N., Meyer, R., Boyer, E. and Dignan, G.

TITLE The sequence of Homo sapiens BAC clone RP11-258B17
 JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 129676)
 Waterston, R. H.

TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108 USA

REFERENCE 4 (bases 1 to 129676)
 Waterston, R. H.

TITLE
JOURNAL
Direct Submission
Submitted (09-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA (bases 1 to 129676)
5 (bases 1 to 129676)
Waterston, R.
AUTHORS
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 9, 2001 this sequence version replaced g1:14488388.
JOURNAL
Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.edu
Summary Statistics
Center project name: H_NH0258B17

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPc1-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(<http://bacpac.med.buffalo.edu>)
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1L22; the clone sequenced
to the right is RP11-159N20, 2000 bp overlap. Actual start of this
clone is at base position 1 of RP11-258B17; actual end is at base
position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES
source
Location/Qualifiers
1..129676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-258B17"
/clone_11b="RPc1-11"
488..779
/rpt_family="MER2_type"
941..1253
/note="match to EST BF804362 (NID:912133351)"
repeat_region
1388..1412
/rpt_family="AT_rich"
1397..3331
/rpt_family="L1"
2346..2370
/rpt_family="(TTTGG)n"
misc_feature
repeat_region
repeat_region
repeat_region

repeat_region 9444..9466
/rpt_family="AT_rich"
misc_feature 11961..11969
/note="match to EST A1054234 (NID:93322021) q177b02.x1"
repeat_region 12697..12739
/rpt_family="(TTC)n"
repeat_region 14016..14171
/rpt_family="MaLR"
repeat_region 14175..14337
/rpt_family="MaLR"
repeat_region 15532..15842
/rpt_family="Alu"
repeat_region 16269..16605
/rpt_family="MaLR"
repeat_region 16629..16712
/rpt_family="MIR"
repeat_region 16810..16939
/rpt_family="MIR"
repeat_region 17238..17381
/rpt_family="MaLR"
repeat_region 17508..17966
/rpt_family="ERV1"
repeat_region 18190..18453
/rpt_family="ERV1"
repeat_region 18434..18801
/rpt_family="ERV1"
repeat_region 18933..19074
/rpt_family="ERV1"
repeat_region 19144..19250
/rpt_family="ERV1"
repeat_region 19260..19628
/rpt_family="ERV1"
repeat_region 20104..20145
/rpt_family="(TG)n"
repeat_region 20170..20305
/rpt_family="MER1_type"
repeat_region 20618..20756
/rpt_family="MER1_type"
repeat_region 21300..21325
/rpt_family="(A)n"
repeat_region 21428..21796
/note="match to EST BF821779 (NID:91261303)"
repeat_region 23084..23228
/rpt_family="MIR"
repeat_region 23967..24256
/rpt_family="Alu"
repeat_region 25108..25208
/rpt_family="MIR"
repeat_region 25485..25805
/rpt_family="MaLR"
repeat_region 26417..26463
/rpt_family="ERV1"
repeat_region 26466..26655
/rpt_family="MER2_type"
repeat_region 26656..27047
/rpt_family="MaLR"
repeat_region 27048..27149
/rpt_family="MER2_type"
repeat_region 27246..27403
/rpt_family="(TA)n"
repeat_region 27309..27380
/rpt_family="L1"
repeat_region 27403..27671
/rpt_family="Alu"
repeat_region 27698..27749
/rpt_family="MER2_type"
repeat_region 27750..27904
/rpt_family="(TA)n"
repeat_region 27926..28052
/rpt_family="L2"
misc_feature 28052..28667
/note="match to EST BF736070 (NID:912062744)"
repeat_region 28834..28958

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repeat_region      /rpl_family="MIR"
                    29414..29696
                    /rpl_family="Alu"
repeat_region      /rpl_family="Alu"
                    29727..30221
                    /rpl_family="MaLR"
repeat_region      30363..30543
                    /rpl_family="MER1_type"
repeat_region      30738..30919
                    /rpl_family="MER1_type"
repeat_region      31494..31783
                    /rpl_family="Alu"
repeat_region      32028..32488
                    /rpl_family="ERV1"
repeat_region      32053..32080
                    /rpl_family="(GA)n"
repeat_region      32667..32787
                    /rpl_family="MIR"
repeat_region      34079..34164
                    /rpl_family="L2"
repeat_region      34271..34348
                    /rpl_family="MER1_type"
misc_feature        34409..34703
                    /note="match to EST BG956501 (MID:g14374672)"
repeat_region      35346..35374
                    /rpl_family="(TTTG)n"
repeat_region      35361..35676
                    /rpl_family="Alu"

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Query Match      47.4%; Score 175; DB 9; Length 129676;
Best Local Similarity 100.0%; Pred. No. 8.2e-94;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGTCCGGG 229
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Db 120741 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGTCCGGG 120682
|||||
QY 230 TACCACTCTTCTGCTCCCGAGGAAGTCACTAGTTCATCAGCTCTGCACACC 289
|||||
Db 120661 TACCACTCTTCTGCTCCCGAGGAAGTCACTAGTTCATCAGCTCTGCACACC 120622
|||||
QY 290 CCTCTTTGTAACGGGCAAGGCCAAGAAAGGGGAAGTCTGCTCGGCGCTCA 344
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Db 120621 CCTCTTTGTAACGGGCAAGGCCAAGAAAGGGGAAGTCTGCTCGGCGCTCA 120567
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```

RESULT 11
AC010974/c        147131 bp      DNA      linear      PRI 01-MAR-2002
LOCUS             AC010974
DEFINITION        Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION         AC010974
VERSION           AC010974.9  GI:19033964
KEYWORDS          HTG.
SOURCE            Homo sapiens.
ORGANISM          Homo sapiens.
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE         1 (bases 1 to 147131)
AUTHORS           Sulston,J.E. and Waterston,R.
TITLE             Toward a complete human genome sequence
JOURNAL           Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE           99063792
PUBMED            9847074
REFERENCE         2 (bases 1 to 147131)
AUTHORS           Vanbrunt,A. and Stromatt,C.
TITLE             The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL           Unpublished (2001)
REFERENCE         3 (bases 1 to 147131)
AUTHORS           Waterston,R.H.
TITLE             Direct Submission
JOURNAL           Submitted (28-SEP-1999) Genome Sequencing Center, Washington
                  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                  MO 63108, USA
REFERENCE         4 (bases 1 to 147131)

```

AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT

Waterston,R.H.
Direct Submission
Submitted (23-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 147131)
Waterston,R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 1, 2002 this sequence version replaced 91:33435273.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu

Summary Statistics
Center project name: H_NH0159N20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCR-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Teleno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the clone sequenced to the right is RP11-258B17. Actual start of this clone is at base position 1 of RP11-159N20; actual end is at base position 147131 of RP11-159N20.

There are polymorphic base differences in the overlap between the clone RP11-159N20 and RP11-258B17.

FEATURES

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source            location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-159N20"
/clone_lib="RPCR-11"
21..67
/rpl_family="MIR"
118..1013
/rpl_family="L1"
984..1176
/note="match to EST BG200048 (MID:g13721735)"
991..1176
/note="match to EST BG184021 (MID:g13705708)"
misc_feature
misc_feature
misc_feature

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misc_feature      991..1176
                   /note="match to EST BG187166 (NID:g13708853)"
repeat_region     1035..1200
                   /rpt_family="Alu"
repeat_region     1525..1552
                   /rpt_family="(TTTA)n"
repeat_region     1526..1814
                   /rpt_family="Alu"
repeat_region     2299..2596
                   /rpt_family="Alu"
repeat_region     4890..5129
                   /rpt_family="MALR"
repeat_region     5738..5757
                   /rpt_family="(TG)n"
repeat_region     6131..6178
                   /rpt_family="GA-rich"
misc_feature      7310..7364
                   /note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
repeat_region     7811..7881
                   /rpt_family="MIR"
repeat_region     8227..8260
                   /rpt_family="(CATTC)n"
repeat_region     8373..8683
                   /rpt_family="11"
misc_feature      8640..9120
                   /note="match to EST BF112212 (NID:g10941902)"
repeat_region     8776..8838
                   /rpt_family="MIR"
misc_feature      8810..9257
                   /note="match to EST AA434316 (NID:g2139230) zw24e08.r1"
repeat_region     9348..9395
                   /rpt_family="GA-rich"
misc_feature      9731..9895
                   /note="match to EST BF347279 (NID:g11294874)"
misc_feature      9743..9895
                   /note="match to EST BG184021 (NID:g13705708)"
misc_feature      9743..9895
                   /note="match to EST BG187166 (NID:g13708853)"
repeat_region     10053..10359
                   /rpt_family="Alu"
repeat_region     12424..12509
                   /rpt_family="MIR"
repeat_region     12505..12671
                   /rpt_family="MERL_type"
misc_feature      13456..13776
                   /note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
misc_feature      13834..13855
                   /note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
misc_feature      15183..15321
                   /note="match to EST BE386060 (NID:g9331425)"
misc_feature      15183..15321
                   /note="match to EST BG704350 (NID:g13977603)"
misc_feature      15183..15321
                   /note="match to EST BG753617 (NID:g14064270)"
misc_feature      15183..15321
                   /note="match to EST H06756 (NID:g870288) y183b07.r1"
misc_feature      15184..15321
                   /note="match to EST BF347279 (NID:g11294874)"
misc_feature      15184..15321
                   /note="match to EST BG184021 (NID:g13705708)"
misc_feature      15184..15320
                   /note="match to EST BG187166 (NID:g13708853)"
misc_feature      15184..15320
                   /note="match to EST BG200048 (NID:g13721735)"
repeat_region     15767..15789
                   /rpt_family="AT-rich"
misc_feature      15864..18081
                   /note="CPG_island (%GC=68.0, o/e=0.80, #CPGs=194)"
misc_feature      16665..17055
                   /note="match to EST BG704350 (NID:g13977603)"
misc_feature      16665..16984
                   /note="match to EST BF347279 (NID:g11294874)"
misc_feature      16665..16728

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misc_feature      /note="match to EST BG753617 (NID:g14064270)"
misc_feature      16665..16686
                   /note="match to EST H06756 (NID:g870288) y183b07.r1"
misc_feature      17965..18209
                   /note="match to EST BE386060 (NID:g9331425)"
repeat_region     18319..18352
                   /rpt_family="(TCCC)n"
misc_feature      18637..19184
                   /note="match to EST BF940247 (NID:g12357567)"
misc_feature      18931..19137
                   /note="similar to Homo sapiens EST R54936 (NID:g819192)
                   yj75b04.s1"
misc_feature      18938..19409
                   /note="similar to Homo sapiens EST AAT779875 (NID:g2839206)
                   af46b10.s1"
misc_feature      19225..19616
                   /note="match to EST R54748 (NID:g819270) yj75b04.r1"
repeat_region     19406..19426
                   /rpt_family="AT-rich"
misc_feature      19407..19710
                   /note="similar to Bos taurus EST BE750540 (NID:g10164532)"
misc_feature      19498..19795
                   /note="similar to Bos taurus EST BE682268 (NID:g1067956)"
misc_feature      19873..20090
                   /note="match to EST BG200485 (NID:g13722172)"
misc_feature      19926..20089
                   /note="similar to Homo sapiens EST BE963800
                   (NID:g11767217)"

Query Match      38.5%; Score 142; DB 9; Length 147131;
Best Local Similarity 100.0%; Pred. No. 7.2e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCGCGTGCAGACAGACT 89
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DB      15324 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCGCGTGCAGACAGACT 15265

QY      90 GCTCCGCCCGCGATGATGTAATTCGACGCTGAAGCTGACAGTGTGCAGAAAG 149
         |||||
DB      15264 GCTCCGCCCGCGATGATGTAATTCGACGCTGAAGCTGACAGTGTGCAGAAAG 15205

QY      150 AAGTATGAGCAAAAGTCCGG 171
         |||||
DB      15204 AAGTATGAGCAAAAGTCCGG 15183

RESULT 12
AC124493      209885 bp      DNA      linear      HTG 05-JUL-2002
LOCUS      AC124493/C
DEFINITION      Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
ACCESSION      AC124493
VERSION      AC124493.2 GI:21699722
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
ORGANISM      Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 209885)      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS      McPherson,J.D. and Waterston,R.H.
TITLE      The sequence of Mus musculus clone
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 209885)
AUTHORS      McPherson,J.D. and Waterston,R.H.
TITLE      Direct Submission
JOURNAL      Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
3 (bases 1 to 209885)      Parkway, St. Louis, MO 63108, USA
AUTHORS      McPherson,J.D. and Waterston,R.H.
TITLE      Direct Submission
JOURNAL      Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT      On Jul 5, 2002 this sequence version replaced gi:21426614.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project information
Center project name: M_BA0462Pl3
-----
----- Summary Statistics -----
Sequencing vector: M13, 0%
Sequencing vector: plasmid, 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208484 bases at least Q40
Consensus quality: 208911 bases at least Q30
Consensus quality: 209285 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 212112; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; agarose-fp
Quality coverage: 11.62 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 11331: contig of 11331 bp in length
* 11332: gap of unknown length
* 11432: contig of 17186 bp in length
* 28617: gap of unknown length
* 28718: contig of 20737 bp in length
* 49454: gap of unknown length
* 49555: gap of unknown length
* 107385: gap of unknown length
* 107484: gap of unknown length
* 209885: contig of 102401 bp in length.
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Location/Qualifiers
1. 209885
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-462Pl3"
1. 11331
/note="assembly_name:Contig8"
11432. 28617
/note="assembly_name:Contig9"
28718. 49454
/note="assembly_name:Contig10"
49555. 107384
/note="assembly_name:Contig11"
107485. 209885
/note="assembly_name:Contig12"
BASE COUNT 59789 a 44784 c 46164 g 58745 t 403 others
ORIGIN
Query Match 12.7%; Score 47; DB 2; Length 209885;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 122 GTGAACGTTCAACATGTGTGTCAGAAAGAGTGTGAGCAAACTGC 168
|||||
DB 103249 GTGAACGTTCAACATGTGTGTCAGAAAGAGTGTGAGCAAACTGC 103203
|||||
RESULT 13
LOCUS AB041649 1797 bp mRNA linear ROD 30-JUN-2000
DEFINITION Mus musculus brain cDNA, clone MNCB-0671.
ACCESSION AB041649

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```

VERSION AB041649.1 GI:7670499
KEYWORDS f1s (full insert sequence).
SOURCE Mus musculus (strain:C57BL/6) adult female cDNA to mRNA,
clone_11b:Sugano mouse brain mncb clone:MNCB-0671.
ORGANISM Mus musculus
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (sites)
Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and
Hashimoto,K.
Isolation of full-length cDNA clones from mouse brain cDNA library
made by oligo-capping method
Unpublished
2 (bases 1 to 1797)
Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (13-APR-2000) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail:khashim@nih.go.jp, URL:http://www.nih.go.jp/yoken/genbank/,
Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
URL: http://www.nih.go.jp/yoken/genbank/
Lib Name: Sugano mouse brain mncb
Lib host: TOP10
Vector: pME18S-FL3
1st strand cDNA was primed with an oligo(dN) primer
[ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Library
was constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing ( 5' end primer
[CTTCTGCTTAAAGCTGCG]; 3' end primer
[CGACCTGAGCTCGACCA]).
A part of this sequence is reported in AU035640.
Location/Qualifiers
1. 1797
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MNCB-0671"
/sex="female"
/clone_11b="Sugano mouse brain mncb"
/dev_stage="adult"
325..750
/note="unnamed protein product"
/codon_start=1
/protein_id="BA95101.1"
/db_xref="GI:7670500"
/translation="MWVLGIAATFCGLFPLPGLALQIQCYOCSEFOLNNDSSPEFIV
NCTVNDMDCKEYTESGIMYRKSSASACLIASAGYOSFSPKRLNSVCISCN
TFLCNGRPKRKRGSSASAIRPGLTTLTFLPILALCLANC"
BASE COUNT 391 a 487 c 511 g 408 t
ORIGIN
Query Match 10.3%; Score 38; DB 10; Length 1797;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 50 CAGTCTACCACTGTGAGACATTCACGCTGACACACGA 87
|||||
DB 394 CAGTCTACCACTGTGAGACATTCACGCTGACACACGA 431
|||||
RESULT 14
LOCUS AL512284 113920 bp DNA linear PRI 31-JAN-2002
DEFINITION Human DNA sequence from clone RP11-248M22 on chromosome 10,
complete sequence.
ACCESSION AL512284
VERSION AL512284.20 GI:18477310

```

KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 113920)
AUTHORS Sehra, H.
TITLE Direct Submission
JOURNAL Submitted (31-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humgen@sanger.ac.uk
COMMENT On Feb 1, 2002 this sequence version replaced g1:18476636. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>
RP11-248M22 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-248M22. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-248M22 is at 1 in this sequence. The true left end of clone RP11-495F22 is at 111921 in this sequence. The true right end of clone RP11-481F7 is at 53678 in this sequence.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
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/clone_1fb="RPCT-11.1"
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/note="Sequence from overlapping clone RP11-481F7 (AL603717). Assembly confirmed by restriction digest."
BASE COUNT 28142 a 25061 c 27839 g 32878 t
ORIGIN

Query Match 5 0%; Score 22; DB 9; Length 113920;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 233 CAGTCTCTCTGCTCCAGGGA 254
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DB 38431 CAGTCTCTCTGCTCCAGGGA 38410
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RESULT 15
AC118794 161084 bp DNA linear HTG 18-JUL-2002
LOCUS
DEFINITION Rattus norvegicus clone CH230-179C24, *** SEQUENCING IN PROGRESS
ACCESSION AC118794

VERSION

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AC118794.5 GI:21746956
HTG; HTGS; PHASE1.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 161084)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alpbrouks, S.L., Amaralunga, H.C., Are, J.R., Ayala, M., Banks, T., Barbarella, J., Benton, J., Blinag, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Britova, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Datborne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthett, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Giller, R., Gorrell, J.H., Guevara, M., Gunarene, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hughes, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, V., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Lonsayed, H., Lozano, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Martin, R., Matindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabhat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwenkwo, S., Ogih, M., Okunou, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Plims, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Rollet, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Slisson, I., Sodergren, E., Sonalake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.
Unpublished
Direct Submission
Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 161084)
Worley, K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced g1:20387310.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVHE
Center clone name: CH230-179C24
----- Summary Statistics
Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 103889 bases at least Q40
 Consensus quality: 110038 bases at least Q30
 Consensus quality: 114035 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 69 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1021: contig of 1021 bp in length
 1022 1121: gap of unknown length
 1122 2137: contig of 1016 bp in length
 2138 2237: gap of unknown length
 2238 3416: contig of 1179 bp in length
 3417 3516: gap of unknown length
 3517 5162: contig of 1646 bp in length
 5163 5262: gap of unknown length
 5263 6867: contig of 1605 bp in length
 6868 6967: gap of unknown length
 6968 8084: gap of unknown length
 8085 8184: gap of unknown length
 8185 9615: contig of 1431 bp in length
 9616 9715: gap of unknown length
 9716 10989: contig of 1274 bp in length
 10990 11089: gap of unknown length
 11090 12368: contig of 1279 bp in length
 12369 12468: gap of unknown length
 12469 13619: contig of 1151 bp in length
 13620 13719: gap of unknown length
 13720 15310: contig of 1591 bp in length
 15311 15410: gap of unknown length
 15411 16945: contig of 1535 bp in length
 16946 17045: gap of unknown length
 17046 18097: contig of 1052 bp in length
 18098 18197: gap of unknown length
 18198 19225: contig of 1028 bp in length
 19226 19325: gap of unknown length
 19326 20651: contig of 1326 bp in length
 20652 20751: gap of unknown length
 20752 22409: contig of 1658 bp in length
 22410 22509: gap of unknown length
 22510 24206: contig of 1697 bp in length
 24207 24306: gap of unknown length
 24307 26107: contig of 1801 bp in length
 26108 26207: gap of unknown length
 26208 27712: contig of 1505 bp in length
 27713 27812: gap of unknown length
 27813 29889: contig of 2077 bp in length
 29890 29989: gap of unknown length
 29990 31375: contig of 1386 bp in length
 31376 31475: gap of unknown length
 31476 33181: contig of 1706 bp in length
 33182 33281: gap of unknown length
 33282 35480: contig of 2199 bp in length
 35481 35580: gap of unknown length
 35581 37361: contig of 1781 bp in length
 37362 37461: gap of unknown length
 37462 38681: contig of 1220 bp in length
 38682 38781: gap of unknown length
 38782 40433: contig of 1652 bp in length
 40434 40533: gap of unknown length
 40534 42882: contig of 2349 bp in length
 42883 42982: gap of unknown length
 42983 44757: contig of 1775 bp in length
 44758 44857: gap of unknown length
 44858 45952: contig of 1095 bp in length

45953 46052: gap of unknown length
 46053 47292: contig of 1240 bp in length
 47293 47392: gap of unknown length
 47393 48841: contig of 1549 bp in length
 48842 49041: gap of unknown length
 49042 51345: contig of 2304 bp in length
 51346 51445: gap of unknown length
 51446 53727: contig of 2282 bp in length
 53728 53827: gap of unknown length
 53828 55744: contig of 1917 bp in length
 55745 55844: gap of unknown length
 55845 57208: contig of 1364 bp in length
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 57309 60348: contig of 3040 bp in length
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 62849 62948: gap of unknown length
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 64638 66822: contig of 2185 bp in length
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 66923 68818: contig of 1896 bp in length
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 71561 73738: contig of 2178 bp in length
 73739 73838: gap of unknown length
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 78357 79698: contig of 1342 bp in length
 79699 82434: gap of unknown length
 82435 82534: gap of unknown length
 82535 84744: contig of 2210 bp in length
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 84845 86510: contig of 1666 bp in length
 86511 89257: contig of 2647 bp in length
 89258 89357: gap of unknown length
 89358 90516: contig of 1159 bp in length
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 97201 97300: gap of unknown length
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Query Match 6.0%; Score 22; DB 2; Length 161084;
 Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 308 AGGCCCAAGAAAGGGAAGTT 329
 Db 156950 AGGCCCAAGAAAGGGAAGTT 156971

RESULT 16
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 LOCUS Homo sapiens chromosome 15 clone RP11-232J12 map 15q21.3, complete
 DEFINITION
 sequence.
 ACCESSION AC024061
 VERSION AC024061.7 GI:14647263
 KEYWORDS
 SOURCE HTG.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 157042)

AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 157042)
AUTHORS	Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T., and Hood, L.
TITLE	Direct Submission
JOURNAL	Submitted (22-Feb-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA
REFERENCE	3 (bases 1 to 157042)
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
TITLE	Direct Submission
JOURNAL	Submitted (10-Jul-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
COMMENT	On Jul 10, 2001 this sequence version replaced gi:13162487. ----- Genome Center Center: Multimegabase Sequencing Center Center code: UWMSC Web site: http://chroma.mbl.washington.edu/msg.www Contact: leerowen@systemsbiology.org ----- Summary Statistics Sequencing vector: pUC18; 108752 Chemistry: Dye-terminator Big Dye; 90% of reads Chemistry: Dye-Primer Big Dye; 10% of reads Assembly program: Phrap; version 0.990399 Note: data AC066614 [Drafting center UWMSC] and AC066611 [Drafting center UWMSC] were added for finishing. Location/Qualifiers 1. 157042 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="15" /map="15q21.3" /clone="RP11-323J12" /clone_11b="RPC1 Human BAC library 11" /note="this clone overlaps RP11-8068 AC066614 and RP11-348P16 AC066611. Data from overlapping BACs were combined and the consensus sequence determined from RP11-323J12 to the extent possible." 1. 26818 /note="Overlap with RP11-8068 AC066614" 8723 /note="low quality data." 31605. 31610 /note="low quality data." 34826 /note="low quality data." 42795. 42800 /note="low quality data." 63513. 63514 /note="low quality data." 124490. 124492 /note="low quality data." 143570. 157042 /note="Overlap with RP11-348P16 AC066611."
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Best Local Similarity	100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
07 250 AGGGAACCTGAACACTGAGTTT 269	
Db 75943 AGGGAACCTGAACACTGAGTTT 75962	

LOCUS	AC068808	171146 bp	DNA	Linear	ROD 01-MAR-2001
DEFINITION	Mus musculus 11 BAC RP23-479J7 (Roswell Park Cancer Institute Mouse BAC Library) complete sequence.				
ACCESSION	AC068808				
VERSION	AC068808.20	GI:11496332			
KEYWORDS	HTG.				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 171146)				
AUTHORS	Meeker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okumaru,G., Carlack,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Bunlay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S., Kovar,C., Li,J., Liu,W., Louiseged,H., Lozado,R.J., Martin,R., Massey,E., McLeod,M.P., Mel,G., Moore,S., Morgan,M., Morris,S., Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Ogul,M., Parish,B., Perez,L., Relter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williams,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Murthy,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R.				
TITLE	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 171146)				
AUTHORS	Worley,K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
REFERENCE	3 (bases 1 to 171146)				
AUTHORS	Worley,K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-DEC-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
REFERENCE	5 (bases 1 to 171146)				
AUTHORS	Worley,K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
COMMENT	On Dec 1, 2000 this sequence version replaced gi:11321701. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.				
FEATURES	The repeat regions shown were identified using RepeatMasker by Adrian Smlt.				
SOURCE	Sequence similarities were identified using Powerblast by Jinghui Zhang.				
	Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.				
	Location/Qualifiers				
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2909.3037
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4746.4989
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complement(5674.5684)
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Best Local Similarity 100.0%; Pred.No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 220 CTCGCGGGTACCACTCT 239
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Db 156695 CTCGCGGGTACCACTCT 156714

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RESULT 18
AC099049/c AC099049 180339 bp DNA linear PRI 12-JAN-2002
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-291P10, complete sequence.
ACCESSION AC099049 AC021722
VERSION AC099049.2 GI:18139443

```

KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 180339)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Karen, P.K.A., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 180339)
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 180339)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Karen, P.K.A., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jan 12, 2002 this sequence version replaced gi:16799007.
COMMENT ----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web Site: http://www.genome.washington.edu
Contact: uwgchls@u.washington.edu
Drafting Center: BCM
----- Project Information
Center Project name: chr-3
Center Clone name: RP11-291P10 (bc0345)
----- Summary Statistics
Sequencing vector: unknown; 60% of reads
Sequencing vector: plasmid; 40% of reads
Chemistry: Dye-terminator Big Dye; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180276 bases at least 40
Consensus quality: 180338 bases at least Q40
Consensus quality: 180339 bases at least Q20
Insert size: 180339; sum-of-contigs
Quality coverage: 10.6x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:
57: RP11-442C9 (UWGC:bc0425) AC025029
37: RP11-59E22 (UWGC:bc0181) AC022071

----- Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

----- This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear

in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII		EcoRI		HindIII	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2267	2314	8696	8865	1626	1573
2067	2064	6	<800	6382	6296
4428	4708	7365	7655	512	<800
1965	2064	3768	3808	449	<800
4344	4422	5698	5660	4042	4009
4291	4422	1158	1226	6044	6055
9652	9511	2511	2474	123	<800
5596	5698	1375	1449	618	<800
3081	3247	4214	4275	311	<800
2672	2606	1526	1566	1409	1347
1784	1803	1618	1566	43	<800
4280	4422	135	<800	1543	1573
560	<800	1775	1770	128	<800
3554	3719	5084	5074	6374	6296
2492	2606	3600	3566	2035	2052
1858	1803	3578	3566	2420	2410
3394	3499	365	<800	6424	6515
963	963	146	<800	6075	6296
3591	3719	16	<800	1654	1573
268	<800	782	<800	109	<800
2836	2932	4634	4628	3408	3459
2447	2606	1065	1078	4620	4606
1993	2064	1272	1357	3060	3257
2593	2606	7693	7655	4720	4776
818	815	4017	3990	1752	1730
1430	1373	609	<800	2026	2052
5478	5488	7658	7655	1547	1573
7564	7629	1425	1449	10077	9960
87	<800	11265	11368	12507	12577
799	<800	1832	1770	1338	1347
1992	2064	537	<800	4829	4776
2224	2314	1456	1449	417	<800

847	843	3134	3114	1542	1573
1307	1230	1015	1078	1343	1347
845	843	3274	3263	5165	5042
169	<800	14151	14076	3344	3257
4268	4422	72	<800	4165	4154
3568	3719	1156	1078	6272	6296
4957	5278	644	<800	1190	1160
803	800	1636	1566	7782	7809
3139	3247	789	<800	5084	5042
4708	4986	10043	9956	1981	2052
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8081	8247	2482	2319	2657	2673
4403	4708	2306	2319	2098	2052
2714	2932	5512	5457	3026	3053
2758	2932	8025	8039	2041	2052
5229	5278	1941	1916	856	878
2406	2314	11676	11368	5163	5042
975	963	179	<800	4657	4606
2859	2932	615	<800	1234	1231
794	<800	2419	2474	762	<800
71	<800	9795	9956	27	<800
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6545	6536	-----	-----	958	981

Query Match 5.4%: Score 20: DB 9: Length 180339;
 Best Local Similarity 100.0%: Pred. No. 3.9;
 Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 308 AGGCCCAAGAAAGGGAAG 327
 |||||
 Db 178159 AGGCCCAAGAAAGGGAAG 178140

RESULT 19
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 LOCUS Homo sapiens chromosome 3 clone RP11-442C9, WORKING DRAFT SEQUENCE,
 DEFINITION 25 unordered pieces.
 ACCESSION AC025029 GI:22203847
 VERSION AC025029.14 HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 190914)

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
 Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T.,
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 Davila, M.L., Davis, C., Day-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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 Weinstein, G., and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 11, 2002 this sequence version replaced gi:19438348.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
 Drafting Center Code: BCM

Contact: hgsc-help@bcm.tmc.edu
 Project Information

Center project name: HAVK
 Center clone name: RP11-442C9

Summary Statistics
 Sequencing vector: M13;

Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329

Consensus quality: 168264 bases at least Q40
 Consensus quality: 176241 bases at least Q20

Consensus quality: 181136 bases at least Q20
 Estimated insert size: 191206; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
 (see http://www.bosc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 25 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 2204: contig of 2204 bp in length
 2205 2304: gap of unknown length
 2305 4408: contig of 2104 bp in length
 4409 4508: gap of unknown length
 4509 7590: contig of 3082 bp in length
 7591 7690: gap of unknown length
 7691 10151: contig of 2461 bp in length
 10152 10251: gap of unknown length
 10252 13389: contig of 3138 bp in length
 13390 13489: gap of unknown length
 13490 16745: contig of 3256 bp in length
 16746 16845: gap of unknown length
 16846 20094: contig of 3245 bp in length
 20095 20194: gap of unknown length
 20195 22395: contig of 2101 bp in length
 22396 22977: contig of 4682 bp in length
 22978 27177: gap of unknown length
 27178 30971: contig of 3794 bp in length
 30972 31071: gap of unknown length
 31072 35083: contig of 4012 bp in length
 35084 35183: gap of unknown length
 35184 39480: contig of 4297 bp in length
 39481 39580: gap of unknown length
 39581 44949: contig of 5369 bp in length
 44950 45049: gap of unknown length
 45050 54872: contig of 9823 bp in length
 54873 54972: gap of unknown length
 54973 60941: contig of 5969 bp in length
 60942 61041: gap of unknown length
 61042 68203: contig of 7162 bp in length
 68204 68304: gap of unknown length
 68305 77920: contig of 9617 bp in length
 77921 78020: gap of unknown length
 78021 85714: contig of 7694 bp in length
 85715 85814: gap of unknown length
 85815 95784: contig of 9970 bp in length
 95785 95884: gap of unknown length
 95885 106591: contig of 10707 bp in length
 106592 106691: gap of unknown length
 106692 120378: contig of 13687 bp in length
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 120479 135023: contig of 14545 bp in length
 135024 135123: gap of unknown length
 135124 151718: contig of 16595 bp in length
 151719 151818: gap of unknown length
 151819 170792: contig of 18974 bp in length
 170793 170892: gap of unknown length
 170893 190914: contig of 20022 bp in length.

FEATURES

Location/Qualifiers

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 /db_xref="taxon:9606"
 /chromosome="3"

BASE COUNT 60335 a 33063 c 33135 g 61952 t 2429 others
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 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 AGCCCAAGAAAGGAG 327
 Db 75305 AGCCCAAGAAAGGAG 75324

RESULT 20
 AL596204 205606 bp DNA linear ROD 05-APR-2002
 LOCUS
 DEFINITION Mouse DNA sequence from clone RP23-180B18 on chromosome 11,
 complete sequence.

ACCESSION AL596204.8 GI:20068505
 VERSION
 KEYWORDS HTG.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Griffiths, C.
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Apr 7, 2002 this sequence version replaced gi:15591682.

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
<http://www.sanger.ac.uk/projects/C.elegans/wormpep>

from the RPI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6.

FEATURES

source

Location/Qualifiers
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 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="11"
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BASE COUNT 56071 a 47639 c 47696 g 54200 t
 ORIGIN

Query Match 5.4%; Score 20; DB 10; Length 205606;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 CTCTGCCGGGTACCACTCT 239
 Db 15409 CTCTGCCGGGTACCACTCT 15428

RESULT 21
 AX392969/c 2080 bp DNA linear PAT 23-MAR-2002
 LOCUS
 DEFINITION Sequence 11 from Patent WO0214358.
 ACCESSION AX392969
 VERSION AX392969.1 GI:19701016
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and
Wang, H.
Novel secreted proteins and their uses
Patent: WO 0214358-A 11 21-FEB-2002;
ELI LILLY AND COMPANY (US)

TITLE
JOURNAL
ELI LILLY AND COMPANY (US)

FEATURES
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1. 2080
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ORIGIN

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96. .1682
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335
DB 1811 AAAGGGGAAGTTCTGCCT 1793

RESULT 22
AX392971/c 2222 bp DNA linear PAT 23-MAR-2002
LOCUS
DEFINITION Sequence 13 from Patent WO0214358.
ACCESSION AX392971
VERSION AX392971.1 GI:19701018
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and
Wang, H.
Novel secreted proteins and their uses
Patent: WO 0214358-A 13 21-FEB-2002;
ELI LILLY AND COMPANY (US)

TITLE
JOURNAL
ELI LILLY AND COMPANY (US)

FEATURES
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1. 2222
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BASE COUNT 319 a 862 c 767 g 352 t

ORIGIN

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127. .192

Query Match 5.1%; Score 19; DB 6; Length 2300;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2031 AAAGGGGAAGTTCTGCCT 2013

RESULT 24
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LOCUS

LSHNPSTVPGSFRDYLRLLEHLHAGLAVEPQAFILGRQIRLNLSTLESTHSVNTLETLRYDGNPLACDCLMLIVORKTLPACATPAEVGDAIRNLPSVLEFEYFCRKPRIERRLOVATAGEDVRFICRAEGRAPATVAVMPQHRPVATTSAGRAVALPGLDITLIYSTAMGCTIFLGVLFCFVLLFVMSRGQRQHNKNSVEYSFRVDSPPAALAGGAKRKRMKMI"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335
DB 1953 AAAGGGGAAGTTCTGCCT 1935

RESULT 23
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LOCUS
DEFINITION Sequence 9 from Patent WO0248361.
ACCESSION AX463719
VERSION AX463719.1 GI:21886478
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Micanovic, R., Mills, B.J., Su, E.W., Varga, G., Wang, H.,
Basinski, M.B., Sankhavarani, P.R. and Tschang, S.H.
Novel secreted proteins and their use
Patent: WO 0248361-A 9 20-JUN-2002;
LILLY CO ELI (US)

TITLE
JOURNAL
LILLY CO ELI (US)

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1. 2300
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/db_xref="taxon:9606"
127. .1905
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DIVVSRAPAGLALBELTLERCLNLTALSGESIGHRSISALRLRLHLAIALEQDNF
RRLPGLHLLEIDNMPLEEVAGSLRGNTLSISVTNRNITRPAALRHQAHLTCLN
LSHPISIVPGSFRDYLRLLEHLHAGLAVEPQAFILGRQIRLNLSTLESTHSVNT
LETLRYDGNPLACDCLMLIVORKTLPACATPAEVGDAIRNLPSVLEFEYFCRKP
RIERRLOVATAGEDVRFICRAEGRAPATVAVMPQHRPVATTSAGRAVALPGLD
ITLIYSTAMGCTIFLGVLFCFVLLFVMSRGQRQHNKNSVEYSFRVDSPPAALAG
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BASE COUNT 319 a 862 c 767 g 352 t

ORIGIN

sig_peptide
127. .192

Query Match 5.1%; Score 19; DB 6; Length 2300;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335
DB 2031 AAAGGGGAAGTTCTGCCT 2013

RESULT 24
AF213399/c 2349 bp mRNA linear PLN 10-DEC-2000
LOCUS

DEFINITION Nicotiana tabacum SLT1 protein mRNA, complete cds.
 ACCESSION AF213399
 VERSION AF213399.1 GI:11611666
 KEYWORDS
 SOURCE
 ORGANISM Nicotiana tabacum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 2349)
 REFERENCE
 AUTHORS Matsuno, T.K., Pardo, J.M., Takeda, S., Bressan, R.A. and Hasegawa, P.M.
 TITLE Tobacco and Arabidopsis SLT1 suppresses salt sensitivity of calcineurin-deficient yeast mutants through the regulation of ion homeostasis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2349)
 AUTHORS Matsuno, T.K., Pardo, J.M., Takeda, S., Bressan, R.A. and Hasegawa, P.M.
 TITLE Direct Submission
 JOURNAL Submitted (07-DEC-1999) Horticulture and Landscape Architecture, Purdue University, 1165 Horticulture Building, West Lafayette, IN 47907-1165, USA
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 GLEVPSPNLMVLDSEERKRMKELTRGVNFTIPPSADSSWRNLPTPELEMPAP
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 TSQIPDLIEHNPYWLNEFGVMVDYGCPTAAKSTYEDDEGYLITISLPVDLOR
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BASE COUNT 656 a 407 c 532 g 754 t
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 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGCCCCAGAAAG 322
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 Db 168 GCCAAGCCCCAGAAAG 150

RESULT 25
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 DEFINITION American cockroach clone PL25 mRNA for lectin-related protein, complete cds.
 ACCESSION D49515
 KEYWORDS lectin-related protein.
 SOURCE Periplaneta americana fat body cDNA to mRNA, clone:PL25.
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattoidea; Periplaneta.
 1 (sites)
 REFERENCE
 AUTHORS Kawasaki, K., Kubo, T. and Natori, S.

TITLE Presence of the Periplaneta lectin-related protein family in the American cockroach Periplaneta americana
 JOURNAL Insect Biochem. Mol. Biol. 26 (4), 355-364 (1996)
 MEDLINE 96245436
 REFERENCE
 AUTHORS Kawasaki, K., Kubo, T. and Natori, S.
 TITLE Presence of a lectin family in Periplaneta americana, revealed by analysis of cDNA clones of lectins related to Periplaneta lectin
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 2901)
 AUTHORS Kawasaki, K.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1995) Kiyoshi Kawasaki, University of Tokyo, Faculty of Pharmaceutical Sciences, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111 (ex.4820), Fax:03-5684-2973)
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 DTPLENGEFLKWPQPNPDGDKDKDCGFRFRNFTLGDIPCSAKIAFIQEG"

BASE COUNT 1004 a 512 c 561 g 823 t 1 others
 ORIGIN
 Query Match 5.1%; Score 19; DB 3; Length 2901;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 TTCACGCTGAACAGACT 89
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 Db 2420 TTCACGCTGAACAGACT 2402

RESULT 26
 LOCUS AB017043 3914 bp DNA linear ROD 27-AUG-1998
 DEFINITION Rattus norvegicus gene for hepatocyte nuclear factor 3 gamma, partial cds.
 ACCESSION AB017043
 VERSION AB017043.1 GI:3461893
 KEYWORDS HNF-3G; hepatocyte nuclear factor 3 gamma.
 SOURCE Rattus norvegicus (strain:Wistar) DNA.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (sites)
 REFERENCE
 AUTHORS Saito, K., Nakamura, T., Komoda, H., Hori, N., Adachi, K., Ito, K. and Sato, K.
 TITLE Isolation and characterization of the rat hepatocyte nuclear factor-3gamma (HNF-3G) gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3914)
 AUTHORS Saito, K., Nakamura, T., Komoda, H., Hori, N., Adachi, K., Ito, K. and Sato, K.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1998) Kenzo Sato, Tottori University Faculty of Medicine, Department of Molecular Biology, 86 Nishimachi, Yonago, Tottori 685-8503, Japan (E-mail:kensato@grape.med.tottori-u.ac.jp, Tel:+81-859-34-8039, Fax:+81-859-34-8274)
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 /strain="Wistar"


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repeat_region complement(4912. .5079)
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frame: 1, quality: excellent, score: 93.000"
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/rpt_family="AluSc"
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AA317001 EST188650 HCC cell line (metastasis to liver in
mouse) II Homo sapiens cDNA 5' end similar to similar to
ornithine decarboxylase antizyme (1. .200); 100%
identity. -AA308557 EST179376 HCC cell line (metastasis to
liver in mouse) II Homo sapiens cDNA 5' end similar to
similar to ornithine decarboxylase antizyme (1. .200); 100%
identity. - (14748. .14942) AA307682 EST178550 Colon
carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar
to similar to ornithine decarboxylase antizyme (1. .195);
100% identity. - (14758. .14942) L49059/HUM010907F Homo
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gene

CDS

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/Note="translation of first 68 residues of ODC antizyme:
Ornithine decarboxylase antizyme is likely expressed
through translational frameshifting which results in the
products of ORF1 and ORF2 being synthesized as a single
polypeptide. In rat (D10706) the mRNA sequence at the
junction of the two ORFs, UCC UGA U (253. .259, shown as
ORF1 codons), is decoded as Ser-Asp through +1
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identity. -AA308557 EST179376 HCC cell line (metastasis to
liver in mouse) II Homo sapiens cDNA 5' end similar to
similar to ornithine decarboxylase antizyme (201. .346);
100% identity. -AA307682 EST178550 Colon carcinoma (HCC)
cell line Homo sapiens cDNA 5' end similar to similar to

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Query Match

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Best Local Similarity 5.1%; Score 19; DB 9; Length 37635;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 AAAAGGGAAGTTCTGCCT 335
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Db 35070 AAAAGGGAAGTTCTGCCT 35088

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RESULT 29
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 DEFINITION
 Rattus norvegicus clone CH230-432K14, *** SEQUENCING IN PROGRESS
 *** 45 unordered pieces.
 AC128189 142329 bp DNA linear HTG 19-JUL-2002
 AC128189
 AC128189.1 GI:21908793
 HTG: HTGS_Phasel.
 Rattus norvegicus
 SOURCE
 ORGANISM
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus.
 1 (bases 1 to 142329)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alspbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowls,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gablisl,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrill,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
 Homsl,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Joliver,S., Joudah,S.,
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 Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
 Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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 Nguyen,N., Nickerson,E., Nwokenwo,S., Ogih,M., Okunou,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
 Scherger,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,
 Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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 Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.
 Direct Submission
 2 (bases 1 to 142329)
 Unpublished
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: G2NK
 Center clone name: CH230-432K14
 Summary Statistics
 Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 103440 bases at least Q40
 Consensus quality: 108530 bases at least Q30
 Consensus quality: 112007 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 45 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 1331: gap of unknown length
 1332: contig of 1031 bp in length
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 1334: contig of 2038 bp in length
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 1338: contig of 1982 bp in length
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 1342: contig of 1665 bp in length
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 1350: contig of 1506 bp in length
 1351: gap of unknown length
 1352: contig of 2163 bp in length
 1353: gap of unknown length
 1354: contig of 1495 bp in length
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* 61731 64986: contig of 3256 bp in length
* 64987 65086: gap of unknown length
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* 69207 72414: contig of 3108 bp in length
* 72415 72514: gap of unknown length
* 72515 74919: contig of 2405 bp in length
* 74920 75019: gap of unknown length
* 75020 78722: contig of 3703 bp in length
* 78723 78822: gap of unknown length
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* 88409 88509: gap of unknown length
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* 93945 94044: gap of unknown length
* 94045 99586: contig of 5542 bp in length
* 99587 99686: gap of unknown length
* 99687 106051: contig of 6365 bp in length
* 106052 106151: gap of unknown length
* 106152 112416: contig of 6265 bp in length
* 112417 112516: gap of unknown length
* 112517 123175: contig of 10659 bp in length
* 123176 123275: gap of unknown length
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 CTCGCCAGGGAAGTGAAC 262
DB 65792 CTCGCCAGGGAAGTGAAC 65774
RESULT 30
AC105316/c 148571 bp DNA linear PRI 29-MAY-2002
LOCUS Homo sapiens BAC clone RP11-524B5 from 4, complete sequence.
AC105316 AC105316 GI:20522215
VERSION AC105316.5
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 148571)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 148571)
AUTHORS Buatsi, D., Haakenson, W., Boyer, E. and Spalding, L.
TITLE The sequence of Homo sapiens BAC clone RP11-524B5
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 148571)
AUTHORS Waterston, R.H.
TITLE Direct Submission

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```

JOURNAL Submitted (29-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 148571)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 148571)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 148571)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 10, 2002 this sequence version replaced g1:20340527.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0524B05
-----
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pterle de Jong
and coworkers at http://www.chori.org
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-620C21, 2000 bp overlap;
the clone sequenced to the right is RP11-138A23, 2000 bp overlap.
Actual start of this clone is at base position 70882 of
RP11-620C21; actual end is at base position 47389 of RP11-138A23.
Location/Qualifiers
  1. 148571
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="4"
    /map="4"
    /clone="RP11-524B5"
    /clone_id="RP11-11"
repeat_region 138..322

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repeat_region	/rpt_family="MIR"	4629.4818
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repeat_region	/rpt_family="Alu"	6450.6756
repeat_region	/rpt_family="Alu"	6769.6798
repeat_region	/rpt_family="AT_rich"	7072.7174
repeat_region	/rpt_family="MIR"	8053.8105
repeat_region	/rpt_family="L2"	8355.8649
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repeat_region	/rpt_family="MER2_type	14982.15391
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repeat_region      36111..36413
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repeat_region      36931..36981
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repeat_region      38261..38318
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repeat_region      38498..38635
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repeat_region      38748..39113
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	Query Match	5.1%;	Score 19	Length 148571
	Best Local Similarity	100.0%;	Pred. No. 16	
	Matches 19	Conservative 0	Mismatches 0	Indels 0
QY	315	AGAAAAGGGGAAGTCTG	353	
DB	22080	AGAAAAGGGGAAGTCTG	22062	

RESULT	31
AC084750	
LOCUS	AC084750 154693 bp DNA linear PRI 09-JAN-2002
DEFINITION	Homo sapiens BAC clone RP11-215J17 from 4, complete sequence.
ACCESSION	AC084750
VERSION	AC084750.3 GI:17155079
KEYWORDS	HTC.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 154693) Sullivan,J.E. and Waterston,R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
AUTHORS	99063792
TITLE	JOURNAL MEDLINE
PUBMED	9847074
REFERENCE	2 (bases 1 to 154693) Isak,A. and Kozlowicz,A. The sequence of Homo sapiens BAC clone RP11-215J17 Unpublished (2001)
JOURNAL	3 (bases 1 to 154693) Waterston,R.H. Direct Submission Submitted (11-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 154693) Waterston,R.H. Direct Submission Submitted (30-NOV-2001) Genome Sequencing Center, Washington

REFERENCE
AUTHORS
TITLE
JOURNAL

University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 154693)
Waterston, R. H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 154693)
Waterston, R.

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 30, 2001 this sequence version replaced g1:16799050.
----- Genome Center

COMMENT

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0215J17

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(<http://daccpac.med.buffalo.edu>)
VECTOR: pBACE3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-362M19, 2000 bp overlap.
The clone sequenced to the right is RP11-509I10. Actual start of
this clone is at base position 151949 of RP11-362M19; actual end is
at base position 154693 of RP11-215J17.

FEATURES

SOURCE

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-215J17"
/clone_lib="RPC1-11"
145..272
/rpt_family="L1"
repeat_region
4574..4607
/rpt_family="AT_rich"
6208..6327
/rpt_family="MaLR"
repeat_region

Data from AC091490 was used to finish this clone, AC084750.

repeat_region 6322..6349
/rpt_family="AT_rich"
repeat_region 6496..6526
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repeat_region 7110..7251
/rpt_family="L2"
repeat_region 8487..8763
/rpt_family="Alu"
repeat_region 9234..10888
/rpt_family="L1"
repeat_region 10870..10920
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repeat_region 11857..11907
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repeat_region 14191..14480
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repeat_region 14936..15017
/rpt_family="A-rich"
repeat_region 16176..16228
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repeat_region 18134..18177
/rpt_family="(CA)n"
repeat_region 20262..20282
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repeat_region 20678..20764
/rpt_family="MIR"
repeat_region 20805..21091
/rpt_family="L1"
repeat_region 21089..21139
/rpt_family="AT_rich"
repeat_region 21164..21361
/rpt_family="L1"
repeat_region 21358..21757
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repeat_region 21764..22238
/rpt_family="L1"
repeat_region 22285..23509
/rpt_family="L1"
repeat_region 23610..24135
/rpt_family="L1"
repeat_region 24332..24403
/rpt_family="GA-rich"
repeat_region 25117..26953
/rpt_family="L1"
repeat_region 27180..27360
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repeat_region 28399..28549
/rpt_family="MIR"
repeat_region 30843..30915
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repeat_region 30909..31192
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repeat_region 31329..31365
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repeat_region 31372..31446
/rpt_family="CRL"
repeat_region 31892..31917
/rpt_family="AT_rich"
repeat_region 32244..32278
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repeat_region 32993..33269


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* 11953 12052: gap of unknown length
* 12053 13451: contig of 1399 bp in length
* 13452 13551: gap of unknown length
* 13552 14859: contig of 1308 bp in length
* 14860 14959: gap of unknown length
* 14960 15983: contig of 1024 bp in length
* 15984 16083: gap of unknown length
* 16084 17352: contig of 1269 bp in length
* 17353 17452: gap of unknown length
* 17453 18905: contig of 1453 bp in length
* 18906 19005: gap of unknown length
* 19006 20634: contig of 1629 bp in length
* 20635 20734: gap of unknown length
* 20735 21951: contig of 1217 bp in length
* 21952 22051: gap of unknown length
* 22052 23512: contig of 1461 bp in length
* 23513 23612: gap of unknown length
* 23613 25111: contig of 1499 bp in length
* 25112 25211: gap of unknown length
* 25212 26295: contig of 1084 bp in length
* 26296 26395: gap of unknown length
* 26396 28255: contig of 1860 bp in length
* 28256 28355: gap of unknown length
* 28356 29759: contig of 1404 bp in length
* 29760 29859: gap of unknown length
* 29860 30988: contig of 1139 bp in length
* 30989 31098: gap of unknown length
* 31099 32270: contig of 1172 bp in length
* 32271 32370: gap of unknown length
* 32371 34072: contig of 1702 bp in length
* 34073 34172: gap of unknown length
* 34173 35716: contig of 1544 bp in length
* 35717 35816: gap of unknown length
* 35817 37261: contig of 1445 bp in length
* 37262 37361: gap of unknown length
* 37362 38480: contig of 1119 bp in length
* 38481 38580: gap of unknown length
* 38581 39609: contig of 1029 bp in length
* 39610 39709: gap of unknown length
* 39710 41831: contig of 2122 bp in length
* 41832 41931: gap of unknown length
* 41932 43536: contig of 1605 bp in length
* 43537 43636: gap of unknown length
* 43637 45470: contig of 1834 bp in length
* 45471 45570: gap of unknown length
* 45571 46972: contig of 1402 bp in length
* 46973 47072: gap of unknown length
* 47073 48378: contig of 1306 bp in length
* 48379 48478: gap of unknown length
* 48479 49869: contig of 1391 bp in length
* 49870 49969: gap of unknown length
* 49970 52101: contig of 2132 bp in length
* 52102 52201: gap of unknown length
* 52202 53702: contig of 1501 bp in length
* 53703 53802: gap of unknown length
* 53803 55595: contig of 1793 bp in length
* 55596 55695: gap of unknown length
* 55696 58025: contig of 2330 bp in length
* 58026 58125: gap of unknown length
* 58126 60175: contig of 2050 bp in length
* 60176 60275: gap of unknown length
* 60276 61611: contig of 1336 bp in length
* 61612 61711: gap of unknown length
* 61712 63647: contig of 1936 bp in length
* 63648 63747: gap of unknown length
* 63748 65445: contig of 1698 bp in length
* 65446 65545: gap of unknown length
* 65546 67327: contig of 1782 bp in length
* 67328 67427: gap of unknown length
* 67428 69058: contig of 1631 bp in length
* 69059 69158: gap of unknown length
* 69159 70888: contig of 1730 bp in length

```

```

Query Match          5.1%: Score 19; DB 2; Length 154772;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 96 CCCCAGGATTCATTGTGAA 114
Db 59719 CCCCAGGATTCATTGTGAA 59737

```

RESULT 33

AC113265/c

LOCUS

DEFINITION

MUS musculus chromosome 17 clone rp23-46k8 strain C57BL/6J, WORKING

DRAFT SEQUENCE, 6 ordered pieces.

AC113265

VERSION

AC113265.18 GI:22038589

KEYWORDS

HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

MILLAM, J. and ROE, B.A.

1 (bases 1 to 156128)

JOURNAL

MUS musculus BAC clone rp23-46k8

Unpublished

2 (bases 1 to 156128)

REFERENCE

MILLAM, J. and ROE, B.A.

Submitted Submission

Direct Submission

The University (28-FEB-2002) Department of Chemistry And Biochemistry,

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

On Aug 1, 2002 this sequence version replaced gi:22002191.

Genome Center

Center: Department of Chemistry And Biochemistry

The University of Oklahoma

Center code:UOKNOR

NOTE: This is a 'working draft' sequence. It currently

consists of 6 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

been provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 2249: contig of 2249 bp in length

2250 2349: gap of unknown length

REFERENCE JOURNAL
 TITLE
 AUTHORS
 JOURNAL
 COMMENT

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Jul 14, 2002 this sequence version replaced gi:20467689.

Center: Baylor College of Medicine
 Genome Center
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: GTXN
 Center clone name: CH230-354C23
 Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 116366 bases at least Q40
 Consensus quality: 120870 bases at least Q30
 Consensus quality: 124554 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>)
 NOTE: This is a working draft sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
 1097 1196: contig of 1096 bp in length
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 1197 2600: contig of 1404 bp in length
 2601 2700: gap of unknown length
 2701 3999: contig of 1299 bp in length
 4000 4099: gap of unknown length
 4100 5207: contig of 1108 bp in length
 5208 5307: gap of unknown length
 5308 7024: contig of 1717 bp in length
 7025 7125: gap of unknown length
 7125 8165: contig of 1041 bp in length
 8166 8265: gap of unknown length
 8266 9509: contig of 1244 bp in length
 9510 9609: gap of unknown length
 9610 10764: contig of 1155 bp in length
 10765 10865: gap of unknown length
 10865 12046: contig of 1182 bp in length
 12047 12145: gap of unknown length
 12147 13186: contig of 1040 bp in length
 13187 13286: gap of unknown length
 13287 14687: contig of 1401 bp in length

* 104540 109623: contig of 5084 bp in length
 * 109624 109723: gap of unknown length
 * 109724 113402: contig of 3679 bp in length
 * 113403 113502: gap of unknown length
 * 113503 117935: contig of 4433 bp in length
 * 117936 118035: gap of unknown length
 * 118036 122534: contig of 4499 bp in length
 * 122535 122634: gap of unknown length
 * 122635 127202: contig of 4568 bp in length
 * 127203 127302: gap of unknown length
 * 127303 132412: contig of 5110 bp in length
 * 132413 132512: gap of unknown length
 * 132513 135347: contig of 2835 bp in length

Query Match 5.18; Score 19; DB 2; Length 163041;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CCCCCGAGTCATTGTGAA 114
 Db 39872 CCCCCGAGTCATTGTGAA 39890

RESULT 36 165873 bp DNA linear PRI 05-APR-2002
 AC066593 Homo sapiens chromosome 3 clone RP11-34405 map 3p, complete
 LOCUS AC066593
 DEFINITION sequence.
 AC066593 GI:10799383
 VERSION HTG: HTGS.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 165873)
 AUTHORS Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
 Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C.,
 Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
 Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L.,
 Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,
 Wang, J., Wang, J., Wang, L., Wang, R., Wang, X., Wang, X.,
 Wang, X., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X.,
 Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, L., Zhang, M.,
 Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,
 Yu, J. and Yang, H.
 TITLE Chromosome 3p genomic sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165873)
 AUTHORS Kang, N., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B.,
 Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y.,
 Qi, X., Li, Y., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y.,
 Li, G., Li, C., Bao, Q., Bao, J., Song, L., Zhang, L., Guo, D.,
 Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.,
 and Yang, H.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Human Genomic Center, Institute of
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
 100101, P.R.China
 REFERENCE 3 (bases 1 to 165873)
 AUTHORS Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
 He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G.,
 Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W.,
 Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L., Song, S., Sun, M.,
 Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J.,
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 Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yang, X., Zhang, G.,
 Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X.,
 Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.
 TITLE Direct Submission
 JOURNAL Submitted (12-Oct-2000) Human Genomic Center, Institute of

REFERENCE 4 (bases 1 to 165873)
 AUTHORS Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
 Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C.,
 Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
 Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Qi, Q., Qi, X., Song, L.,
 Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,
 Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y.,
 Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yang, X.,
 Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M.,
 Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,
 Yu, J. and Yang, H.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2002) Human Genomic Center, Institute of
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
 100101, P.R.China
 COMMENT On Oct 12, 2000 this sequence version replaced gi:10719643.
 -----Genome Center
 Center: Beijing Center
 Center code: Beijing
 Website: http://hgci.gtp.ac.cn
 http://www.genomics.org.cn
 Contact: hgci.gtp.ac.cn
 -----Project Information
 Center project name: 1# project
 Center clone name: RP11-34405
 -----Summary Statistics
 Sequencing vector: pUC18; 100% of reads
 Chemistry: Dye-terminator; 5% of reads
 Chemistry: Dye-terminator Big Dye; 45% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 167281 bases at least Q40
 Consensus quality: 169056 bases at least Q30
 Consensus quality: 169188 bases at least Q20
 Insert size: 165873; sum-of-contigs
 Quality coverage: 6.54x in Q20 bases; sum-of-contigs

FEATURES
 source
 location/Qualifiers
 1..165873
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /map="3p"
 /clone="RP11-34405"
 BASE COUNT 50270 a 30351 c 31859 g 53393 t
 ORIGIN

Query Match 5.18; Score 19; DB 9; Length 165873;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 TCAGAAAGAGTGTGAG 160
 Db 65260 TCAGAAAGAGTGTGAG 65278

RESULT 37 177070 bp DNA linear HTG 18-FEB-2001
 AC018875/c Homo sapiens chromosome 3 clone RP11-28956, WORKING DRAFT
 LOCUS AC018875
 DEFINITION sequence, 31 unordered pieces.
 AC018875
 AC018875 GI:12963043
 VERSION HTG: HTGS-PHASE1; HTGS-DRAFT; HTGS-FULLTOP.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 177070)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Unpublished
2 (bases 1 to 177070)
Waterson, R.H.
Direct Submission
Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis
MO 63108, USA
On Feb 18, 2001 this sequence version replaced gi:11192196.

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0289506
----- Summary Statistics -----
Sequencing vector: M13: 86%
Sequencing vector: Plasmid: 14%
Chemistry: Dye-terminator ET: 86% of reads
Chemistry: Dye-terminator Big Dye: 14% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163528 bases at least Q40
Consensus quality: 169714 bases at least Q30
Consensus quality: 173054 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 176607; sum-of-configs
Quality coverage: 5.28 in Q20 bases; agarose-fp
Quality coverage: 5.08 in Q20 bases; sum-of-configs

```

NOTE: this is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	1367	contlig of 1367 bp in length
1368	1467	gap of unknown length
1468	2665	contlig of 1198 bp in length
2666	2765	gap of unknown length
2766	3873	contlig of 1108 bp in length
3874	3973	gap of unknown length
3974	5142	contlig of 1169 bp in length
5143	5242	gap of unknown length
5243	6835	contlig of 1593 bp in length
6836	6935	gap of unknown length
6936	8704	contlig of 1769 bp in length
8705	8804	gap of unknown length
8806	10231	contlig of 1427 bp in length
10232	10331	gap of unknown length
10332	12457	contlig of 2126 bp in length
12458	12557	gap of unknown length
12558	14011	contlig of 1454 bp in length
14012	14111	gap of unknown length
14112	15897	contlig of 1786 bp in length
15898	15997	gap of unknown length
15998	17916	contlig of 1919 bp in length
17917	18016	gap of unknown length
18017	19872	contlig of 1856 bp in length
19873	19972	gap of unknown length
19973	22611	contlig of 2639 bp in length
22612	22711	gap of unknown length
22712	25838	contlig of 3127 bp in length
25839	25938	gap of unknown length
25939	27145	contlig of 1207 bp in length
27146	27245	gap of unknown length
27246	29836	contlig of 2591 bp in length
29837	31395	gap of unknown length
31396	31495	contlig of 1459 bp in length
31496	35219	gap of unknown length
35220	35319	contlig of 3724 bp in length
35320	35319	gap of unknown length

FEATURES

SOURCE

	*	35320	36695:	contig of 1376 bp in length
	*	36696	36799:	gap of unknown length
	*	36796	36796:	contig of 2753 bp in length
	*	39549	39648:	gap of unknown length
	*	39649	41067:	contig of 1419 bp in length
	*	41168	41600:	gap of unknown length
	*	41168	44600:	contig of 3433 bp in length
	*	44601	44700:	gap of unknown length
	*	47437	47436:	contig of 2736 bp in length
	*	47537	47536:	gap of unknown length
	*	51070	51169:	contig of 3533 bp in length
	*	51170	56386:	contig of 5217 bp in length
	*	56387	56486:	gap of unknown length
	*	56487	61787:	contig of 5301 bp in length
	*	61788	61887:	gap of unknown length
	*	65441	65440:	contig of 3535 bp in length
	*	65541	65540:	gap of unknown length
	*	70097	70096:	contig of 4556 bp in length
	*	70197	79053:	contig of unknown length
	*	79054	79153:	gap of unknown length
	*	79154	109291:	contig of 30138 bp in length
	*	109282	109391:	gap of unknown length
	*	109392	117070:	contig of 67679 bp in length
source			Location/Qualifiers	
			1. 117070	
misc_feature			/organism="Homo sapiens"	
misc_feature			/db_xref="taxon:9606"	
misc_feature			/chromosome="YUNK"	
misc_feature			/clone="RP11-289E6"	
misc_feature			1. 1367	
misc_feature			/note="assembly_name:Contig18"	
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misc_feature			/note="assembly_name:Contig17"	
misc_feature			2766. 3873	
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misc_feature			6336. 8704	
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misc_feature			8805. 10231	
misc_feature			/note="assembly_name:Contig26"	
misc_feature			10332. 12457	
misc_feature			/note="assembly_name:Contig27"	
misc_feature			12558. 14011	
misc_feature			/note="assembly_name:Contig28"	
misc_feature			14112. 15897	
misc_feature			/note="assembly_name:Contig29"	
misc_feature			15998. 17916	
misc_feature			/note="assembly_name:Contig30"	
misc_feature			18017. 19872	
misc_feature			/note="assembly_name:Contig31"	
misc_feature			19973. 22611	
misc_feature			/note="assembly_name:Contig33"	
misc_feature			22712. 25838	
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misc_feature			/note="assembly_name:Contig36"	
misc_feature			29937. 31195	
misc_feature			/note="assembly_name:Contig37"	
misc_feature			31496. 35219	
misc_feature			/note="assembly_name:Contig38"	
misc_feature			35320. 36695	
misc_feature			/note="assembly_name:Contig39"	
misc_feature			36796. 39548	
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misc-feature      41168..44600
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misc-feature      44701..47436
                   /note="assembly_name:Contig43"
misc-feature      47537..51069
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misc-feature      51170..56386
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misc-feature      56487..61787
                   /note="assembly_name:Contig46"
misc-feature      61888..65440
                   /note="assembly_name:Contig47"
misc-feature      65541..70096
                   /note="assembly_name:Contig48"
misc-feature      70197..79053
                   /note="assembly_name:Contig49"
misc-feature      79154..109291
                   /note="assembly_name:Contig50"
                   clone_end:T7
misc-feature      vector_side:right"
                   109392..177070
                   /note="assembly_name:Contig51"
BASE COUNT      44893 a 41640 c 40959 g 46560 t 3018 others
ORIGIN

```

```

Query Match      5.1%: Score 19: DB 2: Length 177070:
Best Local Similarity 100.0%: Pred. NO. 16;
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
OY      45 AAATCAGTGTCTACCACTG 63
        |||||||
Db 20274 AAATCAGTGTCTACCACTG 20256

```

```

RESULT 38
AC021222      177426 bp DNA linear HTG 07-JUL-2000
LOCUS      Homo sapiens chromosome 11 clone RP11-567M21, WORKING DRAFT
DEFINITION
AC021222.4 GI:7770692
VERSION      HTG: HTGS-PHASE1; HTGS-DRAFT.
KEYWORDS
SOURCE      Homo sapiens
ORGANISM
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 177426)
JOURNAL      Waterston,R.H.
REFERENCE      The sequence of Homo sapiens clone
AUTHORS      Unpublished
TITLE      2 (bases 1 to 177426)
JOURNAL      Waterston,R.H.
REFERENCE      Direct Submission
AUTHORS      Submitted (15-JAN-2000) Genome Sequencing Center, Washington
TITLE      University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL      MO 63108, USA
COMMENT      On May 12, 2000 this sequence version replaced gi:7233676.

```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0567M21
----- Summary Statistics -----
Sequencing vector: MJ3, 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154559 bases at least Q40
Consensus quality: 161804 bases at least Q30
Consensus quality: 166430 bases at least Q20

```

FEATURES

```

Insert size: 189000; agarose-fp
Insert size: 174526; sum-of-contigs
Quality coverage: 2.77 in Q20 bases; agarose-fp
Quality coverage: 3.06 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1045      1044: contig of 1044 bp in length
1145      1144: gap of unknown length
1230      2529: contig of 1385 bp in length
2530      2629: gap of unknown length
2630      3739: contig of 1110 bp in length
3740      3839: gap of unknown length
3840      5188: contig of 1349 bp in length
5189      5288: gap of unknown length
5289      6861: contig of 1573 bp in length
6862      6961: gap of unknown length
6962      8387: contig of 1426 bp in length
8388      8487: gap of unknown length
8488      9957: contig of 1470 bp in length
9958      10057: gap of unknown length
10058      11934: contig of 1877 bp in length
11935      12034: gap of unknown length
12035      15639: contig of 3605 bp in length
15640      15739: gap of unknown length
15740      18805: contig of 3066 bp in length
18806      18905: gap of unknown length
18906      21750: contig of 2845 bp in length
21751      21850: gap of unknown length
21851      24673: contig of 2823 bp in length
24674      24773: gap of unknown length
24774      27874: contig of 3101 bp in length
27875      27974: gap of unknown length
27975      32401: contig of 4427 bp in length
32402      32501: gap of unknown length
32502      35859: contig of 3358 bp in length
35860      35959: gap of unknown length
35960      38608: contig of 2649 bp in length
38609      38708: gap of unknown length
38709      43983: contig of 5275 bp in length
43984      44083: gap of unknown length
44084      50370: contig of 6287 bp in length
50371      50470: gap of unknown length
50471      55419: contig of 4949 bp in length
55420      55519: gap of unknown length
55520      60146: contig of 4627 bp in length
60147      60247: gap of unknown length
60248      65990: contig of 5744 bp in length
65991      66090: gap of unknown length
66091      72519: contig of 6429 bp in length
72520      72619: gap of unknown length
72620      79368: contig of 6749 bp in length
79369      79468: gap of unknown length
79469      88631: contig of 9163 bp in length
88632      88731: gap of unknown length
88732      98171: gap of unknown length
98172      98271: contig of 9440 bp in length
98272      108874: contig of 10603 bp in length
108875      108974: gap of unknown length
108975      120856: contig of 11882 bp in length
120857      120956: gap of unknown length
120957      133832: contig of 12876 bp in length
133833      133932: gap of unknown length
133933      151337: contig of 17405 bp in length
151338      151438: gap of unknown length
151439      177426: contig of 25989 bp in length.
Location/Qualifiers

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/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-567M21"
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3840. 5188
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6962. 8387
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66091. 72519
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98272. 108874
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108975. 120856
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120957. 133832
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133933. 151337
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151438. 177426
/note="assembly_name:Contig41"
BASE COUNT 4881 a 38792 c 37341 g 49554 t 2928 others
ORIGIN

Query Match 5.1%; Score 19; DB 2; Length 177426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Einhart,C., Edgar,D., Edwards,C.C., Elina,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hayes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Huik,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolyvet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., Kling,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabadi,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,S.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwundu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivas,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshark,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usumani,K., Vasquez,L., Vera,V., Vialation,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 185551)
Worley,K.C.
Direct Submission
Submitted (21-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 185551)
Worley,K.C.
Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

```


COMMENT

Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20303368.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSSY
Center clone name: CH230-191H11
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap version 0.990329
Consensus quality: 138102 bases at least Q40
Consensus quality: 143613 bases at least Q30
Consensus quality: 148883 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length.
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1002: contig of 1002 bp in length
1003 1102: gap of unknown length
1103 2102: contig of 1000 bp in length
2103 2202: gap of unknown length
2203 3426: contig of 1224 bp in length
3427 3526: gap of unknown length
3527 4701: contig of 1175 bp in length
4702 4801: gap of unknown length
4802 6301: contig of 1500 bp in length
6302 6401: gap of unknown length
6402 7861: contig of 1460 bp in length
7862 7961: gap of unknown length
7962 8994: contig of 1033 bp in length
8995 9094: gap of unknown length
9095 10209: contig of 1115 bp in length
10210 10309: gap of unknown length
10310 11813: contig of 1504 bp in length
11814 11913: gap of unknown length
11914 13306: contig of 1393 bp in length
13307 13406: gap of unknown length
13407 14854: contig of 1448 bp in length
14855 14954: gap of unknown length
14955 15959: contig of 1015 bp in length
15970 16069: gap of unknown length
16070 17610: contig of 1541 bp in length
17611 17710: gap of unknown length
17711 19243: contig of 1533 bp in length
19244 19343: gap of unknown length
19344 21972: contig of 2629 bp in length
21973 23072: gap of unknown length
23073 23420: contig of 1348 bp in length
23421 23520: gap of unknown length
23521 25976: contig of 2456 bp in length
25977 26076: gap of unknown length
26077 27910: contig of 1834 bp in length
27911 28010: gap of unknown length
28011 29116: contig of 1106 bp in length
29117 29216: gap of unknown length
29217 30272: contig of 1056 bp in length
30273 30372: gap of unknown length
30373 31532: contig of 1160 bp in length
31533 31632: gap of unknown length
31633 33259: contig of 1627 bp in length
33260 33359: gap of unknown length
33360 34755: contig of 1396 bp in length

34756 34855: gap of unknown length
34856 35954: contig of 1099 bp in length
35955 36054: gap of unknown length
36055 37883: contig of 1829 bp in length
37884 37983: gap of unknown length
37984 40017: contig of 2034 bp in length
40018 40117: gap of unknown length
40118 42375: contig of 2258 bp in length
42376 42475: gap of unknown length
42475 44342: contig of 1867 bp in length
44343 44442: gap of unknown length
44443 46003: contig of 1561 bp in length
46004 46103: gap of unknown length
46104 47435: contig of 1332 bp in length
47436 47535: gap of unknown length
47536 50415: contig of 2860 bp in length
50416 50515: gap of unknown length
50516 54064: contig of 3549 bp in length
54064 54164: gap of unknown length
54165 57106: contig of 2942 bp in length
57107 57206: gap of unknown length
57207 59706: contig of 2500 bp in length
59707 59806: gap of unknown length
59806 62287: contig of 2481 bp in length
62288 62387: gap of unknown length
62388 65758: contig of 3371 bp in length
65759 65858: gap of unknown length
65859 68739: contig of 2881 bp in length
68740 68839: gap of unknown length
68840 70238: contig of 1399 bp in length
70239 70338: gap of unknown length
70339 73742: contig of 3404 bp in length
73743 73842: gap of unknown length
73843 76328: contig of 2486 bp in length
76329 76428: gap of unknown length
76429 79753: contig of 3325 bp in length
79754 79853: gap of unknown length
79853 82522: contig of 2659 bp in length
82523 82622: gap of unknown length
82623 84875: contig of 2253 bp in length
84876 84975: gap of unknown length
84976 88118: contig of 3143 bp in length
88119 88218: gap of unknown length
88219 90713: contig of 2495 bp in length
90714 90813: gap of unknown length
90814 94914: contig of 4101 bp in length
94915 95014: gap of unknown length
95015 99367: contig of 4353 bp in length
99368 99467: gap of unknown length
99468 104476: contig of 5009 bp in length
104477 104576: gap of unknown length
104577 107621: contig of 3045 bp in length
107622 107721: gap of unknown length
107722 113653: contig of 5932 bp in length
113654 113753: gap of unknown length
113754 117798: contig of 4045 bp in length
117799 117898: gap of unknown length
117899 121628: contig of 3730 bp in length
121629 121728: gap of unknown length
121729 125896: contig of 4168 bp in length
125897 125996: gap of unknown length
125997 129919: contig of 3923 bp in length

Query Match 5.1%; Score 19; DB 2; Length 185551;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 GAAGTGAATGAGCAATG 167
|||||

Db 42662 GAAGTGAATGAGCAATG 42680

RESULT 40

AP003041/c 188172 bp DNA linear PRI 10-AUG-2002
 LOCUS AP003041 Homo sapiens genomic DNA, chromosome 11 clone:RP11-567M21, complete
 DEFINITION sequence.
 ACCESSION AP003041 GI:22202826
 VERSION AP003041.3
 KEYWORDS HTG.
 SOURCE Homo sapiens DNA, clone:RP11-567M21.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
 Fujiyama, A., Yada, T., Totoki, Y., Matsubae, H. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA
 JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 188172)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
 Fujiyama, A., Yada, T., Totoki, Y., Matsubae, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-2000) Masahiro Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel:81-45-503-9111, Fax:81-45-503-9170
 On Aug 9, 2002 this sequence version replaced gi:20334333.
 COMMENT location/Qualifiers
 FEATURES
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 1. 188172
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q"
 /clone="RP11-567M21"
 BASE COUNT 53056 a 40586 c 41718 g 52812 t
 ORIGIN
 Query Match 5.1%; Score 19; DB 9; Length 188172;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 304 GCCAAGGCCCAAGAAAG 322
 Db 42556 GCCAAGGCCCAAGAAAG 42538
 RESULT 41
 AC113489 194769 bp DNA linear HTG 02-JUN-2002
 LOCUS AC113489 Mus musculus clone RP23-358A18, WORKING DRAFT SEQUENCE, 9 ordered
 DEFINITION pieces.
 ACCESSION AC113489
 VERSION AC113489.2 GI:21313864
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 194769)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Mus musculus, clone RP23-358A18
 JOURNAL Unpublished
 2 (bases 1 to 194769)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
 Glude, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
 Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,

McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
 Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Roselli, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 194769)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
 Glude, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
 Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,
 Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
 Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
 Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S.,
 Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S.,
 Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Jun 2, 2002 this sequence version replaced gi:19033670.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L23802
 Center clone name: 358_A_18
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960721
 Consensus quality: 191646 bases at least Q40
 Consensus quality: 193107 bases at least Q40
 Consensus quality: 193517 bases at least Q20
 Insert size: 194000; agarose-ff
 Insert size: 193969; sum-of-contigs
 Quality coverage: 6.0 in Q20 bases; sum-of-contigs
 Quality coverage: 6.0 in Q20 bases; sum-of-contigs
 ----- NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

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*      1      1980: contig of 1980 bp in length
*      1981 2080: gap of 100 bp
*      2081 3501: contig of 1421 bp in length
*      3502 3601: gap of 100 bp
*      3602 6848: contig of 3247 bp in length
*      6849 6948: gap of 100 bp
*      6949 11584: contig of 4636 bp in length
*      11585 11684: gap of 100 bp
*      11685 30031: contig of 18347 bp in length
*      30032 30131: gap of 100 bp
*      30132 88538: contig of 58407 bp in length
*      88539 88638: gap of 100 bp
*      88639 118825: contig of 30187 bp in length
*      118826 118925: gap of 100 bp
*      118926 162363: contig of 43438 bp in length
*      162364 162463: gap of 100 bp
*      162464 194769: contig of 32306 bp in length.
*      Location/Qualifiers
        1. 194769
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /clone="RP23-358A18"
        /clone_1fb="RPC1-23 Female Mouse BAC"
        1. 1980
        /note="assembly_fragment"
        2081. 3501
        /note="assembly_fragment"
        misc_feature
        /note="assembly_fragment"
        3602. 6848
        /note="assembly_fragment"
        misc_feature
        /note="assembly_fragment"
        6949. 11584
        /note="assembly_fragment"
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        /note="assembly_fragment"
        11685. 30031
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        misc_feature
        /note="assembly_fragment"
        30132. 88538
        /note="assembly_fragment"
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        /note="assembly_fragment"
        88639. 118825
        /note="assembly_fragment"
        misc_feature
        /note="assembly_fragment"
        118926. 162363
        /note="assembly_fragment"
        misc_feature
        /note="assembly_fragment"
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        vector_side:right"

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BASE COUNT 56367 a 38216 c 39235 g 60084 t 867 others
ORIGIN

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Query Match

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Best Local Similarity 5.1%; Score 19; DB 2; Length 194769;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 261 ACTCAGTTGCATCAGCTG 279
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Db 68166 ACTCAGTTGCATCAGCTG 68148

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RESULT 42
LOCUS AC122259 209418 bp DNA linear HTG 23-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP23-183E7, WORKING DRAFT
ACCESSION AC122259
VERSION AC122259.1 GI:21105101
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 209418)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 209418)
AUTHORS McPherson,J.D. and Waterston,R.H.

```

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0183E07

----- Summary Statistics -----
Sequencing vector: M13: 0%
Sequencing vector: Plasmid: 100%
Chemistry: Dye-Primer ET: 0% of reads
Chemistry: Dye-Terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 205472 bases at least Q40
Consensus quality: 206680 bases at least Q30
Consensus quality: 207478 bases at least Q20
Insert size: 212000; agarose-fp
Insert size: 208518; sum-of-contigs
Quality coverage: 7.49 in Q20 bases; sum-of-contigs
Quality coverage: 6.37 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

*      1      6482: contig of 6482 bp in length
*      6483 6582: gap of unknown length
*      6583 19747: contig of 13165 bp in length
*      19748 19847: gap of unknown length
*      19848 51248: contig of 31401 bp in length
*      51249 51348: gap of unknown length
*      51349 88682: contig of 37334 bp in length
*      88683 88782: gap of unknown length
*      88783 125635: contig of 36853 bp in length
*      125636 125735: gap of unknown length
*      125736 192346: contig of 66611 bp in length
*      192347 192446: gap of unknown length
*      192447 193492: contig of 1046 bp in length
*      193493 193592: gap of unknown length
*      193593 198088: contig of 4496 bp in length
*      198089 198188: gap of unknown length
*      198189 203515: contig of 5327 bp in length
*      203516 203615: gap of unknown length
*      203616 209418: contig of 5803 bp in length.

```

FEATURES

source

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1. 209418
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-183E7"
1. 6482
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6583. 19747
/note="assembly_name:Contig11"
19848. 51248
/note="assembly_name:Contig12"
51349. 88682
/note="assembly_name:Contig13"
88783. 125635
/note="assembly_name:Contig14
clone_end:SP6
vector_side:right"
125736. 192346
/note="assembly_name:Contig15

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                  vector_side:right"
192447.193492
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193593.198088
misc_feature      /note="assembly_name:Contig7"
198189.203515
misc_feature      /note="assembly_name:Contig8"
203616.209418
                  /note="assembly_name:Contig9"
BASE COUNT      58209 a 45087 c 44929 g 60292 t      901 others
ORIGIN
Query Match      5.1%; Score 19; DB 2; Length 209418;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 CTCGCCAGGGAAGTGAAC 262
Db 159434 CTCGCCAGGGAAGTGAAC 159452

RESULT 43
AC010290/c      238472 bp      DNA      linear      PRI 23-OCT-2001
LOCUS      Homo sapiens chromosome 5 clone CTB-125B20, complete sequence.
DEFINITION      AC010290
ACCESSION      AC010290.7 GI:16328257
VERSION      HTG.
KEYWORDS      Homo sapiens.
SOURCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 238472)
              DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS      Unpublished
              Direct Submission
              2 (bases 1 to 238472)
              DOE Joint Genome Institute.
              Direct Submission
              Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
              3 (bases 1 to 238472)
              DOE Joint Genome Institute and Stanford Human Genome Center.
              Direct Submission
              Submitted (23-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
              Drive, Walnut Creek, CA 94598, USA
              On Oct 23, 2001 this sequence version replaced gi:1711412.
              Draft Sequence produced by DOE Joint Genome Institute
              www.jgi.doe.gov
              Finishing Completed at Stanford Human Genome Center
              www.hgsc.stanford.edu
              Quality: Phrap Quality >=40 99.7% of Sequence;
              Estimated Total Number of Errors is 0.5.
FEATURES
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                  /db_xref="taxon:9606"
                  /chromosome="5"
                  /clone="CTB-125B20"
BASE COUNT      73389 a 52011 c 48279 g 64793 t
ORIGIN
Query Match      5.1%; Score 19; DB 9; Length 238472;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 304 GCCAAGGCCCAAGAAAG 322
Db 134911 GCCAAGGCCCAAGAAAG 134893

RESULT 44

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AC096319
LOCUS      239904 bp      DNA      linear      HTG 11-JUL-2002
DEFINITION      Rattus norvegicus clone CH230-162p21, *** SEQUENCING IN PROGRESS
              *** 44 unordered pieces.
ACCESSION      AC096319
VERSION      AC096319.6 GI:21723476
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Ratus.
              1 (bases 1 to 239904)
              Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
              Alstbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
              Barbista,J., Benton,J., Bimaga,K., Blankenbury,K., Bonnin,D.,
              Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
              Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
              Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
              Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
              Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
              Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
              Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
              Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
              Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
              Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
              Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
              Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
              Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
              Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
              Homs,F., Howard,S., Huber,J., Hulik,S., Hume,J., Jackson,L.E.,
              Jacobson,B., Jia,Y., Johnson,R., Jolyet,S., Joudad,S.,
              Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
              Kratovic,J., Kreshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
              Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,W., Louised,H.,
              Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
              Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
              Massey,E., Mawliny,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
              Miner,G., Miner,Z., Mitchell,T., Mohabat,K., Morgan,M., Morris,S.,
              Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
              Nguyen,N., Nickerson,E., Nwokwenko,S., Ogun,M., Okwomou,G.,
              Orangunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
              Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
              Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Severy,G.,
              Scherer,S., Scott,G., Shen,H., Shoshari,N., Sisson,I.,
              Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
              Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
              Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S.,
              Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
              Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
              Williams,G., Williamson,A., Wlecezyk,R., Wooden,S., Worley,K.,
              Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
              Weinstein,G. and Gibbs,R.
              Direct Submission
              Unpublished
              2 (bases 1 to 239904)
              Worley,K.C.
              Direct Submission
              Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
              of Molecular and Human Genetics, Baylor College of Medicine, One
              Baylor Plaza, Houston, TX 77030, USA
              3 (bases 1 to 239904)
              Worley,K.C.
              Direct Submission
              Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
              of Molecular and Human Genetics, Baylor College of Medicine, One
              Baylor Plaza, Houston, TX 77030, USA
              On Jul 10, 2002 this sequence version replaced gi:18846093.
              ----- Genome Center
              Center: Baylor College of Medicine
              Center code: BCM
              Web site: http://www.hgsc.bcm.tmc.edu/
              Contact: hgsc-help@bcm.tmc.edu

```

```

----- Project Information
Center project name: GEXO
Center clone name: CH230-162P21
----- Summary Statistics
Sequencing vector: plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191179 bases at least Q40
Consensus quality: 196736 bases at least Q30
Consensus quality: 201345 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1019: contig of 1018 bp in length
1118: gap of unknown length
1119: contig of 1222 bp in length
2340: gap of unknown length
2441: contig of 1026 bp in length
3466: gap of unknown length
3567: contig of 1556 bp in length
5123: gap of unknown length
5223: contig of 1102 bp in length
6324: gap of unknown length
6325: contig of 1126 bp in length
7550: gap of unknown length
7650: contig of 1182 bp in length
8833: gap of unknown length
8932: contig of 1117 bp in length
10049: gap of unknown length
10149: contig of 1681 bp in length
10150: gap of unknown length
11831: contig of 1168 bp in length
11931: contig of 1956 bp in length
13099: gap of unknown length
13199: contig of 1854 bp in length
15155: gap of unknown length
15254: contig of 1776 bp in length
15255: gap of unknown length
17109: contig of 2153 bp in length
17209: gap of unknown length
18984: contig of 2137 bp in length
18985: gap of unknown length
19085: contig of 2435 bp in length
21238: gap of unknown length
21338: contig of 3548 bp in length
23773: gap of unknown length
23872: contig of 4102 bp in length
27420: gap of unknown length
27421: contig of 5056 bp in length
31623: gap of unknown length
31624: contig of 3748 bp in length
36778: gap of unknown length
36779: contig of 2097 bp in length
36878: gap of unknown length
40626: contig of 4098 bp in length
40727: gap of unknown length
42824: contig of 6543 bp in length
42825: gap of unknown length
47021: contig of 3830 bp in length
47121: gap of unknown length
47122: contig of 5078 bp in length
53664: gap of unknown length
53665: contig of 4980 bp in length
57594: gap of unknown length
57595: contig of 5005 bp in length
57695: gap of unknown length
62772: contig of 5005 bp in length
62773: gap of unknown length
67852: contig of 5005 bp in length
67853: gap of unknown length
72957: contig of 5005 bp in length
72958: gap of unknown length
73057: gap of unknown length

```

```

* 73058 81506: contig of 8449 bp in length
* 81507 81506: gap of unknown length
* 81607 87909: contig of 6303 bp in length
* 87910 88009: gap of unknown length
* 88010 88009: gap of unknown length
* 94461 94561: gap of unknown length
* 94562 94561: gap of unknown length
* 101192 101192: contig of 6631 bp in length
* 101193 101192: gap of unknown length
* 101293 107536: contig of 6244 bp in length
* 107537 107536: gap of unknown length
* 107637 112983: contig of 5347 bp in length
* 112983 113083: gap of unknown length
* 113084 120878: contig of 7755 bp in length
* 120879 120978: gap of unknown length
* 120978 127185: contig of 6206 bp in length
* 127185 127284: gap of unknown length
* 127284 133119: contig of 5835 bp in length
* 133119 133120: gap of unknown length
* 133120 143648: contig of 10429 bp in length
* 143649 143748: gap of unknown length
* 143749 143748: gap of unknown length
* 143748 154717: contig of 10969 bp in length
* 154718 154817: gap of unknown length
* 154818 164405: contig of 9588 bp in length
* 164406 164505: gap of unknown length
* 164506 170277: contig of 5772 bp in length
* 170278 170377: gap of unknown length
* 170378 179323: contig of 8946 bp in length
* 179324 179423: gap of unknown length
* 179424 193498: contig of 14075 bp in length
* 193499 193598: gap of unknown length
* 193599 208152: contig of 14554 bp in length
* 208153 208252: gap of unknown length
* 208253 223131: contig of 14879 bp in length
* 223132 223231: gap of unknown length
* 223232 239904: contig of 16673 bp in length.

```

```

FEATURES
source 1..239904
Location/Qualifiers
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-162P21"

```

```

BASE COUNT 68735 a 49743 c 49983 g 64401 t 7042 others
ORIGIN

```

```

Query Match 5.1% Score 19; DB 2; Length 239904;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 62 TGTGAAGATTCCAGCTGA 80
|||||
Db 87434 TGTGAAGATTCCAGCTGA 87452

```

```

RESULT 45
AC097172/c 247865 bp DNA linear HTG 24-AUG-2002
LOCUS Rattus norvegicus clone CH230-2616, *** SEQUENCING IN PROGRESS ***
DEFINITION 40 unordered pieces.
AC097172
AC097172.3 GI:21953449
VERSION HTG: HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE

```

```

ORGANISM

```

```

REFERENCE
AUTHORS

```

```

1 (bases 1 to 247865)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbata, J., Benton, J., Blum, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Boyle, S., Brieval, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burdett, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

```

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earnhardt, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, A.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
 Homsl, F., Howard, S., Huber, J., Huliy, S., Hume, J., Jackson, L.E.,
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 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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 Nguyen, N., Nickerson, E., Nwokkwo, S., Ogun, M., Okunolu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G.,
 Scherer, S., Scott, G., Shen, H., Shoochari, N., Sisson, I.,
 Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Swatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Umanal, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 247865)
 Worley, K.C.

Direct Submission
 Submitted (11-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 247865)
 Worley, K.C.

Direct Submission
 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 24, 2002 this sequence version replaced gi:17063105.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: TUVU
 Center clone name: CH230-2G16
 ----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 211853 bases at least Q40
 Consensus quality: 215254 bases at least Q30
 Consensus quality: 217501 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length
 * (see <http://www.hgsc.bcm.tmc.edu/docs/genbank/draft.data.html>).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 40 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1
 1097 1096: contig of 1096 bp in length
 1197 1196: gap of unknown length
 1197 2530: contig of 1334 bp in length
 2531 2530: gap of unknown length
 2631 3702: contig of 1072 bp in length
 3703 3802: gap of unknown length
 3803 4896: contig of 1094 bp in length
 4897 4996: gap of unknown length
 4997 6170: contig of 1174 bp in length
 6171 6270: gap of unknown length
 6271 7322: contig of 1052 bp in length
 7323 7422: gap of unknown length
 7423 8427: contig of 1005 bp in length
 8428 8527: gap of unknown length
 8528 9546: contig of 1019 bp in length
 9547 9646: gap of unknown length
 9647 11320: contig of 1674 bp in length
 11321 11420: gap of unknown length
 11421 13074: contig of 1654 bp in length
 13075 13174: gap of unknown length
 13175 14255: contig of 1081 bp in length
 14256 14355: gap of unknown length
 14356 15668: gap of unknown length
 15669 16720: contig of 1052 bp in length
 16721 16820: gap of unknown length
 16821 18498: contig of 1678 bp in length
 18499 18599: gap of unknown length
 18599 21960: contig of 3362 bp in length
 21961 22060: gap of unknown length
 22061 23501: contig of 1441 bp in length
 23502 23601: gap of unknown length
 23602 26241: contig of 2640 bp in length
 26242 26341: gap of unknown length
 26342 29052: contig of 2711 bp in length
 29053 29152: gap of unknown length
 29153 34283: contig of 5131 bp in length
 34284 34383: gap of unknown length
 34384 37721: contig of 3338 bp in length
 37722 37821: gap of unknown length
 37822 42562: contig of 4641 bp in length
 42563 42762: gap of unknown length
 42763 48044: contig of 5282 bp in length
 48045 48144: gap of unknown length
 48145 53928: contig of 5784 bp in length
 53929 54028: gap of unknown length
 54029 59505: contig of 5477 bp in length
 59506 59605: gap of unknown length
 59606 67767: contig of 8162 bp in length
 67768 75525: gap of unknown length
 75526 75525: contig of 7658 bp in length
 75526 83842: gap of unknown length
 83843 83942: gap of unknown length
 83943 91792: contig of 7850 bp in length
 91793 91892: gap of unknown length
 91893 99982: contig of 8090 bp in length
 99983 100082: gap of unknown length
 100083 108887: contig of 8805 bp in length
 108888 108987: gap of unknown length
 108988 116779: contig of 7792 bp in length
 116780 116879: gap of unknown length
 116879 126915: contig of 10036 bp in length
 126916 127015: gap of unknown length
 127016 138752: contig of 11737 bp in length
 138753 138852: gap of unknown length
 138853 149877: contig of 11025 bp in length
 149878 149977: gap of unknown length
 149978 161922: contig of 11945 bp in length
 161923 162022: gap of unknown length
 162023 174262: contig of 12240 bp in length
 174263 174362: gap of unknown length

* 174363 188460: contig of 14098 bp in length
 * 188461 188560: gap of unknown length
 * 188561 203563: contig of 15003 bp in length
 * 203564 203663: gap of unknown length
 * 203664 221346: contig of 17683 bp in length
 * 221347 221446: gap of unknown length
 * 221447 247865: contig of 26419 bp in length.

FEATURES
 source 1. .247865
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone="CH230-2G16"

BASE COUNT 67196 a 54622 c 53919 g 67619 t 4509 others
 ORIGIN

Query Match 5.1%; Score 19; DB 2; Length 247865;
 Best Local Similarity 100.0%; Pred. NO. 16;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GAAGTGATGGAGCAAACTG 167
 ||||||||||||||||
 Db 44325 GAAGTGATGGAGCAAACTG 44307

Search completed: November 7, 2002, 21:51:28
 Job time : 2444.62 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 : Search time 72.6545 Seconds
(without alignments)
11437.514 Million cell updates/sec

```

Title:          US-09-970-966-199
Perfect score:  369
Sequence:       1 ggcacacttttgcgatatgt.....tggctcgcgaccaccatcct 369

```

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 458492

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Listing first 45 summaries

Database :
N_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	369	100.0	369	22	AAE95007	Human ovarian carc
2	369	100.0	369	24	ABT03274	Human ovarian carc
3	369	100.0	369	24	ABL48956	Ovarian carcinoma
4	315	85.4	1524	24	ABK33543	CDNA encoding huma
5	315	85.4	1619	24	ABT03277	Human ovarian carc
5	315	85.4	1619	24	ABT03281	Human ovarian carc
7	315	85.4	1619	24	ABL40345	Ovarian carcinoma
8	315	85.4	1619	24	ABL40349	Ovarian carcinoma
9	315	85.4	1890	22	AAE93845	Human CDNA encodin

C	10	315	85.4	1897	24	ABT03284
C	11	315	88.4	1897	24	ABL043052
C	12	314	89.1	2528	22	AAD16690
C	13	283	76.7	1953	21	AAF22400
C	14	283	76.7	1956	22	AAF624188
C	15	281	76.2	396	22	AAF94818
C	16	281	76.2	396	24	ABT03085
C	17	281	76.2	396	24	ABL48768
C	18	271	73.4	1010	24	ABT03282
C	19	271	73.4	1010	24	ABL043050
C	20	221	59.9	591	22	AAE940044
C	21	142	38.5	1608	24	ABO54231
C	22	117	31.7	480	24	ABT03283
C	23	117	31.7	480	24	ABL40351
C	24	55	14.9	430	24	ABL81273
C	25	19	5.1	1226	22	AAI07456
C	26	19	5.1	2080	22	ABK62080
C	27	19	5.1	2222	24	ABK62081
C	28	18	4.9	737	24	ABL75913
C	29	18	4.9	256	24	ABL76635
C	30	18	4.9	286	24	ABL75647
C	31	18	4.9	484	22	AAK66539
C	32	18	4.9	484	22	AAK66540
C	33	18	4.9	1152	22	AAE52496
C	34	18	4.9	1562	23	AAE58379
C	35	18	4.9	1567	24	ABN91662
C	36	18	4.9	1566	24	ABN92620
C	37	18	4.9	1633	21	AAE54968
C	38	18	4.9	1791	21	AAA55968
C	39	18	4.9	2253	23	AAAS91414
C	40	18	4.9	3281	22	AAH54960
C	41	18	4.9	3566	22	AAI59083
C	42	18	4.9	3633	22	AAH54943
C	43	18	4.9	4106	22	AAH541744
C	44	18	4.9	6399	23	ABL13144
C	45	18	4.9	8268	23	ABL15972

ALIGNMENTS

RESULT 1

AAF95007 standard; DNA; 369 BP.

AA AC AAF95007;

DT 23-MAY-2001 (first entry)

Human ovarian cancer associated coding sequence SEQ ID NO: 199.

Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.

aa
05 Homo sapiens.

PN WO200118046-A2.

AA
PD 15-MAR-2001.

08-SEP-2000; 2000WO-US24827.

PR 10-SEP-1999; 99US-0394374.

15-AUG-2000; 2000US-0640173.

[illegible]

CONFIDENTIAL

[illegible]

WFL, 2001 211000/211000
XX

P1 Isolated polypeptide

PT nucleic acids that encode them, useful for the prevention diagnosis and
 PT treatment of ovarian cancers -
 PS
 XX
 PS Claim 18; Page 189; 189pp; English.

CC The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences.
 XX

SO Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 100.0%; Score 369; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.5e-187;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGTTCTTCTTNCAGGCTTTGGCGTGAATCCAGTGTACCA 60
 DB 1 GGCACTTTTGGCGATTGTTCTTCTTNCAGGCTTTGGCGTGAATCCAGTGTACCA 60
 QY 61 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 120
 DB 61 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 120
 QY 121 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 180
 DB 121 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 180
 QY 181 CGGCAAGTCTGTGCATCATCATGAGCGGCTGTCTCATGCTCCGCCGAGTCAATGGAATTGCAC 240
 DB 181 CGGCAAGTCTGTGCATCATCATGAGCGGCTGTCTCATGCTCCGCCGAGTCAATGGAATTGCAC 240
 QY 241 CTGCTCCCGAGGAACTGAAGTCAAGTTCATGAGTGTGCAACACCCCTTTTGA 300
 DB 241 CTGCTCCCGAGGAACTGAAGTCAAGTTCATGAGTGTGCAACACCCCTTTTGA 300
 QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTTCANGCCATGCTCCGCAC 360
 DB 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTTCANGCCATGCTCCGCAC 360
 QY 361 CACCATCCT 369
 DB 361 CACCATCCT 369

RESULT 2

ABT03274
 ID ABT03274 standard; cDNA; 369 BP.

XX
 AC ABT03274;

XX
 DT 05-SEP-2002 (first entry)

XX
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

XX
 KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX
 KW cytoskeletal; gene; ss.

XX
 OS Homo sapiens.

XX
 PN WO200239885-A2.

XX
 PD 23-MAY-2002.

XX
 PF 13-NOV-2001; 2001WO-US45395.

XX
 PR 14-NOV-2000; 2000US-0713550.

XX
 PR 03-APR-2001; 2001US-0825294.

XX
 PR 02-OCT-2001; 2001US-0970966.

XX
 PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
 XX
 DR WPI; 2002-500186/53.

XX
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX
 PS Example 1; Page 187; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.

SO Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 100.0%; Score 369; DB 24; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.5e-187;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGTTCTTCTTNCAGGCTTTGGCGTGAATCCAGTGTACCA 60
 DB 1 GGCACTTTTGGCGATTGTTCTTCTTNCAGGCTTTGGCGTGAATCCAGTGTACCA 60
 QY 61 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 120
 DB 61 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 120
 QY 121 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 180
 DB 121 GTGTAAAGAAATTCAGCTGAACAACGACTGCTCCGCCGAGTCAATGGAATTGCAC 180
 QY 181 CGGCAAGTCTGTGCATCATCATGAGCGGCTGTCTCATGCTCCGCCGAGTCAATGGAATTGCAC 240
 DB 181 CGGCAAGTCTGTGCATCATCATGAGCGGCTGTCTCATGCTCCGCCGAGTCAATGGAATTGCAC 240
 QY 241 CTGCTCCCGAGGAACTGAAGTCAAGTTCATGAGTGTGCAACACCCCTTTTGA 300
 DB 241 CTGCTCCCGAGGAACTGAAGTCAAGTTCATGAGTGTGCAACACCCCTTTTGA 300
 QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTTCANGCCATGCTCCGCAC 360
 DB 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCGCTCGGCTTCANGCCATGCTCCGCAC 360
 QY 361 CACCATCCT 369
 DB 361 CACCATCCT 369

RESULT 3

ABL48956
 ID ABL48956 standard; cDNA; 369 BP.

XX
 AC ABL48956;

XX
 DT 18-JUN-2002 (first entry)

XX
 DE Ovarian carcinoma sequence isolate 57887.

XX
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

XX
 KW ss.

XX
 OS Homo sapiens.

XX
 PN US2002004491-A1.

XX
 PD 10-JAN-2002.

XX
 PF 03-APR-2001; 2001US-0825294.

XX
 PR 10-SEP-1999; 99US-0394374.

```

PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656688.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP.
XX
XX WPI: 2002-171027/22.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX
XX Claim 1a; Page 116; 131pp; English.
XX
CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilized in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The sequences
CC given in records ABL48760-ABL48956 represent polynucleotides encoding
CC ovarian carcinoma proteins.
XX
XX Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other:
XX
XX Query Match 100.0%; Score 369; DB 24; Length 369;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-187;
XX Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGCACCTTTTGGCGATTGTTGCTTTCAGCGCTTTCGCTCAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGCGATTGTTGCTTTCAGCGCTTTCGCTCAATCCAGTCTACCA 60
OY 61 GGTGAAGATTCCAGCTGTAACACGACGCTCTCCCGAGTTCAATTGTAATGCAC 120
DB 61 GGTGAAGATTCCAGCTGTAACACGACGCTCTCCCGAGTTCAATTGTAATGCAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
OY 181 CGGCAAGTCTGTGATCATCAGCGCTGTCTCATCGCTTCCCGGGATACCAAGTCTT 240
DB 181 CGGCAAGTCTGTGATCATCAGCGCTGTCTCATCGCTTCCCGGGATACCAAGTCTT 240
OY 241 CGTGTCCCGGAGGAAATCAATCACTTTCATCAGCTGCTGTGCAACACCCCTTTTGTAA 300
DB 241 CGTGTCCCGGAGGAAATCAATCACTTTCATCAGCTGCTGTGCAACACCCCTTTTGTAA 300
OY 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTCTGCTCGGCCCTCANGSCATGAGCTCCGAC 360
DB 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTCTGCTCGGCCCTCANGSCATGAGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

ABK33543
ID ABK33543 standard; cDNA; 1524 BP.
XX
XX AC ABK33543;
XX
XX 08-MAY-2002 (first entry)
XX
XX cDNA encoding human PRO protein, Seq ID No 15.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001WO-US4280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GENE ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2002-172001/22.
XX P-PSDB: AAU83599.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour.
XX
XX Claim 2; Figure 15; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for stimulating
XX the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX

```

RESULT 4

CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 4.1e-158;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89
   |||||||
DB 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTTGAACGTTTGTGTGAGAAG 149
   |||||||
DB 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTTGAACGTTTGTGTGAGAAG 149
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
   |||||||
DB 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
QY 210 GTCTCATCGCTCTGCGGGATCAGTCTGTCTCCCAAGGAACTGAACAGTTT 269
   |||||||
DB 210 GTCTCATCGCTCTGCGGGATCAGTCTGTCTCCCAAGGAACTGAACAGTTT 269
QY 270 GCATCAGCTGTGTGCAACACCCCTTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
   |||||||
DB 270 GCATCAGCTGTGTGCAACACCCCTTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
QY 330 CTGCTCTGGGCTCTCA 344
   |||||||
DB 330 CTGCTCTGGGCTCTCA 344

RESULT 7
ABL40345
ID ABL40345 standard; CDNA; 1619 BP.
XX
AC ABL40345;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 57887 extended CDNA.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KM ss.
XX
OS Homo sapiens.
XX
PN US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PF 03-APR-2001; 2001US-0825294.
XX
PR 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOL/) STOL J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
DR WPI: 2002-171027/22.
XX
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

```

PT prevention and/or treatment of cancer, especially ovarian cancer
XX
XX Claim 1a; Page 119-120; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the extended CDNA sequence of ovarian carcinoma
CC isolate 57887 given in record ABL48956.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 4.1e-158;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89
   |||||||
DB 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTTGAACGTTTGTGTGAGAAG 149
   |||||||
DB 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTTGAACGTTTGTGTGAGAAG 149
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
   |||||||
DB 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
QY 210 GTCTCATCGCTCTGCGGGATCAGTCTGTCTCCCAAGGAACTGAACAGTTT 269
   |||||||
DB 210 GTCTCATCGCTCTGCGGGATCAGTCTGTCTCCCAAGGAACTGAACAGTTT 269
QY 270 GCATCAGCTGTGTGCAACACCCCTTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
   |||||||
DB 270 GCATCAGCTGTGTGCAACACCCCTTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
QY 330 CTGCTCTGGGCTCTCA 344
   |||||||
DB 330 CTGCTCTGGGCTCTCA 344

RESULT 8
ABL40349
ID ABL40349 standard; CDNA; 1619 BP.
XX
AC ABL40349;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma 05915 nucleotide sequence.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KM ss.
XX
OS Homo sapiens.
XX
PN US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PF 03-APR-2001; 2001US-0825294.

```

[illegible]

AC	AAFG93845.
XX	
DT	23-MAY-2001 (first entry)
XX	
DE	Human cDNA encoding a membrane or secretory protein clone PSEC0181.
XX	
KW	Human; secretory protein; membrane protein; vaccine; gene therapy;
XX	rheumatoid arthritis; diabetes; ss.
OS	Homo sapiens.
PX	
PN	EPI067182-A2.
PD	
XX	10-JAN-2001.
PF	
XX	07-JUL-2000; 2000EP-0114090.
PR	
XX	08-JUL-1999; 99GP-0194179.
PR	11-JAN-2000; 2000JP-0118775.
XX	02-MAY-2000; 2000JP-0183766.
PA	(HELI-) HELIX RES INST.
PX	
P1	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
DR	WPI; 2001-093989/11.
XX	F-PADB; AAB88418.
CC	
PT	Nucleic acids encoding secretory proteins/membrane proteins, useful in
PS	gene therapy or as candidate target molecules in drug development -
XX	Claim 1; SEQ ID 203; 609BP + CD ROM; English.
XX	
CC	This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC	which encode human secretory or membrane proteins represented by
CC	AAB88317 - AAB88419. Included in the invention are primers
CC	AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC	cDNA sequences of the invention. The invention also includes methods for
CC	the production of antibodies directed against the proteins, and cDNA
CC	sequences, which can be used in vaccines. The polynucleotide sequences
CC	can be used in gene therapy. The polynucleotide sequences and the
CC	proteins they encode may be used in the prevention, treatment and
CC	diagnosis of diseases associated with inappropriate secretory
CC	protein/membrane protein expression. The nucleic acids and complementary
CC	sequences may also be used as DNA probes in diagnostic assays
CC	(e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC	presence of similar nucleic acid sequences in samples. They may also be
CC	used to study the expression and function of secretory proteins/membrane
CC	polypeptides and their role in metabolism. The polypeptides may be used
CC	as antigens in the production of antibodies against them and in assays to
CC	identify modulators (agonists and antagonists) of expression and
CC	activity. The antibodies and antagonists may also be used as therapeutic
CC	agents to down regulate expression and activity. The antibodies may also
CC	be used as diagnostic agents for detecting the presence of the
CC	polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC	(ELISA). Examples of diseases which may be treated include rheumatoid
CC	arthritis and diabetes.
XX	
SQ	Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other:
	Query Match 85.4%; Score 315; DB 22; Length 1890;
	Best Local Similarity 100.0%; Pred. NO. 4.2e-158;
	Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	30 CAGGCTTGGCGGTGCAAAATCCAGTGCTACCACTGTGAAGAATTCCAGTCGAACAACGACT 89
Db	323 CAGGCTTTGCCGTGCATAATCCAGTGCTACCACTGTGAAGAATTCCAGTCGAACAACGACT 382
OY	90 GCTCCTCCCCCGAGTTCATGTGAATTGACAGCGTGAAGCTTAACAACATGTGTCAGAAG 149
Db	383 GCTCCTCCCCCGAGTTCATGTGAATTGCACGCGTGAACGTTCAACACATGTGTCAGAAG 442
OY	150 AAGTAGTAGGAGCAAGTCCCGGATCATGTACCGCAAGTCCCTGCATCATCATAGGCGGCT 209

```

Db 443 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAGTCTGTGCTATCATCAGCGGCT 502
    |||
Oy 210 GGTCTATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTGAACTCAGTTT 269
    |||
Db 503 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTGAACTCAGTTT 562
    |||
Oy 270 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCCAAGGCCCCAAGAAAGGGGAAGTT 329
    |||
Db 563 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCCAAGGCCCCAAGAAAGGGGAAGTT 622
    |||
Oy 330 CTGCTCTGGGCTCTCA 344
    |||
Db 623 CTGCTCTGGGCTCTCA 637

```

RESULT 10

ABT03284
ID ABT03284 standard; cDNA; 1897 BP.

AC ABT03284;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI: 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Claim 2; Page 196; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

XX Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

SO Query Match 85.4%; Score 315; DB 24; Length 1897;

Best Local Similarity 100.0%; Pred. NO. 4.2e-158;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 CAGGCTTCCGCGCAATCCAGTGTACAGTGTGAAGATTCACCTGAAACGACT 89

Db 309 CAGGCTTCCGCGCAATCCAGTGTACAGTGTGAAGATTCACCTGAAACGACT 368

Oy 90 GCTCTCCCGCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGCAGAAAG 149

Db 369 GCTCTCCCGCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGCAGAAAG 428

```

Oy 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAGTCTGTGCTATCATCAGCGGCT 209
    |||
Db 429 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAGTCTGTGCTATCATCAGCGGCT 488
    |||
Oy 210 GGTCTATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTGAACTCAGTTT 269
    |||
Db 489 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTGAACTCAGTTT 548
    |||
Oy 270 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCCAAGGCCCCAAGAAAGGGGAAGTT 329
    |||
Db 549 GCATCAGCTGCTGCAACACCCCTTTGTGAACGGGCCCAAGGCCCCAAGAAAGGGGAAGTT 608
    |||
Oy 330 CTGCTCTGGGCTCTCA 344
    |||
Db 609 CTGCTCTGGGCTCTCA 623

```

RESULT 11

ABL40352
ID ABL40352 standard; cDNA; 1897 BP.

AC ABL40352;

DT 28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C/0591S consensus nucleotide sequence.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

FN Key Location/Qualifiers

FT CDS 260..685

FT /*tag= a

FT /product= "Ovarian carcinoma protein O1034C/0591S"

PN US2002004491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;

DR WPI: 2002-171027/22.

DR P-PSDB: ABB09417.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PT prevention and/or treatment of cancer, especially ovarian cancer

PS Claim 1a; Page 127-128; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides

CC that may be utilized in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are

CC useful for detecting a cancer in a patient, for stimulating and/or

CC expanding T-cells specific for a tumour protein, and for inhibiting the

CC development of a cancer in a patient. They are also useful for

CC stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their

CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polyptides in tumour cells. Polyptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma O1034C/0591S consensus
 CC nucleotide sequence.

XX Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

Query Match 85.4%; Score 315; DB 24; Length 1897;
 Best Local Similarity 100.0%; Pred. No. 4.2e-158;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCTGCAATCCAGTCACTGTCGTAAGATTCAGTGAACACGACT 89
 Db 309 CAGGCTTGGCTGCAATCCAGTCACTGTCGTAAGATTCAGTGAACACGACT 368
 QY 90 GCTCCCTCCCGAGTTCATTTGTAATTCACAGGTCGTAAGATTCAGTGAAC 149
 Db 369 GCTCCCTCCCGAGTTCATTTGTAATTCACAGGTCGTAAGATTCAGTGAAC 428
 QY 150 AAGTATGAGGACAAAGTCCGGGATTCATTCGCAAGTCTGTCATCATCAGCGCT 209
 Db 429 AAGTATGAGGACAAAGTCCGGGATTCATTCGCAAGTCTGTCATCATCAGCGCT 488
 QY 210 GTCATCATGCTGCTGCGGGATTCAGTCTTCTCCCAAGGAACTGACATCATTT 269
 Db 489 GTCATCATGCTGCTGCGGGATTCAGTCTTCTCCCAAGGAACTGACATCATTT 548
 QY 270 GCATCAGCTCTGCAACACCCCTCTTTTAAAGGGCCCAAGGCGGGAAGTT 329
 Db 549 GCATCAGCTCTGCAACACCCCTCTTTTAAAGGGCCCAAGGCGGGAAGTT 608
 QY 330 CTGCTCGGGCCCTCA 344
 Db 609 CTGCTCGGGCCCTCA 623

RESULT 12
 AAD18690/c
 ID AAD18690 standard; cDNA; 2528 BP.

XX AAD18690;

DT 18-DEC-2001 (first entry)

DE Human G protein coupled receptor (GPCR) 4941 cDNA.

KW Human: cardiovascular; tumourigenic disorder; aberrant angiogenesis;
 KW gene therapy; aberrant vascularisation; arteriosclerosis; ovarian cancer;
 KW ischaemia/reperfusion injury; hypertension; arterial inflammation;
 KW psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
 KW myocardial infarction; Grave's disease; G protein coupled receptor;
 KW GPCR 4941; vasotropic; hypotensive; antiinflammatory; cytostatic;
 KW antidiabetic; antipsoriatic; leukaemia; ss.

XX Homo sapiens.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 42..1403

FT /tag= a
 FT /product= "Human GPCR 4941"
 FT /note= "The CDS is specifically claimed in claim 1 of
 the specification"

XX WO200181634-A2.

XX 01-NOV-2001.

XX 25-APR-2001; 2001WO-US13788.

PR 26-APR-2000; 2000US-199908P.
 PR 09-AUG-2000; 2000US-0635521.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Galvin KA, Rudolph-owen LA;
 DR WPI: 2001-611743/70.
 DR P-PSDB: AAE11751.

PT Identifying nucleic acids for the diagnosis and treatment of
 PT cardiovascular and tumorigenic disorders, comprises identifying G
 PT protein coupled receptor (GPCR)-4941

PS Example 1; Fig 1; 118pp: English.

XX The present invention relates to a method for identifying a nucleic acid
 CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a
 CC cardiovascular or tumorigenic disorder. The method comprising contacting
 CC a sample containing a nucleic acid molecule with a hybridisation probe or
 CC amplification primers and detecting the presence. The invention is used
 CC in gene therapy. The method of the invention is used for identifying
 CC nucleic acids or polypeptides associated with a cardiovascular or
 CC tumorigenic disorder such as aberrant angiogenesis, aberrant
 CC vascularisation, arteriosclerosis, or ovarian cancer, ischaemia/
 CC reperfusion injury, hypertension, restenosis, arterial inflammation,
 CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
 CC infarction, Grave's disease and leukaemia. The methods can also detect
 CC mRNA or genomic DNA in a sample. The present sequence is G protein
 CC coupled receptor (GPCR) 4941 cDNA.

XX Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other;

Query Match 85.1%; Score 314; DB 22; Length 2528;
 Best Local Similarity 100.0%; Pred. No. 1.4e-157;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTGGCTGCAATCCAGTCACTGTCGTAAGATTCAGTGAACACGACTG 90
 Db 2217 AGGCTTGGCTGCAATCCAGTCACTGTCGTAAGATTCAGTGAACACGACTG 2158
 QY 91 CTCCTCCCGAGTTCATTTGTAATTCACAGGTCGTAAGATTCAGTGAAC 150
 Db 2157 CTCCTCCCGAGTTCATTTGTAATTCACAGGTCGTAAGATTCAGTGAAC 2098
 QY 151 AGTATGAGGACAAAGTCCGGGATTCATTCGCAAGTCTGTCATCATCAGCGCT 210
 Db 2097 AGTATGAGGACAAAGTCCGGGATTCATTCGCAAGTCTGTCATCATCAGCGCT 2038
 QY 211 TCTCATGCTCTGCGGGATTCAGTCTTCTCCCAAGGAACTGAACTCAGTTTG 270
 Db 2037 TCTCATGCTCTGCGGGATTCAGTCTTCTCCCAAGGAACTGAACTCAGTTTG 1978
 QY 271 CATCAGCTGTCGAACACCCCTCTTTTAAAGGGCCCAAGGCGGGAAGTTG 330
 Db 1977 CATCAGCTGTCGAACACCCCTCTTTTAAAGGGCCCAAGGCGGGAAGTTG 1918
 QY 331 TGCCTCGGGCCCTCA 344
 Db 1917 TGCCTCGGGCCCTCA 1904

RESULT 13
 AAF22400/c
 ID AAF22400 standard; cDNA; 1953 BP.

XX AAF22400;

DT 26-MAR-2001 (first entry)

DE Human secreted protein gene 28 SEQ ID NO:38.

KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;

KM antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KM cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KM fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KM rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KM cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing; skin aging;
KM food additive; preservative; ss.
XX
OS Homo sapiens.
XX
PM WO200061629-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000MO-US09071.
XX
PR 09-APR-1999; 99US-0128694.
PR 20-JAN-2000; 2000US-0176931.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-647420/62.
DR P-PSDB; AAB63161.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 1; Page 440; 533pp; English.
XX
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
XX to AAB63187. AAB63183 to AAB63231 represent more human secreted proteins
XX and polypeptides homologous to them. Human secreted proteins have
XX activities based on the tissues and cells the genes are expressed in.
XX Examples of activities include: immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
XX fungicide; and ophthalmological. The polynucleotides and proteins can be
XX used to prevent, treat or ameliorate a medical condition in e.g. humans,
XX mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
XX also used in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular
XX disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
XX ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's
XX disease, infections caused by bacteria, viruses and fungi and ocular
XX disorders e.g. corneal infection. The polypeptides can also be used to
XX aid wound healing and epithelial cell proliferation, to prevent skin
XX aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis. The polypeptides can also be used as a food additive or
XX preservative to increase or decrease storage capabilities. AAF22374 to
XX AAF22372 and AAB63133 represent sequences used in the exemplification of
XX the present invention.
XX
SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 76.7%; Score 283; DB 21; Length 1953;
Best Local Similarity 100.0%; Pred. No. 5,3e-141;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCGTTTCCGCTGCAAAATTCAGTGCACAGTGTGAAGATTCCAGCTGACAAACGACT 89
DB 1645 CAGGCTTTCCGCTGCAAAATTCAGTGCACAGTGTGAAGATTCCAGCTGACAAACGACT 1586
OY 90 GCCTCTCCCGCAGTTCATGTGTAATGACACGGTGAACGTTCAAGACATGTGTGAGAAG 149
DB 1585 GCTCTCTCCCGCAGTTCATGTGTAATGACACGGTGAACGTTCAAGACATGTGTGAGAAG 1526

OY 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCCT 209
DB 1525 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCCT 1466
OY 210 GTCATATGCGCCCTCTGCGGGGTACCACTCTTCTGCTGCCAGGGAATCACTCACTT 269
DB 1465 GTCATATGCGCCCTCTGCGGGGTACCACTCTTCTGCTGCCAGGGAATCACTCACTT 1406
OY 270 GCATCAGCTGCTGCAACACCCCTCTTGTACGGGGCAAGGCC 312
DB 1405 GCATCAGCTGCTGCAACACCCCTCTTGTACGGGGCAAGGCC 1363

RESULT 14
AAF64188/c
ID AAF64188 standard; cDNA; 1956 BP.
XX
AC AAF64188;
XX
DT 06-APR-2001 (first entry)
XX
DE Human secreted protein gene 13 SEQ ID NO:23.
XX
XX Human, secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
XX nootropic; neuroprotective; antibacterial; virucide; fungicide;
XX ophthalmological; vulnerability; autoimmune disease; cardiovascular disorder;
XX hyperproliferative disorders; cerebrovascular disorder; wound healing;
XX nervous system disorder; ocular disorder; skin aging; chemotaxis;
XX food additive; ss.
XX
OS Homo sapiens.
XX
PM WO200077026-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000MO-US14973.
XX
PR 11-JUN-1999; 99US-0138630.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-071258/08.
DR P-PSDB; AAB75318.
XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
XX Claim 1; Page 443-444; 542pp; English.
XX
XX Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide
XX sequences AAF64176 - AAF64224. The specification includes amino acid
XX sequences AAB75555 - AAB75606 which represent fragments of the human
XX secreted proteins, and protein sequences with which they share homology.
XX The proteins and polynucleotides, their agonists and antagonists have
XX activities dependent on the tissues and cells in which they are
XX expressed, examples of these activities include; immunosuppressive;
XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
XX vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
XX virucide; fungicide; ophthalmological; and vulnary. The proteins,
XX polynucleotides, agonists and antagonists can be used to treat or detect
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders
XX e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX infections caused by bacteria, viruses and fungi and ocular disorders
XX e.g. corneal infection. The polypeptides can also be used to aid wound

CC healing and epithelial cell proliferation, to prevent skin ageing due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which
CC are used in the isolation, identification and characterisation of the
CC proteins of the invention.

XX Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match 76.7%; Score 283; DB 22; Length 1956;

Best Local Similarity 100.0%; Pred. No. 5,3e-141; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGGCTGCAATTCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 89
DB 1645 CAGGCTTTCGGCTGCAATTCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 1586
QY 90 GCTCTCTCCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGCATGTGTCAAGAAG 149
DB 1585 GCTCTCTCCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGCATGTGTCAAGAAG 1526
QY 150 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 1525 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 1466
QY 210 GTCATTCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 269
DB 1465 GTCATTCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 1406
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCCAGGCC 312
DB 1405 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCCAGGCC 1363

RESULT 15

AAF94818
ID AAF94818 standard; cDNA; 396 BP.

XX AAF94818;

AC 23-MAY-2001 (first entry)

DE Human ovarian cancer associated coding sequence SEQ ID NO: 9.

XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

OS Homo sapiens.

PN WO200118046-A2.

PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24827.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA;

DR WPI; 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the
XX nucleic acids that encode them, useful for the prevention diagnosis and
XX treatment of ovarian cancers -
PS Claim 5; Page 119; 189pp; English.
XX

CC The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 76.2%; Score 281; DB 22; Length 396;

Best Local Similarity 100.0%; Pred. No. 6e-140; Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGGCTGCAATTCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 89
DB 40 CAGGCTTTCGGCTGCAATTCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 99
QY 90 GCTCTCTCCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGCATGTGTCAAGAAG 149
DB 100 GCTCTCTCCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGCATGTGTCAAGAAG 159
QY 150 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 160 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 219
QY 210 GTCATTCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 269
DB 220 GTCATTCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 279
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCCAGGCC 310
DB 280 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCCAGGCC 320

RESULT 16

ABT03085
ID ABT03085 standard; cDNA; 396 BP.

XX ABT03085;

AC 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;

DR WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX -
PS Example 1; Page 116; 197pp; English.
XX

CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:

Query Match 76.2%; Score 281; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e-140;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAAAATCCAGTGTACGAGTGTGAAGTAATCCAGCTGAACACGACT 89
DB 40 CAGGCTTTCGCTGCAAAATCCAGTGTACGAGTGTGAAGTAATCCAGCTGAACACGACT 99
QY 90 GCTCCCTCCCGAGTTCATGTGAATGACGAGTGAAGTTCAGACATGTGTGAGAAAG 149
DB 100 GCTCCCTCCCGAGTTCATGTGAATGACGAGTGAAGTTCAGACATGTGTGAGAAAG 159
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 209
DB 160 AAGTGTGAGCAAAAGTCCGGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 219
QY 210 GTCTCATTCGCTTGCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 269
DB 220 GTCTCATTCGCTTGCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 279
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAG 310
DB 280 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAG 320

RESULT 17

ABL48768
ID ABL48768 standard; cDNA; 396 BP.

XX ABL48768:

XX 18-JUN-2002 (first entry)

XX Ovarian carcinoma sequence isolate 21920.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.

OS Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOL/) STOLK J A.

XX (ALGA/) ALGATE P A.

XX (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP;

XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer,
XX Claim 1a; Page 41-42; 131pp; English.
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The sequences
CC given in records ABL48760-ABL48956 represent polynucleotides encoding
CC ovarian carcinoma proteins.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:

Query Match 76.2%; Score 281; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e-140;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAAAATCCAGTGTACGAGTGTGAAGTAATCCAGCTGAACACGACT 89
DB 40 CAGGCTTTCGCTGCAAAATCCAGTGTACGAGTGTGAAGTAATCCAGCTGAACACGACT 99
QY 90 GCTCCCTCCCGAGTTCATGTGAATGACGAGTGAAGTTCAGACATGTGTGAGAAAG 149
DB 100 GCTCCCTCCCGAGTTCATGTGAATGACGAGTGAAGTTCAGACATGTGTGAGAAAG 159
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 209
DB 160 AAGTGTGAGCAAAAGTCCGGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 219
QY 210 GTCTCATTCGCTTGCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 269
DB 220 GTCTCATTCGCTTGCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 279
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAG 310
DB 280 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAG 320

RESULT 18

ABF03282
ID ABF03282 standard; cDNA; 1010 BP.

XX ABF03282:

XX 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 212.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX cytoskeletal; gene; ss.

XX Homo sapiens.

XX WO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 XX
 PS Claim 2; Page 195; 197pp; English.
 XX
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 XX
 SQ Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;
 Query Match 73.4%; Score 271; DB 24; Length 1010;
 Best Local Similarity 100.0%; Pred. No. 1.4e-134;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 31 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGCTGAACAAGCAGCTG 90
 DB 258 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGCTGAACAAGCAGCTG 317
 OY 91 CTCCTCCCCAGATTCATGTGTAATGTCAGCGTGAACGTTCAAGCATGTGTGAGAAAGA 150
 DB 318 CTCCTCCCCAGATTCATGTGTAATGTCAGCGTGAACGTTCAAGCATGTGTGAGAAAGA 377
 OY 151 AGTGATGAGCAAGATGCGGGATCATGTACCGCAAGTCCTGTGATCATCAGCGGCTG 210
 DB 378 AGTGATGAGCAAGATGCGGGATCATGTACCGCAAGTCCTGTGATCATCAGCGGCTG 437
 OY 211 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGAATCAGTTTG 270
 DB 438 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGAATCAGTTTG 497
 OY 271 CATCAGCTGCTGCAACAACCCCTCTTTGTAAAC 301
 DB 498 CATCAGCTGCTGCAACAACCCCTCTTTGTAAAC 528
 RESULT 19
 ABL40350
 ID ABL40350 standard; cDNA; 1010 BP.
 XX
 AC ABL40350;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Ovarian carcinoma BF345141 nucleotide sequence.
 XX
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW ss.
 XX
 OS Homo sapiens.
 OS
 PN US2002004491-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 03-APR-2001; 2001US-0825294.
 XX
 PR 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XUJ/) XU J.
 PA (STOLK/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 XX
 PI XU J, Stolk JA, Algate PA, Fling SP;

XX
 DR WPI; 2002-171027/22.
 XX
 XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially ovarian cancer
 XX
 PS Claim 1a; Page 126-127; 131pp; English.
 XX
 CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour and
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma BF345141 nucleotide
 CC sequence.
 XX
 SQ Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;
 Query Match 73.4%; Score 271; DB 24; Length 1010;
 Best Local Similarity 100.0%; Pred. No. 1.4e-134;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 31 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGCTGAACAAGCAGCTG 90
 DB 258 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGCTGAACAAGCAGCTG 317
 OY 91 CTCCTCCCCAGATTCATGTGTAATGTCAGCGTGAACGTTCAAGCATGTGTGAGAAAGA 150
 DB 318 CTCCTCCCCAGATTCATGTGTAATGTCAGCGTGAACGTTCAAGCATGTGTGAGAAAGA 377
 OY 151 AGTGATGAGCAAGATGCGGGATCATGTACCGCAAGTCCTGTGATCATCAGCGGCTG 210
 DB 378 AGTGATGAGCAAGATGCGGGATCATGTACCGCAAGTCCTGTGATCATCAGCGGCTG 437
 OY 211 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGAATCAGTTTG 270
 DB 438 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGAATCAGTTTG 497
 OY 271 CATCAGCTGCTGCAACAACCCCTCTTTGTAAAC 301
 DB 498 CATCAGCTGCTGCAACAACCCCTCTTTGTAAAC 528
 RESULT 20
 AAF94044
 ID AAF94044 standard; DNA; 591 BP.
 XX
 AC AAF94044;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 478.
 XX
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes; PCR primer; ss.
 XX
 OS Synthetic.
 OS
 PN EP1067182-A2.
 PN 10-JAN-2001.
 PD
 PF 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-018775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 XX (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K.
 DR WPI: 2001-093989/11.
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 XX gene therapy or as candidate target molecules in drug development -
 XX
 PS Claim 4: SEQ ID 478; 609pp + CD ROM; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g., polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g., by enzyme linked immunosorbent assay
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 CC
 XX
 SQ Sequence 591 BP; 108 A; 198 C; 173 G; 109 T; 3 other;
 XX
 Query Match 59.9%; Score 221; DB 22; Length 591;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-108;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 30 CAGGCTTGGCGCTCAATCCAGTGTGAGAGATTCAGCTGAACAACGACT 89
 DB 323 CAGGCTTGGCGCTCAATCCAGTGTGAGAGATTCAGCTGAACAACGACT 382
 QY 90 GCTCCTCCCGGAGTTCATGTAATGCAAGGTAAGCAATGTCGAAGA 149
 DB 383 GCTCCTCCCGGAGTTCATGTAATGCAAGGTAAGCAATGTCGAAGA 442
 QY 150 AAGTATGAGAGCAAGTCCGGGATCATGTCAGCAAGTCTGTGCATCATCAGCGGCT 209
 DB 443 AAGTATGAGAGCAAGTCCGGGATCATGTCAGCAAGTCTGTGCATCATCAGCGGCT 502
 QY 210 GTCTCATGCGCTGTGCGGGTACCAAGTCTTGTCTCCCA 250
 DB 503 GTCTCATGCGCTGTGCGGGTACCAAGTCTTGTCTCCCA 543
 XX
 RESULT 21
 AB054231
 ID AB054231 standard; cDNA; 1608 BP.
 XX
 AC AB054231;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.

XX Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Blise CE, Rosen CA;
 XX
 DR WPI: 2002-147878/19.
 XX
 DR P-PSDB: ABP41154.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT used in the prevention, treatment and diagnosis of cancer (e.g.,
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 XX Claim 1: SEQ ID No 111; 2922pp; English.
 XX
 PS The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;
 XX
 Query Match 38.5%; Score 142; DB 24; Length 1608;
 Best Local Similarity 100.0%; Pred. No. 1, 2e-65;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGGT 230
DB 106 GGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGGT 165
QY 231 ACCAGTCTTCTCTCTCCCGGAGAACTGAACTGAGTTTGCATCAGCTGTGCAACACC 230
DB 166 ACCAGTCTTCTCTCTCCCGGAGAACTGAACTGAGTTTGCATCAGCTGTGCAACACC 225
QY 291 CTCTTTGTAAAGGCGGCAAGGCC 312
DB 226 CTCTTTGTAAAGGCGGCAAGGCC 247

RESULT 22
ABF03283
ID ABF03283 standard; cDNA; 480 BP.
XX
AC ABF03283;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX
KW Cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
PR 03-APR-2001; 2001US-0825294.
XX
PR 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX PA
XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX
XX PS Claim 2; Page 196; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
XX
XX Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;
XX

Query Match 31.7%; Score 117; DB 24; Length 480;
Best Local Similarity 99.4%; Pred. No. 2.8e-52;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAATTCAGTGTGAGAGAAATTCAGCTGAACAAGACT 89
DB 309 CAGGCTTTCGCTGCAATTCAGTGTGAGAGAAATTCAGCTGAACAAGACT 368
QY 90 GGTCTCCCGCGAGTTTCATGTGATGACGCTGAACCTTAAAGCATGTGTGAGAAG 149
DB 369 GGTCTCCCGCGAGTTTCATGTGATGACGCTGAACCTTAAAGCATGTGTGAGAAG 428
QY 150 AAGTATGAGCAAGTGCAGGATCATGTACCAAGTCTGTGCAT 197
XX

DB 429 AAGTATGAGCAAGTGCAGGATCATGTACCAAGTCTGTGCAT 476
RESULT 23
ABF0351
ID ABL40351 standard; cDNA; 480 BP.
XX
AC ABL40351;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma BE336607 nucleotide sequence.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.
XX
OS Homo sapiens.
XX
PN US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PF 03-APR-2001; 2001US-0825294.
XX
PR 10-SEP-1999; 99US-0394374.
XX
PR 01-MAY-2000; 2000US-0561778.
XX
PR 15-AUG-2000; 2000US-0640173.
XX
PR 07-SEP-2000; 2000US-0656668.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
XX (XUJ/) XU J.
XX (STOL/) STOLK J A.
XX (ALGA/) ALGATE P A.
XX (FLIN/) FLING S P.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP;
XX WPI: 2002-171027/22.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX
XX
XX PS Claim 1a; Page 127; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The current
XX sequence represents the ovarian carcinoma BE336607 nucleotide sequence.
XX

Query Match 31.7%; Score 117; DB 24; Length 480;
Best Local Similarity 99.4%; Pred. No. 2.8e-52;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAATTCAGTGTGAGAGAAATTCAGCTGAACAAGACT 89
DB 309 CAGGCTTTCGCTGCAATTCAGTGTGAGAGAAATTCAGCTGAACAAGACT 368
QY 90 GGTCTCCCGCGAGTTTCATGTGATGACGCTGAACCTTAAAGCATGTGTGAGAAG 149
DB 369 GGTCTCCCGCGAGTTTCATGTGATGACGCTGAACCTTAAAGCATGTGTGAGAAG 428
QY 150 AAGTATGAGCAAGTGCAGGATCATGTACCAAGTCTGTGCAT 197
XX

DB 369 GCNCTCCCCCGATGTCATGTGATTCGACGGTGAACGTTCAAGACATGCTGGAAG 428
OY 150 AAGTATGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAT 197
DB 429 AAGTATGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAT 476

RESULT 24
ABL81273
ID ABL81273 standard; cDNA; 430 BP.
XX
AC ABL81273;
XX
XX 17-MAY-2002 (first entry)
DE Human ovarian cancer related cDNA clone SEQ ID NO:4251.
XX
XX Human: ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200192581-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US17756.
XX
XX 26-MAY-2000; 2000US-207484P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Algate PA, Harlocker SL, Jones R;
XX
XX WPI; 2002-122075/16.
XX
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide -

Claim 1; SEQ ID 4251; 489pp; English.

XX
PS The present invention describes a composition (I) comprising: carriers
XX and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (31) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (32), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (31) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (31) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
XX techniques.

XX
SQ Sequence 430 BP; 92 A; 121 C; 108 G; 109 T; 0 other:

Query Match 14.9%; Score 55; DB 24; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 TCCCGAGGAACGACACAGTTCGATCAGCTGCTGCAACCCCTCTTGTGA 299
DB 1 TCCCGAGGAACGACACAGTTCGATCAGCTGCTGCAACCCCTCTTGTGA 55

RESULT 25
AAL07456/C
ID AAL07456 standard; DNA; 1226 BP.
XX
XX AAL07456;
XX
XX 21-NOV-2001 (first entry)
DE Human reproductive system related antigen DNA SEQ ID NO: 10144.
XX
XX Human: reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX WO200155320-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
XX
XX 04-FEB-2000; 2000US-0180628.
XX
XX 24-FEB-2000; 2000US-0184664.
XX
XX 02-MAR-2000; 2000US-0186350.
XX
XX 16-MAR-2000; 2000US-0189874.
XX
XX 17-MAR-2000; 2000US-0190076.
XX
XX 18-APR-2000; 2000US-0198123.
XX
XX 19-MAY-2000; 2000US-0205515.
XX
XX 07-JUN-2000; 2000US-0209467.
XX
XX 28-JUN-2000; 2000US-0214886.
XX
XX 30-JUN-2000; 2000US-0215135.
XX
XX 07-JUL-2000; 2000US-0216647.
XX
XX 07-JUL-2000; 2000US-0216880.
XX
XX 11-JUL-2000; 2000US-0217487.
XX
XX 11-JUL-2000; 2000US-0217496.
XX
XX 14-JUL-2000; 2000US-0218290.
XX
XX 26-JUL-2000; 2000US-0220963.
XX
XX 26-JUL-2000; 2000US-0220964.
XX
XX 14-AUG-2000; 2000US-0224518.
XX
XX 14-AUG-2000; 2000US-0224519.
XX
XX 14-AUG-2000; 2000US-0225213.
XX
XX 14-AUG-2000; 2000US-0225214.
XX
XX 14-AUG-2000; 2000US-0225266.
XX
XX 14-AUG-2000; 2000US-0225267.
XX
XX 14-AUG-2000; 2000US-0225268.
XX
XX 14-AUG-2000; 2000US-0225270.
XX
XX 14-AUG-2000; 2000US-0225447.
XX
XX 14-AUG-2000; 2000US-0225757.
XX
XX 14-AUG-2000; 2000US-0225758.
XX
XX 14-AUG-2000; 2000US-0225759.
XX
XX 14-AUG-2000; 2000US-0225759.
XX
XX 18-AUG-2000; 2000US-0226279.
XX
XX 22-AUG-2000; 2000US-0226681.
XX
XX 22-AUG-2000; 2000US-0226868.
XX
XX 22-AUG-2000; 2000US-0227182.
XX
XX 23-AUG-2000; 2000US-0227009.
XX
XX 30-AUG-2000; 2000US-0228924.
XX
XX 01-SEP-2000; 2000US-0229287.
XX
XX 01-SEP-2000; 2000US-0229343.
XX
XX 01-SEP-2000; 2000US-0229344.
XX
XX 01-SEP-2000; 2000US-0229345.
XX
XX 05-SEP-2000; 2000US-0229509.
XX
XX 05-SEP-2000; 2000US-0229513.
XX
XX 06-SEP-2000; 2000US-0230437.
XX
XX 06-SEP-2000; 2000US-0230438.
XX
XX 08-SEP-2000; 2000US-0231242.
XX
XX 08-SEP-2000; 2000US-0231243.
XX
XX 08-SEP-2000; 2000US-0231244.
XX
XX 08-SEP-2000; 2000US-0231413.
XX
XX 08-SEP-2000; 2000US-0231414.
XX
XX 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.	PR 01-DEC-2000; 2000US-0250160.
PR 12-SEP-2000; 2000US-0231968.	PR 01-DEC-2000; 2000US-0250391.
PR 14-SEP-2000; 2000US-0232397.	PR 05-DEC-2000; 2000US-0251030.
PR 14-SEP-2000; 2000US-0232398.	PR 05-DEC-2000; 2000US-0251988.
PR 14-SEP-2000; 2000US-0232399.	PR 05-DEC-2000; 2000US-0256719.
PR 14-SEP-2000; 2000US-0232400.	PR 06-DEC-2000; 2000US-0251479.
PR 14-SEP-2000; 2000US-0232401.	PR 08-DEC-2000; 2000US-0251856.
PR 14-SEP-2000; 2000US-0233063.	PR 08-DEC-2000; 2000US-0251868.
PR 14-SEP-2000; 2000US-0233064.	PR 08-DEC-2000; 2000US-0251869.
PR 21-SEP-2000; 2000US-0234223.	PR 08-DEC-2000; 2000US-0251889.
PR 21-SEP-2000; 2000US-0234224.	PR 08-DEC-2000; 2000US-0251990.
PR 25-SEP-2000; 2000US-0234997.	PR 11-DEC-2000; 2000US-0254097.
PR 25-SEP-2000; 2000US-0234998.	PR 05-JAN-2001; 2001US-0259678.
PR 26-SEP-2000; 2000US-0235484.	XX
PR 27-SEP-2000; 2000US-0235834.	PA (HUMA-) HUMAN GENOME SCI INC.
PR 27-SEP-2000; 2000US-0235836.	XX
PR 29-SEP-2000; 2000US-0236327.	PI Rosen CA, Barash SC, Ruben SM;
PR 29-SEP-2000; 2000US-0236367.	XX
PR 29-SEP-2000; 2000US-0236368.	DR WPI: 2001-465570/50.
PR 29-SEP-2000; 2000US-0236369.	XX
PR 29-SEP-2000; 2000US-0236370.	PT Isolated nucleic acid molecule encoding a reproductive system antigen
PR 02-OCT-2000; 2000US-0236802.	XX is used in preventing, treating or ameliorating a medical condition -
PR 02-OCT-2000; 2000US-0237037.	XX
PR 02-OCT-2000; 2000US-0237038.	PS Disclosure; SEQ ID NO 10144; 1297pp + Sequence Listing: English.
PR 02-OCT-2000; 2000US-0237039.	XX
PR 02-OCT-2000; 2000US-0237040.	CC The present invention provides the protein and coding sequences of a
PR 13-OCT-2000; 2000US-0239335.	CC number of human reproductive system related antigens. These can be used
PR 13-OCT-2000; 2000US-0239337.	CC in the prevention and treatment of reproductive system disorders,
PR 20-OCT-2000; 2000US-0240960.	CC including cancer. The present sequence is a genomic sequence encoding a
PR 20-OCT-2000; 2000US-0241221.	XX protein of the invention.
PR 20-OCT-2000; 2000US-0241785.	XX
PR 20-OCT-2000; 2000US-0241786.	SQ Sequence 1226 BP; 188 A; 438 C; 403 G; 197 T; 0 other;
PR 20-OCT-2000; 2000US-0241787.	
PR 20-OCT-2000; 2000US-0241808.	
PR 20-OCT-2000; 2000US-0241809.	
PR 20-OCT-2000; 2000US-0241826.	
PR 01-NOV-2000; 2000US-0244617.	
PR 08-NOV-2000; 2000US-0246474.	QY 317 AAAGGGAAGTTCGCT 335
PR 08-NOV-2000; 2000US-0246475.	
PR 08-NOV-2000; 2000US-0246476.	Db 977 AAAGGGAAGTTCGCT 959
PR 08-NOV-2000; 2000US-0246477.	
PR 08-NOV-2000; 2000US-0246478.	
PR 08-NOV-2000; 2000US-0246523.	
PR 08-NOV-2000; 2000US-0246524.	
PR 08-NOV-2000; 2000US-0246525.	
PR 08-NOV-2000; 2000US-0246526.	
PR 08-NOV-2000; 2000US-0246527.	
PR 08-NOV-2000; 2000US-0246528.	
PR 08-NOV-2000; 2000US-0246532.	
PR 08-NOV-2000; 2000US-0246609.	
PR 08-NOV-2000; 2000US-0246610.	
PR 08-NOV-2000; 2000US-0246611.	
PR 17-NOV-2000; 2000US-0249207.	
PR 17-NOV-2000; 2000US-0249208.	
PR 17-NOV-2000; 2000US-0249209.	
PR 17-NOV-2000; 2000US-0249210.	
PR 17-NOV-2000; 2000US-0249211.	
PR 17-NOV-2000; 2000US-0249212.	
PR 17-NOV-2000; 2000US-0249213.	
PR 17-NOV-2000; 2000US-0249214.	
PR 17-NOV-2000; 2000US-0249215.	
PR 17-NOV-2000; 2000US-0249216.	
PR 17-NOV-2000; 2000US-0249217.	
PR 17-NOV-2000; 2000US-0249218.	
PR 17-NOV-2000; 2000US-0249219.	
PR 17-NOV-2000; 2000US-0249244.	
PR 17-NOV-2000; 2000US-0249245.	
PR 17-NOV-2000; 2000US-0249264.	
PR 17-NOV-2000; 2000US-0249265.	
PR 17-NOV-2000; 2000US-0249287.	
PR 17-NOV-2000; 2000US-0249289.	
PR 17-NOV-2000; 2000US-0249299.	
PR 17-NOV-2000; 2000US-0249300.	

PA (ELIL) LILLY & CO ELLI.
 PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;
 XX WPI; 2002-304057/34.
 DR P-PSDB; AAU91328.
 XX
 PT Novel polypeptides and polynucleotides of secreted proteins useful for
 PT treating various diseases such as multiple sclerosis, cancer,
 PT autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's
 XX disease -
 PS Claim 1; Page 154-157; 235pp; English.
 XX
 CC The invention relates to a novel human secreted polypeptide having
 CC sequence 90% identical to the polypeptide sequences of LP105, LP061,
 CC LP224, LP240, LP239(a), LP243(b), LP253, LP218, LP251(a),
 CC LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP253(b),
 CC or LP223(b). Also included are the nucleic acids encoding the LP
 CC proteins (including complement, fragments encoding mature forms of the
 CC polypeptide or variant), a vector comprising the nucleic acid, a
 CC host cell comprising the vector, the preparation of the protein,
 CC an anti-LP antibody, and/agonists of LP and anti-LP-encoding mRNA
 CC ribozymes. The secreted protein or its agonist is useful in the
 CC manufacture of a medicament for treating a mammal suffering from a
 CC disease (and in diagnosis), condition or disorder associated with
 CC aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,
 CC arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,
 CC meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,
 CC mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid
 CC arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple
 CC sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,
 CC sleep patterns, balance, and perception. The secreted protein is further
 CC useful for identifying compounds that bind to the secreted protein. The
 CC present sequence encodes a novel secreted protein of the invention.
 CC
 SQ Sequence 2080 BP; 303 A; 758 C; 676 G; 342 T; 1 other;
 XX
 Query Match 5.1%; Score 19; DB 24; Length 2080;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 317 AAAAGGGGAAGTTCTGCTT 335
 Db 1811 AAAAGGGGAAGTTCTGCTT 1793
 XX
 RESULT 27
 ABK62081/c
 ID ABK62081 standard; cDNA: 2222 BP.
 XX
 AC ABK62081;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human cDNA encoding novel secreted protein LP243(b).
 XX
 KW Human; ss: gene: secreted protein; cancer; autoimmune disease;
 KW arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease;
 KW meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction;
 KW mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia;
 KW rheumatoid arthritis; hypothyroidism; allergic response; liver failure;
 KW multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;
 KW autism; panic disorder; learning disability; feeding disorder;
 KW sleep pattern disorder; balance; perception; Th1-dependent insulinitis;
 KW adult respiratory distress syndrome; ARDS.
 KW
 XX Homo sapiens.
 OS
 XX WO200214358-A2.
 PN

XX 21-FEB-2002.
 PD
 XX
 XX 30-JUL-2001; 2001WO-US21124.
 PF
 XX 11-AUG-2000; 2000US-224642P.
 PR
 XX 19-OCT-2000; 2000US-241779P.
 PR
 PA (ELIL) LILLY & CO ELLI.
 XX
 PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;
 XX WPI; 2002-304057/34.
 DR P-PSDB; AAU91329.
 XX
 PT Novel polypeptides and polynucleotides of secreted proteins useful for
 PT treating various diseases such as multiple sclerosis, cancer,
 PT autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's
 XX disease -
 PS Claim 1; Page 160-163; 235pp; English.
 XX
 CC The invention relates to a novel human secreted polypeptide having
 CC sequence 90% identical to the polypeptide sequences of LP105, LP061,
 CC LP224, LP240, LP239(a), LP243(b), LP253, LP218, LP251(a),
 CC LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP253(b),
 CC or LP223(b). Also included are the nucleic acids encoding the LP
 CC proteins (including complement, fragments encoding mature forms of the
 CC polypeptide or variant), a vector comprising the nucleic acid, a
 CC host cell comprising the vector, the preparation of the protein,
 CC an anti-LP antibody, and/agonists of LP and anti-LP-encoding mRNA
 CC ribozymes. The secreted protein or its agonist is useful in the
 CC manufacture of a medicament for treating a mammal suffering from a
 CC disease (and in diagnosis), condition or disorder associated with
 CC aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,
 CC arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,
 CC meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,
 CC mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid
 CC arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple
 CC sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive
 CC disorder, autism, panic disorder, learning disabilities, ALS
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,
 CC sleep patterns, balance, and perception. The secreted protein is further
 CC useful for identifying compounds that bind to the secreted protein. The
 CC present sequence encodes a novel secreted protein of the invention.
 CC
 SQ Sequence 2222 BP; 317 A; 827 C; 733 G; 345 T; 0 other;
 XX
 Query Match 5.1%; Score 19; DB 24; Length 2222;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 317 AAAAGGGGAAGTTCTGCTT 335
 Db 1953 AAAAGGGGAAGTTCTGCTT 1935
 XX
 RESULT 28
 ABL75913
 ID ABL75913 standard; cDNA: 237 BP.
 XX
 AC ABL75913;
 XX
 DT 14-MAY-2002 (first entry)
 XX
 DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5287.
 XX
 KW Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;
 KW inheritance; characteristic; growth; development; disease resistance;
 KW environmental adaptability; quality; yield; molecular marker;
 KW multigene trait; plant breeding; corn tassel; gene; ss.
 XX

OS Zea mays.
 XX
 PN US2001051335-A1.
 XX
 PD 13-DEC-2001.
 XX
 PF 16-APR-1999; 99US-0294093.
 XX
 PR 21-APR-1998; 98US-082567P.
 XX
 PA (LALG/) LALGUDI R V.
 XX (ITOL/) ITO L Y.
 XX (SHER/) SHERMAN B K.
 XX
 PI Laljudi RV, Ito LY, Sherman BK;
 XX
 DR WPI: 2002-163647/21.
 XX
 PT Novel purified corn tassell-derived polynucleotide useful for
 XX determining altered gene expression, to recover regulatory elements and
 PT to follow inheritance of desirable characteristics through hybrid
 PT breeding programs -
 PS
 PS Claim 1: SEQ ID 5287; 201pp: English.

CC The present sequence describes a purified corn tassell-derived
 CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
 CC selected from those given in ABL70627 to ABL76833. The cdps sequences
 CC encode corn tassell-derived polypeptides (CDPs). The cdps sequences (I)
 CC can be used for determining altered gene expression, to recover
 CC regulatory elements and to follow inheritance of desirable
 CC characteristics through hybrid breeding programs. (I) are also useful
 CC in the evaluation, and alteration of desired characteristics associated
 CC with growth and development, disease resistance, environmental
 CC adaptability, quality and yield, and as molecular markers for studying
 CC inheritance of multigene traits in a plant breeding program. (I) can be
 CC used to produce a tassell-specific profile of gene transcription, a
 CC transcript image, to clone regulatory elements for use in transformation
 CC vectors, to express a polypeptide, to identify, isolate or extend
 CC identical or related corn tassell nucleic acid sequences from DNA
 CC libraries, in nucleic acid hybridisation or amplification technologies,
 CC as query sequences to determine homology of known sequences, as probe
 CC for use in Southern or Northern hybridisation, and to identify the
 CC presence of and/or to determine the degree of similarity between two
 CC (or more) nucleic acid sequences.
 CC
 SQ Sequence 237 BP; 60 A; 64 C; 66 G; 46 T; 1 other;

Query Match 4.9%; Score 18; DB 24; Length 237;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209
 ||||||||||||||||
 DB 44 GTGCATCATCAGCGGCT 61

RESULT 29
 ABL76335
 ID ABL76335 standard; cDNA: 256 BP.

AC ABL76335;
 XX
 DT 14-MAY-2002 (first entry)

DE Corn tassell-derived polynucleotide (cdps) SEQ ID NO:5709.

XX Corn: corn tassell-derived polynucleotide; cdps; hybrid breeding; CDPs;
 XX inheritance; characteristic; growth; development; disease resistance;
 KW environmental adaptability; quality; yield; molecular marker;
 KM multigene trait; plant breeding; corn tassell; gene; ss.
 XX
 OS Zea mays.

XX
 PN US2001051335-A1.
 XX
 PD 13-DEC-2001.
 XX
 PF 16-APR-1999; 99US-0294093.
 XX
 PR 21-APR-1998; 98US-082567P.
 XX
 PA (LALG/) LALGUDI R V.
 XX (ITOL/) ITO L Y.
 XX (SHER/) SHERMAN B K.
 XX
 PI Laljudi RV, Ito LY, Sherman BK;
 XX
 DR WPI: 2002-163647/21.
 XX
 PT Novel purified corn tassell-derived polynucleotide useful for
 XX determining altered gene expression, to recover regulatory elements and
 PT to follow inheritance of desirable characteristics through hybrid
 PT breeding programs -
 PS
 PS Claim 1: SEQ ID 5709; 201pp: English.

CC The present sequence describes a purified corn tassell-derived
 CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
 CC selected from those given in ABL70627 to ABL76833. The cdps sequences
 CC encode corn tassell-derived polypeptides (CDPs). The cdps sequences (I)
 CC can be used for determining altered gene expression, to recover
 CC regulatory elements and to follow inheritance of desirable
 CC characteristics through hybrid breeding programs. (I) are also useful
 CC in the evaluation, and alteration of desired characteristics associated
 CC with growth and development, disease resistance, environmental
 CC adaptability, quality and yield, and as molecular markers for studying
 CC inheritance of multigene traits in a plant breeding program. (I) can be
 CC used to produce a tassell-specific profile of gene transcription, a
 CC transcript image, to clone regulatory elements for use in transformation
 CC vectors, to express a polypeptide, to identify, isolate or extend
 CC identical or related corn tassell nucleic acid sequences from DNA
 CC libraries, in nucleic acid hybridisation or amplification technologies,
 CC as query sequences to determine homology of known sequences, as probe
 CC for use in Southern or Northern hybridisation, and to identify the
 CC presence of and/or to determine the degree of similarity between two
 CC (or more) nucleic acid sequences.
 CC
 SQ Sequence 256 BP; 72 A; 60 C; 78 G; 42 T; 4 other;

Query Match 4.9%; Score 18; DB 24; Length 256;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209
 ||||||||||||||||
 DB 77 GTGCATCATCAGCGGCT 94

RESULT 30
 ABL75647
 ID ABL75647 standard; cDNA: 286 BP.

AC ABL75647;
 XX
 DT 14-MAY-2002 (first entry)

DE Corn tassell-derived polynucleotide (cdps) SEQ ID NO:5021.

XX Corn: corn tassell-derived polynucleotide; cdps; hybrid breeding; CDPs;
 XX inheritance; characteristic; growth; development; disease resistance;
 KW environmental adaptability; quality; yield; molecular marker;
 KM multigene trait; plant breeding; corn tassell; gene; ss.
 XX
 OS Zea mays.

PM US2001051335-A1.
XX
PD 13-DEC-2001.
XX
PF 16-APR-1999; 99US-0294093.
XX
PR 21-APR-1998; 98US-082567P.
XX
PA (LALG/) LALGUDI R V.
PA (ITOL/) ITO L Y.
PA (SHER/) SHERMAN B K.
PI Laljudi RV, Ito LY, Sherman BK;
DR WPI: 2002-163647/21.
XX
PT Novel purified corn tassel-derived polynucleotide useful for
PT determining altered gene expression, to recover regulatory elements and
PT to follow inheritance of desirable characteristics through hybrid
PT breeding programs -
XX
PS Claim 1; SEQ ID 5021; 201pp; English.
XX
CC The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL/0627 to ABL/6833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (1)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (1) are also useful
CC in the evaluation, and alteration of desired characteristics associated
CC with growth and development, disease resistance, environmental
CC adaptability, quality and yield, and as molecular markers for studying
CC inheritance of multigene traits in a plant breeding program. (1) can be
CC used to produce a tassel-specific profile of gene transcription, a
CC transcript image, to clone regulatory elements for use in transformation
CC vectors, to express a polypeptide, to identify, isolate or extend
CC identical or related corn tassel nucleic acid sequences from DNA
CC libraries, in nucleic acid hybridisation or amplification technologies,
CC as query sequences to determine homology of known sequences, as probe
CC for use in Southern or Northern hybridisation, and to identify the
CC presence of and/or to determine the degree of similarity between two
CC (or more) nucleic acid sequences.
XX
SQ Sequence 286 BP; 69 A; 74 C; 83 G; 52 T; 8 other:
Query Match 4.9%; Score 18; DB 24; Length 286;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 192 GTGCATCATCAGCGCCT 209
DB 58 GTGCATCATCAGCGCCT 75
RESULT 31
AAK66339/C
ID AAK66339 standard; DNA; 484 BP.
XX
AC AAK66339;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21151.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX WO200157182-A2.
PN
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-0501354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0225279.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0226886.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228287.
PR 01-SEP-2000; 2000US-0228343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.

PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226879.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231988.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PT
XX
PS Disclosure; SEQ ID NO 21152; 3071pp + Sequence Listing; English.
XX
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC to AAH87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAH54942 to AAH54950 and AAH82169
CC represent sequences used in the exemplification of the present invention.
XX

SO Sequence 484 BP; 124 A; 110 C; 69 G; 181 T; 0 other:

Query Match 4.9%; Score 18; DB 22; Length 484;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGTGAG 160
|||||
DB 457 CAGAAAGAGTGTGAG 440

RESULT 33

AAH52496/c
ID AAH52496 standard; DNA; 1152 BP.

AC AAH52496;

DT 03-SEP-2001 (first entry)

DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:385.

KM Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.

OS Staphylococcus epidermidis.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI Kimerly WJ;

DR WPI: 2001-316495/33.

DR P-PSDB; AAH81646.

PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 144; 2188pp; English.

CC AAH5304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAH81454 to AAH83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.

SO Sequence 1152 BP; 429 A; 169 C; 241 G; 313 T; 0 other;

Query Match 4.9%; Score 18; DB 22; Length 1152;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGCTGCAC 286
|||||
DB 864 TGCATCAGCTGCTGCAC 847

RESULT 34

AAH83729/c
ID AAH83729 standard; cDNA; 1542 BP.

AC AAH83729;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19533.

KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG19542.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID NO 19533; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAH64197-AAH94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1542 BP; 416 A; 434 C; 433 G; 259 T; 0 other;

Query Match 4.9%; Score 18; DB 23; Length 1542;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 143 CAGAAAGATGATGAG 160
 |||||
 DB 718 CAGAAAGATGATGAG 701

RESULT 35

ABN91962
 ID ABN91962 standard; DNA; 1587 BP.

AC ABN91962;
 XX

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1425.

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy; gene; ds.

XX Staphylococcus epidermidis.

OS US6380370-B1.

PN 30-APR-2002.

PF 13-AUG-1998; 98US-0134001.

PR 14-AUG-1997; 97US-055779P.

PA 08-NOV-1997; 97US-064964P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

DR P-PSDB; ABP39417.

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
 XX polypeptide, useful for diagnosing and treating bacterial infections -
 CC USPTO web site.

PS Disclosure; SEQ ID 1425; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP3960. The S. epidermidis sequences have

CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life
 CC cycle or inhibit S. epidermidis infection.

CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.

CC

CC

XX Sequence 1587 BP; 605 A; 231 C; 325 G; 426 T; 0 other;

Query Match 4.9%; Score 18; DB 24; Length 1587;
 Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 AATTCAGCTGACACACG 86
 |||||

DB 567 AATTCAGCTGACACACG 584

RESULT 36

ABN92620/c

ID ABN92620 standard; DNA; 1596 BP.

XX ABN92620;
 AC
 XX

DT 24-JUL-2002 (first entry)

XX Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2083.
 DE

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy; gene; ds.

XX Staphylococcus epidermidis.

OS US6380370-B1.

PN 30-APR-2002.

PF 13-AUG-1998; 98US-0134001.

PR 14-AUG-1997; 97US-055779P.

PA 08-NOV-1997; 97US-064964P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

DR P-PSDB; ABP40075.

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
 XX polypeptide, useful for diagnosing and treating bacterial infections -
 CC USPTO web site.

PS Disclosure; SEQ ID 2083; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP3960. The S. epidermidis sequences have

CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life
 CC cycle or inhibit S. epidermidis infection.

CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.

XX

XX

XX

XX Sequence 1596 BP; 616 A; 230 C; 327 G; 423 T; 0 other;

Query Match 4.9%; Score 18; DB 24; Length 1596;
 Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGCGCAC 286
 |||||

DB 1308 TGCATCAGCTGCGCAC 1291

RESULT 37

AACT4983
 ID AACT4983 standard; cDNA; 1633 BP.

AC AACT4983;
 AC

DT 08-FEB-2001 (first entry)

DE Human ORF538 polynucleotide sequence SEQ ID NO:1075.

XX Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; neuroprotective;
 KW anticonvulsant; osteopathic; antiarrhythmic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; anti-diabetic;
 KW hypotensive; dermatological; immunosuppressive; anti-inflammatory;
 KW antiviral; antibacterial; antifungal; antineoplastic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000MO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI: 2000-602362/57.
 DR P-PSDB; AAB40774.
 XX
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 1013-1014; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparasitic; antiparkinsonian; neotrophic; neuroprotective;
 CC osteoplastic; anticoagulant; antithrombotic; immunosuppressive;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antihypertensive; antidiabetic; antitumor; antineoplastic;
 CC antihypertensive; antidiabetic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease, to enhance
 CC coagulation, to inhibit thrombosis, and as a contraceptive.
 XX
 SQ Sequence 1633 BP; 335 A; 515 C; 480 G; 303 T; 0 other;
 XX
 Query Match 4.9%; Score 18; DB 21; Length 1633;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 231 ACCAGTCTTCTGCTCC 248
 DB 315 ACCAGTCTTCTGCTCC 332
 XX
 RESULT 38
 AAAS5968/c
 ID AAAS5968 standard; cDNA; 1791 BP.
 XX
 AC AAAS5968;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Murine G713 encoding cDNA SEQ ID NO:6.
 XX

KM Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia;
 KM diallelic marker; polymorphism; central nervous disease; detection;
 KM neuroleptic; G713 gene expression inhibitor; genotyping;
 KM brain disorder; psychiatric disorder; bipolar disorder; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200022122-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-IB01730.
 XX
 PR 13-OCT-1998; 98US-0103955.
 PR 30-OCT-1998; 98US-0106457.
 XX
 PA (GEST) GENSET.
 XX
 PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essieux L;
 XX
 DR WPI: 2000-317979/27.
 DR P-PSDB; AAY90963.
 XX
 XX Novel polynucleotide of human G713 gene useful for diagnosis and
 PT prophylactic treatment of brain, psychiatric disorders like
 PT schizophrenia and bipolar disorders -
 XX
 PS Claim 1; Page 234-236; 271pp; English.
 XX
 CC The present invention describes an isolated, purified or recombinant
 CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50
 CC nucleotides, where the span includes a G713 or chromosome 13q31-q33
 CC related diallelic marker. (I) has neuroleptic activity and can be used
 CC as a G713 gene expression inhibitor. (I) can be used genotyping to
 CC estimate the frequency of an allele of a G713 or chromosome 13q31-q33
 CC related diallelic marker in a population, and of a haplotype for a set
 CC of diallelic markers in a population. (I) is also useful in detecting
 CC an association between a haplotype and a trait. The frequency is used
 CC for detecting an association between a genotype and a trait being
 CC schizophrenia. The genotype is used to determine whether an individual
 CC is at risk of developing schizophrenia. (I) can also be used as a
 CC medication against several disorders preferably brain, psychiatric
 CC disorders such as schizophrenia and bipolar disorder. Early
 CC identification of risk of developing schizophrenia is possible, which
 CC would enable early and/or prophylactic treatment. AAAS5964 to AAAS5966
 CC represent human G713 genomic DNA sequences; AAAS5967 encodes the human
 CC G713 protein AAY90962; AAAS5968 encodes the murine G713 protein
 CC AAY90963; AAAS5992 to AAAS6030 represent human chromosome 13q31-q33 locus
 CC diallelic markers A12 to A49; AAAS5969 to AAAS5991, and AAAS6031 and
 CC AAAS6032 represent PCR primers used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 1791 BP; 389 A; 531 C; 508 G; 363 T; 0 other;
 XX
 Query Match 4.9%; Score 18; DB 21; Length 1791;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 84 ACGACTGCTCTCCCGG 101
 DB 695 ACGACTGCTCTCCCGG 678
 XX
 RESULT 39
 AAS91414/c
 ID AAS91414 standard; cDNA; 2253 BP.
 XX
 AC AAS91414;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #27218.
 XX

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABC27227.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1: SEQ ID NO 27218; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantifying a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AA564197-AA594364 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 2253 BP; 541 A; 612 C; 527 G; 573 T; 0 other;
Query Match 4.9%; Score 18; DB 23; Length 2253;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 CTCCTCCCCGAGTTCAT 108
XXXXXXXXXXXXXXXXXXXX
DB 739 CTCCTCCCCGAGTTCAT 722
XXXXXXXXXXXXXXXXXXXX
RESULT 40
AAH54960/C
ID AAH54960 standard; DNA; 3281 BP.
XX
XX AAH54960;
AC
XX
XX 03-SEP-2001 (first entry)
DT
XX
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:4324.
DE
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW
KW vaccination; endocarditis; ds.

XX
XX Staphylococcus epidermidis.
OS
XX
XX WO200134809-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30782.
XX
XX 09-NOV-1999; 99US-0164258.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Kimmery NJ;
XX
XX WPI: 2001-316495/33.
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
PT
XX
XX Claim 8: Page 2062-2063; 2180bp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX (II), given in AA68154 to AA683120, from Staphylococcus epidermidis.
XX (I) and (II) can have antibacterial activity and therefore can be used
XX in vaccination. The nucleic acids (I) may be used to produce the
XX S. epidermidis polypeptides (II) via the production of vectors
XX containing them which are used to produce host cells which express the
XX polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX used to vaccinate subjects and to raise antibodies against the bacteria.
XX The polypeptides may also be used to assay for other inhibitors of their
XX activity and therefore identify compounds that may be used for the
XX treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX polynucleotide sequences from the present invention. AAH55091 to
XX AAH55098 represent oligonucleotide sequences and primers which are used
XX in the exemplification of the present invention.
XX N.B. The present invention specifically claims all the polynucleotide
XX sequence given in the sequence listing of the present specification,
XX however the sequence listing only goes up to SEQ ID NO:4454 so even
XX though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
SQ Sequence 3281 BP; 1226 A; 464 C; 636 G; 955 T; 0 other;
Query Match 4.9%; Score 18; DB 22; Length 3281;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 269 TGCATCAGCTGTCGAAC 286
XXXXXXXXXXXXXXXXXXXX
DB 1118 TGCATCAGCTGTCGAAC 1101
XXXXXXXXXXXXXXXXXXXX
RESULT 41
AAI59883
ID AAI59883 standard; cDNA; 3556 BP.
XX
XX AAI59883;
AC
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polynucleotide SEQ ID NO 3872.
DE
XX
XX Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
XX

PN WO200153312-A1.
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000WO-US34263.
PF
XX
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR P-PSDB; AAM40727.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 3872; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 3556 BP; 776 A; 1071 C; 1057 G; 652 T; 0 other;
SQ
Query Match 4.9%; Score 18; DB 22; Length 3556;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 ACCAGTCTCTGCTGCC 248
DB 629 ACCAGTCTCTGCTGCC 646
|||||
AAH54943/c
ID AAH54943 standard; DNA; 3633 BP.
XX
XX AAH54943;
AC
XX
XX 03-SEP-2001 (first entry)
DT
XX
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:4307.
DE
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
XX Staphylococcus epidermidis.
OS
XX
XX WO200134809-A2.
PN

XX
XX 17-MAY-2001.
PD
XX
XX 09-NOV-2000; 2000WO-US30782.
PF
XX
XX 09-NOV-1999; 99US-0164258.
PR
XX
XX (GLAXO) GLAXO GROUP LTD.
PA
XX
XX Kimmery WJ;
PI
XX
XX WPI: 2001-316495/33.
DR
XX
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
XX Claim 8; Page 2042-2043; 2188bp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454, so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 3633 BP; 1340 A; 498 C; 707 G; 1088 T; 0 other;
SQ
Query Match 4.9%; Score 18; DB 22; Length 3633;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 269 TGCATCAGCTGCTGCAAC 286
DB 1763 TGCATCAGCTGCTGCAAC 1746
|||||
AAH54174/c
ID AAH54174 standard; DNA; 4106 BP.
XX
XX AAH54174;
AC
XX
XX 03-SEP-2001 (first entry)
DT
XX
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3538.
DE
XX
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
KW vaccination; endocarditis; ds.
XX
XX Staphylococcus epidermidis.
OS
XX
XX WO200134809-A2.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 09-NOV-2000; 2000WO-US30782.
PF
XX
XX 09-NOV-1999; 99US-0164258.
PR
XX
XX

PA (GLAX) GLAXO GROUP LTD.
XX
PI Kimerly MJ;
XX
DR WPI; 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8; Page 1118-1119; 2188pp; English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG61454 to AAG63120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 4106 BP; 1436 A; 659 C; 643 G; 1368 T; 0 other;
XX
Query Match 4.9%; Score 18; DB 22; Length 4106;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 269 TGCATCAGCTGCTGCAAC 286
DB 2916 TGCATCAGCTGCTGCAAC 2899
XXXXXXXXXXXXXXXX
RESULT 44
ABLI3144/C
ID ABLI3144 standard; cDNA; 6399 BP.
XX
AC ABLI3144;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33914.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB69041.

XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 33914; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU57737-ABU72072) and the encoded proteins
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6399 BP; 1706 A; 1543 C; 1399 G; 1751 T; 0 other;
XX
Query Match 4.9%; Score 18; DB 23; Length 6399;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 GTGAATTGCACGGTGAAC 127
DB 5810 GTGAATTGCACGGTGAAC 5793
XXXXXXXXXXXXXXXX
RESULT 45
ABLI5972/C
ID ABLI5972 standard; cDNA; 8268 BP.
XX
AC ABLI5972;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42398.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB71869.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 42398; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA

476

CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 8268 BP: 2539 A; 1758 C; 1674 G; 2297 T; 0 other;

Query Match 4.9%; Score 18; DB 23; Length 8268;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GTGAATGCACGGTGAC 127
 ||||||||||||||||
 Db 837 GTGAATGCACGGTGAC 820

Search completed: November 7, 2002, 18:15:15
 Job time : 90.6545 secs

ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2083

Query Match 4.9%; Score 18; DB 4; Length 1596;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 TGCATCAGCTGCTGCAC 286
Db 1308 TGCATCAGCTGCTGCAC 1291

RESULT 3
US-09-134-001C-263/C
Sequence 263, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 263
LENGTH: 393
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-263

Query Match 4.6%; Score 17; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCATTTGTGATTCACG 121
Db 389 TCATTTGTGATTCACG 373

RESULT 4
US-09-221-017B-627
Sequence 627, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P11182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P11546
FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 627:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1...603
US-09-221-017B-627

Query Match 4.6%; Score 17; DB 4; Length 603;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 AAGTCCTGTCATCATC 201
Db 104 AAGTCCTGTCATCATC 120

RESULT 5
US-08-532-828B-11/C
Sequence 11, Application US/08532828B
Patent No. 5688671
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: OGAWA, Yuri
APPLICANT: SUZUKI, Tomoko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,828B
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-764-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1263 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
US-08-532-828B-11

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 1263;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 720 CAAAGTCCGGGATCAT 704

RESULT 6
US-08-532-828B-12/c
Sequence 12, Application US/08532828B
Patent No. 5688671
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: OGAWA, Yuri
APPLICANT: SUZUKI, Tomoko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532.828B
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-764-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1263 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: AJ3463
US-08-532-828B-12

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 1263;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 720 CAAAGTCCGGGATCAT 704

RESULT 7
US-08-532-828B-1/c
Sequence 1, Application US/08532828B
Patent No. 5688671
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: OGAWA, Yuri
APPLICANT: SUZUKI, Tomoko
APPLICANT: TANAKA, Akiko
APPLICANT: MATSUI, Hiroshi
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532.828B
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-764-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC 13869
US-08-532-828B-1

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 1643;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: AJ3463
FEATURE:
NAME/KEY: mat peptide
LOCATION: 964..1482
US-08-532-828B-10

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 13
US-08-700-359-7/c
Sequence 7, Application US/08700359
Patent No. 5766925
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: USUDA, YOSHIHIRO
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-819-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC 13869
US-08-700-359-7

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 14
US-08-700-359-8/c
Sequence 8, Application US/08700359
Patent No. 5766925
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: USUDA, YOSHIHIRO
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-819-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat peptide
LOCATION: 217..1479
IDENTIFICATION METHOD: S
US-08-700-359-8

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177

Db 936 CAAAGTCCGGGATCAT 920

RESULT 15

US-08-700-359-10/C

; Sequence 10, Application US/08700359
; Patent No. 5766925

GENERAL INFORMATION:

APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: USUDA, YOSHIHIRO
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKIRO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-819-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1643
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat peptidase
LOCATION: 964..1479
LOCATION: S
US-08-700-359-10

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177
Db 936 CAAAGTCCGGGATCAT 920

RESULT 16

US-08-674-168-21/C

; Sequence 21, Application US/08674168
; Patent No. 5604414
; GENERAL INFORMATION:
; APPLICANT: MORIYA, MIKA

APPLICANT: MATSUI, HIROSHI
APPLICANT: YOKOZEKI, KENZO
APPLICANT: HIRANO, SEIKO
APPLICANT: HAYAKAWA, ATSUSHI
APPLICANT: IZUI, MASAKO
APPLICANT: SUGIMOTO, MASAKAZU
TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
ARTIFICIAL TRANSPOSON
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,168
FILING DATE: 01-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
US-08-674-168-21

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177
Db 936 CAAAGTCCGGGATCAT 920

RESULT 17

US-08-596-366-5/C

; Sequence 5, Application US/08596366
; Patent No. 5876983

GENERAL INFORMATION:

APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsura
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,366
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 217..1482
US-08-596-366-5

Query Match 4.6%; Score 17; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
Db 936 CAAAGTCCGGGATCAT 920

RESULT 18
US-08-596-366-7/C
Sequence 7, Application US/08596366
Patent No. 5876983
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsura
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER, & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,366
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 964..1482
US-08-596-366-7

Query Match 4.6%; Score 17; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
Db 936 CAAAGTCCGGGATCAT 920

RESULT 19
US-08-967-104-5/C
Sequence 5, Application US/08967104
Patent No. 5919694
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsura
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER, & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,104
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,366
FILING DATE: 29-APR-1996
APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 217..1482
US-08-967-104-5

Query Match 4.6%; Score 17; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 20
US-08-967-104-7/c
Sequence 7, Application US/08967104
Patent No. 5919694
GENERAL INFORMATION:
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: IZUI, Katsura
TITLE OF INVENTION: MUTANT PHOSPHENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT, P.C.
ADDRESS: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,104
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,366
FILING DATE: 29-APR-1996
APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-784-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 964..1482
US-08-967-104-7

Query Match 4.6%; Score 17; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 21
US-08-985-908-3/c
Sequence 3, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
US-08-985-908-3

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 22
US-08-985-908-4/c
Sequence 4, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI NA
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869

FEATURE:
NAME/KEY: CDS
LOCATION: 217..1482
US-08-985-908-4

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 23
US-08-985-908-6/c
Sequence 6, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 964..1482
US-08-985-908-6

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 24
US-08-852-730-12/c
Sequence 12, Application US/08852730

Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: Brevibacterium lactofermentum
STRAIN: ATCC 13869
US-08-852-730-12

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 25
US-08-852-730-13/c
Sequence 13, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1482
US-08-852-730-13

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 26
US-08-852-730-15/c
Sequence 15, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 964..1482
US-08-852-730-15

Query Match 4.6%; Score 17; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 27

US-08-985-916-3/C
Sequence 3, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
ZIP: 22152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
US-08-985-916-3

Query Match 4.6%; Score 17; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 28

US-08-985-916-4/C
Sequence 4, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
ZIP: 22152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1482
US-08-985-916-4

Query Match 4.6%; Score 17; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177
|||||
DB 936 CAAAGTCCGGGATCAT 920

RESULT 29

US-08-985-916-6/C
Sequence 6, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
ZIP: 22152
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 964..1482
US-08-985-916-6

Query Match 4.6%; Score 17; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAGTGGCGGATCAT 177
|||||
DB 936 CAAGTGGCGGATCAT 920

RESULT 30
US-08-836-022A-10/c
Sequence 10, Application US/08836022A
Patent No. 6001557
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-836-022A-10

Query Match 4.6%; Score 17; DB 3; Length 19307;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAAGTGTGAGCA 163
|||||
DB 3516 AAGAAGTGTGAGCA 3500

RESULT 31
US-09-427-048A-10/c
Sequence 10, Application US/09427048A
Patent No. 6203975
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10

Query Match 4.6%; Score 17; DB 4; Length 19307;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 AAGAGTGTGAGCA 163
DB 3516 AAGAGTGTGAGCA 3500

RESULT 32

US-09-094-287-8/c
Sequence 8, Application US/09094287
Patent No. 6084071
GENERAL INFORMATION:
APPLICANT: Racie, Lisa
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide
TITLE OF INVENTION: Encoding Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,287
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "EST sequence"
US-09-094-287-8

Query Match 4.3%; Score 16; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGTGCA 284
DB 256 TGCATCAGCTGTGCA 241

RESULT 33

US-09-094-287-1/c
Sequence 1, Application US/09094287
Patent No. 6084071
GENERAL INFORMATION:
APPLICANT: Racie, Lisa
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide
TITLE OF INVENTION: Encoding Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,287
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 80..481
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 149..481
US-09-094-287-1

Query Match 4.3%; Score 16; DB 3; Length 908;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGTGCA 284
DB 342 TGCATCAGCTGTGCA 327

RESULT 34

US-09-094-287-3/c
Sequence 3, Application US/09094287
Patent No. 6084071
GENERAL INFORMATION:
APPLICANT: Racie, Lisa
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide
TITLE OF INVENTION: Encoding Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,287
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 85..519
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..519
US-09-094-287-3

Query Match
Best Local Similarity 100.0%; Score 16; DB 3; Length 932;
Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284
|||||
DB 347 TGCATCAGCTGCTGCA 332

RESULT 35
US-09-612-964-1
Sequence 1, Application US/09612964
Patent No. 6403342
GENERAL INFORMATION:
APPLICANT: Gussatiner Mikhail Markovich
APPLICANT: Lunts Maria Grigorievna
APPLICANT: Kozlov Yuri Ivanovich
APPLICANT: Ivanovskaya Larina Valerievna
APPLICANT: Voroshilova Elvira Borisovna
TITLE OF INVENTION: DNA CODING FOR MUTANT ISOPROPYLMALATE SYNTHASE,
TITLE OF INVENTION: L-LEUCINE-PRODUCING MICROORGANISM AND METHOD FOR PRODUCING
FILE REFERENCE: 193845USO
CURRENT APPLICATION NUMBER: US/09/612,964
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: RU 99114325
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 1
LENGTH: 1572
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1569)
US-09-612-964-1

Query Match
Best Local Similarity 100.0%; Score 16; DB 4; Length 1572;
Pred. No. 49;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ATCAACAGCGGCGCTGT 211
|||||
DB 547 ATCAACAGCGGCGCTGT 562

RESULT 36
US-08-062-472B-2
Sequence 2, Application US/08062472B
Patent No. 5655954
GENERAL INFORMATION:
APPLICANT: Sherwood, Nancy G M

APPLICANT: Parker, David B
APPLICANT: McRoy, John E
APPLICANT: Lescheid, David W
TITLE OF INVENTION: DNA ENCODING TWO FISH NEUROPEPTIDES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUQUIST, SPARKMAN, CAMPBELL, LEIGH &
ADDRESS: WINSTON, LLP
STREET: ONE WORLD TRADE CENTER, SUITE 1600, 121 S.W.
STREET: SALMON STREET
CITY: PORTLAND
STATE: OREGON
COUNTRY: USA
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/062,472B
FILING DATE: 14-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POLLEY, RICHARD J
REGISTRATION NUMBER: 28107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-062-472B-2

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 2502;
Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 TTGCATCAGCTGCTGC 283
|||||
DB 1142 TTGCATCAGCTGCTGC 1157

RESULT 37
US-09-461-697-359
Sequence 359, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COSENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Purnam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: fastseq for Windows Version 4.0
SEQ ID NO 359
LENGTH: 2702
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-359

Query Match 4.3%; Score 16; DB 4; Length 2702;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 260 AACTCAGTTTCATCA 275
 |||||||
 Db 2500 AACTCAGTTTCATCA 2515

RESULT 38

US-09-453-702B-258
 ; Sequence 258, Application US/09453702B
 ; Patent No. 6365723
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 ; Burland, Nicole T.
 ; Plunkett, Guy
 ; Welch, Rod
 ; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Quarles & Brady
 ; STREET: 1 South Pinckney Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: US
 ; ZIP: 53701-2113
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 Inch, 1.44Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 8.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/453,702B
 ; FILING DATE: 03-Dec-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/110,955
 ; FILING DATE: 04-DEC-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J.
 ; REGISTRATION NUMBER: 27386
 ; REFERENCE/DOCKET NUMBER: 960296, 95017
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 251-5000
 ; TELEFAX: (608) 251-9166
 ; INFORMATION FOR SEQ ID NO: 258:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8729 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
 ; US-09-453-702B-258

Query Match 4.3%; Score 16; DB 4; Length 8729;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 311 CCCAAGAAAGGGGAA 326
 |||||||
 Db 371 CCCAAGAAAGGGGAA 386

RESULT 39

US-09-338-907-183/C
 ; Sequence 183, Application US/09338907
 ; Patent No. 6265546
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta

APPLICANT: Ilya, Chumakov
 ; APPLICANT: Bougueleret, Lydie
 ; TITLE OF INVENTION: PROSTATE CANCER GENE
 ; FILE REFERENCE: GENSET, 18CPICP
 ; CURRENT APPLICATION NUMBER: US/09/338,907
 ; CURRENT FILING DATE: 1999-06-23
 ; EARLIER APPLICATION NUMBER: 08/996,306
 ; EARLIER FILING DATE: 1997-12-22
 ; EARLIER APPLICATION NUMBER: 60/099,658
 ; EARLIER FILING DATE: 1998-09-09
 ; EARLIER APPLICATION NUMBER: 09/218,207
 ; EARLIER FILING DATE: 1998-12-22
 ; NUMBER OF SEQ ID NOS: 578
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 183
 ; LENGTH: 37950
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 5259..5328
 ; OTHER INFORMATION: exon2
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 12675..12791
 ; OTHER INFORMATION: exon3
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 14621..14710
 ; OTHER INFORMATION: exon4
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 19822..19912
 ; OTHER INFORMATION: exon5
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 21789..21950
 ; OTHER INFORMATION: exon6
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 23387..23510
 ; OTHER INFORMATION: exon7
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 25520..26016
 ; OTHER INFORMATION: exon8
 ; US-09-338-907-183

Query Match 4.3%; Score 16; DB 4; Length 37950;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 TCAGAAAGAGTGATG 157
 |||||||
 Db 34677 TCAGAAAGAGTGATG 34662

RESULT 40

US-09-218-207-183/C
 ; Sequence 183, Application US/09218207
 ; Patent No. 6346381
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Ilya, Chumakov
 ; APPLICANT: Bougueleret, Lydie
 ; TITLE OF INVENTION: Prostate cancer gene
 ; FILE REFERENCE: GENSET, 018CPI
 ; CURRENT APPLICATION NUMBER: US/09/218,207
 ; CURRENT FILING DATE: 1998-12-22
 ; EARLIER APPLICATION NUMBER: 08/996,306
 ; EARLIER FILING DATE: 1997-12-22
 ; EARLIER APPLICATION NUMBER: 60/099,658

EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 183
LENGTH: 37950
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: exon
LOCATION: 5259..5328
OTHER INFORMATION: exon2
FEATURE:
NAME/KEY: exon
LOCATION: 12675..12791
OTHER INFORMATION: exon3
FEATURE:
NAME/KEY: exon
LOCATION: 14621..14710
OTHER INFORMATION: exon4
FEATURE:
NAME/KEY: exon
LOCATION: 19822..19912
OTHER INFORMATION: exon5
FEATURE:
NAME/KEY: exon
LOCATION: 21789..21950
OTHER INFORMATION: exon6
FEATURE:
NAME/KEY: exon
LOCATION: 23387..23510
OTHER INFORMATION: exon7
FEATURE:
NAME/KEY: exon
LOCATION: 25520..26016
OTHER INFORMATION: exon8
US-09-218-207-183

Query Match
Best Local Similarity 4.3%; Score 16; DB 4; Length 37950;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 142 TCAGAAAGAAGTGTG 157
DB 34677 TCAGAAAGAAGTGTG 34662

RESULT 41
US-08-920-422-17
Sequence 17, Application US/08920422A
Patent No. 6255473
GENERAL INFORMATION:
APPLICANT: Vittek, Michael P.
APPLICANT: Mitsuda, No. 62554731aki
APPLICANT: Roses, Allen D.
TITLE OF INVENTION: Presenilin-1 Gene Promoter
FILE REFERENCE: VITEKPRESENTIN
CURRENT APPLICATION NUMBER: US/08/920,422A
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 48974
TYPE: DNA
ORGANISM: Mus musculus
US-08-920-422-17

Query Match
Best Local Similarity 4.3%; Score 16; DB 4; Length 48974;
Matches 16; Conservative 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 140 TGTCTGAAAGAAGTGA 155
DB 43070 TGTCTGAAAGAAGTGA 43085

RESULT 42
US-09-009-913-1
Sequence 1, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AXY'S Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 72928 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-009-913-1

Query Match
Best Local Similarity 4.3%; Score 16; DB 3; Length 72928;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 45 AAATCCAGTGTACCA 60
DB 42450 AAATCCAGTGTACCA 42465

RESULT 43
US-09-453-702B-57
Sequence 57, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
APPLICANT: Burland, Valerie
APPLICANT: Perna, Nicole T.
APPLICANT: Plunkett, Guy
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plunkett Street
CITY: Madison
STATE: WI
COUNTRY: US

ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-Dec-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296, 95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 87563
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-453-702B-57

Query Match 4.3%; Score 16; DB 4; Length 87563;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 CCCAGAGAAAGGGAA 326
|||||
Db 19587 CCCAGAGAAAGGGAA 19602

RESULT 44
US-08-368-803-21
Sequence 21, Application US/08368803
Patent No. 5733554
GENERAL INFORMATION:
APPLICANT: AUDONNET, Jean-Christophe F
APPLICANT: BOULOT, Michel J
APPLICANT: DARTIEL, Raphael J
APPLICANT: DUINAT, Carole V
APPLICANT: LAPLACE, Eliane L
APPLICANT: RIVIERE, Michel A
TITLE OF INVENTION: Avian Herpesvirus-based live recombinant avian
TITLE OF INVENTION: vaccine, in particular against Gamboro disease
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LARSON AND TAYLOR
STREET: 727 SOUTH 23RD STREET
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,803
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SARRO, Thomas
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 920-7200

TELEFAX: (703) 892-8428
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-368-803-21

Query Match 4.1%; Score 15; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGGCC 208
|||||
Db 3 GCATCATCAGCGGCC 17

RESULT 45
US-08-578-096A-22
Sequence 22, Application US/08578096A
Patent No. 5980906
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Avian herpesvirus-based live recombinant
TITLE OF INVENTION: avian vaccine
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,096A
FILING DATE:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-578-096A-22

Query Match 4.1%; Score 15; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGGCC 208
|||||
Db 3 GCATCATCAGCGGCC 17

Search completed: November 7, 2002, 23:12:13
Job time : 123.827 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 23:08:43 ; Search time 16.0364 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggcacacttttcggatgtt.....tggctcgcacacacatcct 369

Scoring table: OLIGO-MNC
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 10

Total number of hits satisfying chosen parameters: 83090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications-NA:*

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- 2: /cgn2_6/ptoddata/2/pubpna/PCN_NEW_PUB.seq:*
- 3: /cgn2_6/ptoddata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptoddata/2/pubpna/US06_PUBCOMB.seq:*
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- 10: /cgn2_6/ptoddata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptoddata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptoddata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptoddata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptoddata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	US-09-825-294-199	Sequence 199, App
2	315	85.4	1619	US-09-825-294-205	Sequence 205, App
3	315	85.4	1619	US-09-825-294-211	Sequence 211, App
4	315	85.4	1897	US-09-825-294-214	Sequence 214, App
5	281	76.2	396	US-09-825-294-8	Sequence 9, Appli
6	271	73.4	1010	US-09-825-294-212	Sequence 212, App
7	117	31.7	480	US-09-825-294-213	Sequence 213, App
8	55	14.9	430	US-09-867-701-4251	Sequence 4251, Ap
9	18	4.9	237	US-09-294-093B-5287	Sequence 5287, Ap
10	18	4.9	286	US-09-294-093B-5709	Sequence 5709, Ap
11	18	4.9	256	US-09-294-093B-5021	Sequence 5021, Ap
12	18	4.9	1791	US-09-416-384A-6	Sequence 6, Appli
13	17	4.6	1298	US-09-925-300-682	Sequence 682, App
14	17	4.6	1713	US-09-815-242-7853	Sequence 7853, Ap
15	17	4.6	2649	US-09-815-242-6571	Sequence 6571, Ap
16	17	4.6	6252	US-09-964-824A-313	Sequence 313, App
17	17	4.6	8033	US-09-070-927A-121	Sequence 121, App
18	17	4.6	11842	US-09-764-860-1187	Sequence 1187, Ap
19	16	4.3	124	US-09-815-242-2587	Sequence 2587, Ap

C	20	16	4.3	236	10	US-09-923-876-3098	Sequence 3098, Ap
	21	16	4.3	271	10	US-09-878-574-7775	Sequence 7775, Ap
	22	16	4.3	364	10	US-09-960-352-1111	Sequence 1111, Ap
	23	16	4.3	369	10	US-09-960-352-11486	Sequence 11486, A
	24	16	4.3	375	10	US-09-770-791-278	Sequence 278, App
	25	16	4.3	402	9	US-10-057-275-3	Sequence 3, Appli
	26	16	4.3	405	9	US-10-103-852-1	Sequence 1, Appli
	27	16	4.3	406	9	US-09-960-352-3690	Sequence 3690, Ap
	28	16	4.3	411	10	US-09-960-352-11005	Sequence 11005, A
	29	16	4.3	414	10	US-09-983-965-3483	Sequence 3483, Ap
	30	16	4.3	488	10	US-09-864-761-10902	Sequence 10902, A
	31	16	4.3	538	10	US-09-393-634-22	Sequence 22, Appli
	32	16	4.3	615	10	US-09-764-864-423	Sequence 423, Appl
	33	16	4.3	654	10	US-09-833-381-94	Sequence 94, Appl
	34	16	4.3	689	9	US-10-001-887-14	Sequence 14, Appl
	35	16	4.3	1172	10	US-09-815-242-4715	Sequence 4715, Ap
	36	16	4.3	1179	10	US-09-815-242-8625	Sequence 8625, Ap
	37	16	4.3	1549	10	US-09-813-358-34	Sequence 34, Appl
	38	16	4.3	1889	10	US-09-801-368-41	Sequence 41, Appl
	39	16	4.3	2053	10	US-09-822-849A-343	Sequence 343, Appl
	40	16	4.3	2165	10	US-09-802-669-94	Sequence 94, Appl
	41	16	4.3	2702	10	US-09-922-261-359	Sequence 359, Appl
	42	16	4.3	3212	10	US-09-834-291-1	Sequence 1, Appli
	43	16	4.3	3294	10	US-09-764-860-1156	Sequence 1156, Ap
	44	16	4.3	11749	10	US-09-764-877-2431	Sequence 2431, Ap
	45	16	4.3	17581	10	US-09-764-869-2170	Sequence 2170, Ap

ALIGNMENTS

RESULT 1
US-09-825-294-199
Sequence 199, Application US/09825294
Patent No. US20020004921A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 199
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(369)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

Query Match 100.0%; Score 369; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.5e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCAACTTTTGGCGATGTTCTTCTTNCAGGCTTTGGCGTGCACAAATCCAGTGCAC	60
DB	1	GGCAACTTTTGGCGATGTTCTTCTTNCAGGCTTTGGCGTGCACAAATCCAGTGCAC	60
QY	61	GTGTGAAGATTCGAGTGCACAGAGCTCTCCCGAGATTCATTTGTGATTCAC	120
DB	61	GTGTGAAGATTCGAGTGCACAGAGCTCTCTCCCGAGATTCATTTGTGATTCAC	120
QY	121	GGTGAACCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAGAGTCCCGGATCATGTA	180
DB	121	GGTGAACCTTCAAGACATGTGTCAAGAAAGTGTGAGCAAGAGTCCCGGATCATGTA	180

```
QY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTTGCGGGTACAGTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGGCTTGCGGGTACAGTCTT 240
QY 241 CTGCTCCCGCAGGGAAGTCACTCACTTGTGATCATCAGCTCTGCAACACCCCTTTGTAA 300
    |||||||
Db 241 CTGCTCCCGCAGGGAAGTCACTCACTTGTGATCATCAGCTCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCCAAGAAAGGGAAGTCTGCTCGGCTTCAGCCATCGCTCCGCAC 360
    |||||||
Db 301 CGGGCCAAAGGCCCCAAGAAAGGGAAGTCTGCTCGGCTTCAGCCATCGCTCCGCAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369
```

```
RESULT 2
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205
```

```
Query Match      85.4%; Score 315; DB 10; Length 1619;
Best Local Similarity 100.0%; Pred. No. 3.7e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
    |||||||
Db 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
QY 90 GCTCCTCCCGAGTTCATTTGTGAATTGCACGGTGAAGCTTCAAGACATGTGTCAAGAG 149
    |||||||
Db 90 GCTCCTCCCGAGTTCATTTGTGAATTGCACGGTGAAGCTTCAAGACATGTGTCAAGAG 149
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATATGCCCAAGTCTGTGATCATCATCAGCGGCT 209
    |||||||
Db 150 AAGTGTGAGCAAAAGTCCGGGATCATATGCCCAAGTCTGTGATCATCATCAGCGGCT 209
QY 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGCAGGGAAGTGAAGTGT 269
    |||||||
Db 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGCAGGGAAGTGAAGTGT 269
QY 270 GCATCAGCTCTGCAACACCCCTTTGTGAAGGGGCCAAGGCCAAGAAAGGGGAAGTT 329
    |||||||
Db 270 GCATCAGCTCTGCAACACCCCTTTGTGAAGGGGCCAAGGCCAAGAAAGGGGAAGTT 329
QY 330 CTGCTCTGGGCTCTCA 344
    |||||||
Db 330 CTGCTCTGGGCTCTCA 344
```

```
RESULT 3
US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211
```

```
Query Match      85.4%; Score 315; DB 10; Length 1619;
Best Local Similarity 100.0%; Pred. No. 3.7e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
    |||||||
Db 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
QY 90 GCTCCTCCCGAGTTCATTTGTGAATTGCACGGTGAAGCTTCAAGACATGTGTCAAGAG 149
    |||||||
Db 90 GCTCCTCCCGAGTTCATTTGTGAATTGCACGGTGAAGCTTCAAGACATGTGTCAAGAG 149
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATATGCCCAAGTCTGTGATCATCATCAGCGGCT 209
    |||||||
Db 150 AAGTGTGAGCAAAAGTCCGGGATCATATGCCCAAGTCTGTGATCATCATCAGCGGCT 209
QY 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGCAGGGAAGTGAAGTGT 269
    |||||||
Db 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGCAGGGAAGTGAAGTGT 269
QY 270 GCATCAGCTCTGCAACACCCCTTTGTGAAGGGGCCAAGGCCAAGAAAGGGGAAGTT 329
    |||||||
Db 270 GCATCAGCTCTGCAACACCCCTTTGTGAAGGGGCCAAGGCCAAGAAAGGGGAAGTT 329
QY 330 CTGCTCTGGGCTCTCA 344
    |||||||
Db 330 CTGCTCTGGGCTCTCA 344
```

```
RESULT 4
US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
```

```
Query Match      85.4%; Score 315; DB 10; Length 1897;
```


Best Local Similarity 100.0%; Pred. No. 3,7e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 30 CAGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACT 89
    |||||||
Db 309 CAGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACT 368
    |||||||
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 149
    |||||||
Db 369 GCTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 428
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 429 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 488
    |||||||
QY 210 GTCATCAGCTTCGCGGGGTACCACTCTTCTGCTCCCGGAAACTGAAGTCACTGTTT 269
    |||||||
Db 489 GTCATCAGCTTCGCGGGGTACCACTCTTCTGCTCCCGGAAACTGAAGTCACTGTTT 548
    |||||||
QY 270 GCATCAGCTTCGCAACACCCCTTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
Db 549 GCATCAGCTTCGCAACACCCCTTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 608
    |||||||
QY 330 CTGCTCGGCGCTCA 344
    |||||||
Db 609 CTGCTCGGCGCTCA 623
    |||||||
```

RESULT 5
US-09-825-294-9
Sequence 9, Application US/09825294

```
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9
```

Query Match 76.2%; Score 281; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.8e-141;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 30 CAGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACT 89
    |||||||
Db 40 CAGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACT 99
    |||||||
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 149
    |||||||
Db 100 GCTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 159
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 160 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 219
    |||||||
QY 210 GTCATCAGCTTCGCGGGGTACCACTCTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 269
    |||||||
Db 220 GTCATCAGCTTCGCGGGGTACCACTCTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 279
    |||||||
```

```
QY 270 GCATCAGCTTCGCAACACCCCTTTGTAAAGCGGCCCAAG 310
    |||||||
Db 280 GCATCAGCTTCGCAACACCCCTTTGTAAAGCGGCCCAAG 320
    |||||||
```

RESULT 6
US-09-825-294-212

```
Sequence 212, Application US/09825294
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 212
LENGTH: 1010
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-212
```

Query Match 73.4%; Score 271; DB 10; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 31 AGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACTG 90
    |||||||
Db 258 AGGCTTTGCGTGAACATCCAGTGTGTAAGAAATTCACAGTGAACAGACTG 317
    |||||||
QY 91 CTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 150
    |||||||
Db 318 CTCCTCCCGGAGTTCATTTGTAATTCGACGGTGAACGTTCAAGACATGTGTAGAAG 377
    |||||||
QY 151 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTG 210
    |||||||
Db 378 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTG 437
    |||||||
QY 211 TCTCATGCTTCGCGGGGTACCACTCTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 270
    |||||||
Db 438 TCTCATGCTTCGCGGGGTACCACTCTTGTAAAGCGGCCCAAGGCCCAAGAAAGGGAAGTT 497
    |||||||
QY 271 CATCAGCTTCGCAACACCCCTTTGTAAAC 301
    |||||||
Db 498 CATCAGCTTCGCAACACCCCTTTGTAAAC 528
    |||||||
```

RESULT 7

US-09-825-294-213
Sequence 213, Application US/09825294
Patent No. US20020004491A1

```
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 213
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
```

US-09-825-294-213

Query Match 31.7%: Score 117; DB 10; Length 480;
Best Local Similarity 99.4%; Pred. No. 3.6e-53;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 30 CAGCCTTGGCGCTGCAATTCAGTACAGTGTGAAGATTCAGCTGAACAAGACT 89

DB 309 CAGCCTTGGCGCTGCAATTCAGTGTGAAGATTCAGCTGAACAAGACT 368

OY 90 GCTCCTCCCGAGTATTCATTTGATTCAGCGGTGAACGCTTCAAGACATGTGTGAGAAG 149

DB 369 GCTCCTCCCGAGTATTCATTTGATTCAGCGGTGAACGCTTCAAGACATGTGTGAGAAG 428

OY 150 AAGTATGAGCAAGTCCGCGGATCATGTACCGCAAGTCTGTGCAT 197

DB 429 AAGTATGAGCAAGTCCGCGGATCATGTACCGCAAGTCTGTGCAT 476

RESULT 8
US-09-867-701-4251
Sequence 4251, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.497

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4251

LENGTH: 430

TYPE: DNA

ORGANISM: Homo sapien

US-09-867-701-4251

Query Match 14.9%: Score 55; DB 10; Length 430;
Best Local Similarity 100.0%; Pred. No. 5.6e-20;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 TCCCCAGGAACTGCACTGATTTGCATCAGCTGTGCAACACCCCTTTTGTGA 299

DB 1 TCCCCAGGAACTGCACTGATTTGCATCAGCTGTGCAACACCCCTTTTGTGA 55

RESULT 9
US-09-294-093B-5287
Sequence 5287, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

PRIORITY FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5287

LENGTH: 237

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700356180H1

NAME/KEY: unsure

LOCATION: 21

OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-5287

Query Match 4.9%: Score 18; DB 10; Length 237;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209

DB 44 GTGCATCATCAGCGGCT 61

RESULT 10
US-09-294-093B-5709
Sequence 5709, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5709

LENGTH: 236

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700382209H1

LOCATION: 19, 21, 234, 245

OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-5709

Query Match 4.9%: Score 18; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209

DB 77 GTGCATCATCAGCGGCT 94

RESULT 11
US-09-294-093B-5021
Sequence 5021, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

PRIORITY FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5021

LENGTH: 286

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700355590H1

NAME/KEY: unsure
LOCATION: 8, 26, 57, 117, 124, 216, 248, 260
OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-5021

Query Match
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 GTCATCATCAGCGCCT 209
DB 58 GTCATCATCAGCGCCT 75

RESULT 12
US-09-416-384A-6/C
Sequence 6, Application US/09416384A
Patent No. US20020081584A1
GENERAL INFORMATION:
APPLICANT: BLUMENFELD, Marta
APPLICANT: BOUGELERET, Lydie
APPLICANT: CHUMAKOV, Ilya
APPLICANT: COHEN, Daniel
APPLICANT: ESSIOUX, Laurent
TITLE OF INVENTION: Genes, proteins and diallelic markers related to central...
FILE REFERENCE: GENSET.043AUS
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: US/09/416,384A
PRIOR FILING DATE: 1999-10-30
PRIOR APPLICATION NUMBER: 60/106,457
PRIOR FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: 60/103,955
PRIOR FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: 60/132,277
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patent.pm
SEQ ID NO 6
LENGTH: 1791
TYPE: DNA
ORGANISM: mus musculus
US-09-416-384A-6

Query Match
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ACGACTGCTCCTCCCGC 101
DB 695 ACGACTGCTCCTCCCGC 678

RESULT 13
US-09-925-300-682
Sequence 682, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT FILING DATE: 2001-08-10
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 682
LENGTH: 1298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc feature
LOCATION: (1294)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-682

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCCGAGTTCATTGTGAA 114
DB 476 CCCGAGTTCATTGTGAA 492

RESULT 14
US-09-815-242-7853
Sequence 7853, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7853
LENGTH: 1713
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1713)
US-09-815-242-7853

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGCCTG 210
DB 308 GCATCATCAGCGCCTG 324

RESULT 15
US-09-815-242-6571
Sequence 6571, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6571
LENGTH: 2649
TYPE: DNA
ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2649)
US-09-815-242-6571

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 2649;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AAGAGAGTGATGAGCA 162
Db 2563 AAGAGAGTGATGAGCA 2579

RESULT 16
US-09-964-824A-313
Sequence 313, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
PRIORITY FILING DATE: 2001-09-27
PRIORITY APPLICATION NUMBER: US/60/236,033
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: US/60/236,032
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: US/60/236,028
PRIORITY FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 313
LENGTH: 6252
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-313

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 6252;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCCGAGTTCATTGTGAA 114
Db 3521 CCCGAGTTCATTGTGAA 3537

RESULT 17
US-09-070-927A-121
Sequence 121, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 8033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-09-070-927A-121

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 8033;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AAGAGAGTGATGAGCA 162
Db 7402 AAGAGAGTGATGAGCA 7418

RESULT 18
US-09-764-860-1187
Sequence 1187, Application US/09764860
Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860

```
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 1198
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 1187
;; LENGTH: 11842
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-860-1187

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 11842;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 CCTCTGCTCCCGAGG 253
DB 6500 CCTCTGCTCCCGAGG 6516

RESULT 19
US-09-815-242-2587
; Sequence 2587, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2587
; LENGTH: 124
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2587

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 124;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AATCCAGTCTACGAG 61
DB 41 AATCCAGTCTACGAG 56

RESULT 20
US-09-923-876-3098/C
; Sequence 3098, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Lalgudi, Raghunath V.
;; APPLICANT: Kamigaki, Laura Y. (Ito)
;; APPLICANT: Sherman, Bradley K.
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
;; FILE REFERENCE: PL-0012-1 COR
;; CURRENT APPLICATION NUMBER: US/09/923,876
;; CURRENT FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/298,329
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/085,331
;; PRIOR FILING DATE: 1998-05-05
;; NUMBER OF SEQ ID NOS: 6332
;; SOFTWARE: PERL Program
;; SEQ ID NO 3098
;; LENGTH: 236
;; TYPE: DNA
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No. US20020013958A1 700161660H1
US-09-923-876-3098

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 236;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 TCAGCTGCTGCACAC 288
DB 131 TCAGCTGCTGCACAC 116

RESULT 21
US-09-878-574-7775
; Sequence 7775, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 7775
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701100324H1
US-09-878-574-7775

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 271;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTACAGTCTCTTG 243
DB 104 GGTACAGTCTCTTG 119

RESULT 22
US-09-960-352-1111
; Sequence 1111, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
```

;; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
;; FILE REFERENCE: 16511.006/37-21(10298)C
;; CURRENT APPLICATION NUMBER: US/09/960.352
;; CURRENT FILING DATE: 2001-09-24
;; NUMBER OF SEQ ID NOS: 15112
;; SEQ ID NO 1111
;; LENGTH: 364
;; TYPE: DNA
;; ORGANISM: Bos taurus
;; OTHER INFORMATION: Clone ID: 05-LIB34-056-Q1-E1-B1
US-09-960-352-1111

Query Match
Best Local Similarity 4.3%; Score 16; DB 10; Length 364;
Matches 16; Conservative 0; Pred. No. 43;
Mismatches 0; Indels 0; Gaps 0;

OY 41 CTGCAATCCAGTCT 56
Db 194 CTGCAATCCAGTCT 209

RESULT 23
US-09-960-352-11486
; Sequence 11486, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathilagan, Naganan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11486
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 49-LIB34-018-Q1-E1-E10
US-09-960-352-11486

Query Match
Best Local Similarity 4.3%; Score 16; DB 10; Length 369;
Matches 16; Conservative 0; Pred. No. 43;
Mismatches 0; Indels 0; Gaps 0;

OY 41 CTGCAATCCAGTCT 56
Db 21 CTGCAATCCAGTCT 36

RESULT 24
US-09-770-791-278/c
; Sequence 278, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.

;; APPLICANT: Allen, Keith
;; APPLICANT: Hoffman, Neil
;; APPLICANT: Hurbau, Patrick
;; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;; FILE REFERENCE: 2029 (PARA-018PRV)
;; CURRENT APPLICATION NUMBER: US/09/770.791
;; CURRENT FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/178,480
;; PRIOR FILING DATE: 2000-01-27
;; NUMBER OF SEQ ID NOS: 999
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 278
;; LENGTH: 375
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-770-791-278

Query Match
Best Local Similarity 4.3%; Score 16; DB 10; Length 375;
Matches 16; Conservative 0; Pred. No. 43;
Mismatches 0; Indels 0; Gaps 0;

OY 80 AACACGACTGCTCCT 95
Db 323 AACACGACTGCTCCT 308

RESULT 25
US-10-057-275-3/c
; Sequence 3, Application US/10057275
; Patent No. US2002015545A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; Bandman, Olga
; Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/057.275
; FILING DATE: 25-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/390.740A
; FILING DATE: February 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0027 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Human Pancreas
; CLONE: 226152
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-057-275-3

Query Match 4.3%; Score 16; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284
DB 263 TGCATCAGCTGCTGCA 248

RESULT 26

US-10-103-859-1/c
; Sequence 1, Application US/10103859
; Patent No. US20020155094A1
; GENERAL INFORMATION:
; APPLICANT: White, J.R.
; APPLICANT: Pelus, L.M.
; TITLE OF INVENTION: Method of Treating Sepsis and ARDS Using Chemokine Beta-9
; FILE REFERENCE: 1488,1520003 US/10/103,859
; CURRENT APPLICATION NUMBER: US/10/03-25
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/496,273
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 08/852,212
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: US 60/017,871
; PRIOR FILING DATE: 1996-05-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(405)
; OTHER INFORMATION:
US-10-103-859-1

Query Match 4.3%; Score 16; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284
DB 263 TGCATCAGCTGCTGCA 248

RESULT 27

US-09-960-352-3690
; Sequence 3690, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511,006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3690
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 16-LIB34-030-Q1-E1-D11
US-09-960-352-3690

Query Match 4.3%; Score 16; DB 10; Length 406;
Best Local Similarity 100.0%; Pred. No. 43;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGCAATTCAGTGCT 56
DB 205 CTGCAATTCAGTGCT 220

RESULT 28

US-09-960-352-11005
; Sequence 11005, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511,006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11005
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (333),(347),(373),(384)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 47-LIB34-011-Q1-E1-D4
US-09-960-352-11005

Query Match 4.3%; Score 16; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGCAATTCAGTGCT 56
DB 389 CTGCAATTCAGTGCT 404

RESULT 29

US-09-983-965-3483
; Sequence 3483, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 3483
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (76),(81),(87)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 37-LIB3058-007-Q1-R1-B2
US-09-983-965-3483

Query Match 4.3%; Score 16; DB 10; Length 414;

Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 TGTGATCGCTCTGCC 226
|||||
Db 219 TGTGATCGCTCTGCC 234

RESULT 30

US-09-864-761-10902/c
Sequence 10902, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10902
LENGTH: 488
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003103.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
US-09-864-761-10902

Query Match 4.3%; Score 16; DB 10; Length 488;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 TGTGCTCCCGAGGA 254
|||||
Db 102 TGTGCTCCCGAGGA 87

RESULT 31

US-09-393-634-22
Sequence 22, Application US/09393634
Patent No. US20020051997A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
TITLE OF INVENTION: SF, a NO. US20020051997A1el Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 538
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: mouse GR06
US-09-393-634-22

Query Match 4.3%; Score 16; DB 10; Length 538;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 TGTGCGAAGAAGT 153
|||||
Db 175 TGTGCGAAGAAGT 190

RESULT 32

US-09-764-864-423/c
Sequence 423, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 423
LENGTH: 615
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (513)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (536)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (569)


```
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (597)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (610)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-423

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 AAGAAAGGGAAGT 329
DB 565 AAGAAAGGGAAGT 550

RESULT 33
US-09-833-381-94
; Sequence 94, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith F.
; TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 94
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-94

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATGCTGCTGCA 284
DB 535 TGCATGCTGCTGCA 550

RESULT 34
US-10-001-887-14/c
; Sequence 14, Application US/10001887
; Patent No. US2002015464A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Cafierkey, Robert
; APPLICANT: Liu, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PR
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 689
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-887-14

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GGCCCAAGAAAGGG 324
DB 311 GGCCCAAGAAAGGG 296

RESULT 35
US-09-815-242-4715/c
; Sequence 4715, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4715
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4715

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AATCCAGTCTACAG 61
DB 992 AATCCAGTCTACAG 977

RESULT 36
US-09-815-242-8625/c
; Sequence 8625, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
```

APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8625
LENGTH: 1179
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1179)
US-09-815-242-8625

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 1179;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AATCCAGTCTACCAG 61
Db 992 AATCCAGTCTACCAG 977

RESULT 37
US-09-813-358-34
Sequence 34, Application US/09813358
Patent No. US20020048759A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Pyle, Ruth
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
FILE REFERENCE: 210121.501
CURRENT APPLICATION NUMBER: US/09/813,358
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 1549
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(1549)
OTHER INFORMATION: n = A,T,C or G
US-09-813-358-34

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 1549;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 CTGCTGCAACACCCCT 292
Db 57 CTGCTGCAACACCCCT 72

RESULT 38
US-09-801-368-41
Sequence 41, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 1989
TYPE: DNA
ORGANISM: Aspergillus nidulans
US-09-801-368-41

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 1989;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 ACCGCAAGTCCTGTGC 195
Db 1026 ACCGCAAGTCCTGTGC 1041

RESULT 39
US-09-822-849A-343/C
Sequence 343, Application US/09822849A
Patent No. US20020045170A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakara
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 343
LENGTH: 2053
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-849A-343

Query Match 4.3%; Score 16; DB 10; Length 2053;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGATCA 176
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DB 1096 CAAAGTCCCGATCA 1081

RESULT 40
US-09-802-669-94/c
; Sequence 94, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISFH-545
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94

Query Match 4.3%; Score 16; DB 10; Length 2165;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CAAGCCCAAGAAAG 321
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DB 2042 CAAGCCCAAGAAAG 2027

RESULT 41
US-09-922-261-359
; Sequence 359, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Io, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/922,261
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 2702
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-261-359

Query Match 4.3%; Score 16; DB 10; Length 2702;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AACTCAGTTTGCATCA 275
|||||

DB 2500 AACTCAGTTTGCATCA 2515

RESULT 42
US-09-834-291-1/c
; Sequence 1, Application US/09834291
; Patent No. US20020042064A1
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
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; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1

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Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CAAGCCCAAGAAAG 321
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DB 2487 CAAGCCCAAGAAAG 2472

RESULT 43
US-09-764-860-1156
; Sequence 1156, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1156
; LENGTH: 3294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1156

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTACAGTCTTCTG 243
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DB 819 GGTACAGTCTTCTG 834

RESULT 44
US-09-764-877-2431

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; Sequence 2431, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2431
; LENGTH: 11749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2431

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Query Match 4.3%; Score 16; DB 10; Length 11749;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 134 GACATGTCGAGAAAG 149
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Db 4972 GACATGTCGAGAAAG 4987

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RESULT 45
US-09-764-869-2170
; Sequence 2170, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2170
; LENGTH: 17581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2170

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Query Match 4.3%; Score 16; DB 10; Length 17581;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 314 AAGAAAGGGGAGATT 329
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Db 2661 AAGAAAGGGGAGATT 2676

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-970-966-199

Perfect score: 369

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4	369	100.0	369	31	US-09-825-294-199
5	369	100.0	369	36	US-09-970-966-199
6	369	100.0	369	42	US-10-212-677-199
7	317	85.9	483	29	US-09-757-034-340
8	317	85.9	483	42	US-10-235-954-340
9	315	85.4	488	16	US-09-234-611-18421
10	315	85.4	488	16	US-09-277-227-6100
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SUMMARIES

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40 315 85.4 1524 42 US-10-219-067-15 Sequence 15, Appl
41 315 85.4 1524 42 US-10-219-068-15 Sequence 15, Appl
42 315 85.4 1524 42 US-10-219-069-15 Sequence 15, Appl
43 315 85.4 1524 42 US-10-219-070-15 Sequence 15, Appl
44 315 85.4 1524 42 US-10-219-071-15 Sequence 15, Appl
45 315 85.4 1524 42 US-10-219-072-15 Sequence 15, Appl

```

ALIGNMENTS

```

RESULT 1
PCT-US01-45395-199
; Sequence 199, Application PC/TUS0145395
; GENERAL INFORMATION:

```

```

; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 29, 345
; OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-199

```

Query Match 100.0%; Score 369; DB 1; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.1e-188; Mismatches 0; Indels 0; Gaps 0;

```

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATTCAGTGTACCA 60
DB 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATTCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGCAAGACGACGCTCCGCCGAGTTTCATTTGTAATGCAC 120
DB 61 GTGTGAAGATTCAGCTGCAAGACGACGCTCCGCCGAGTTTCATTTGTAATGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTAGATGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTAGATGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CGCAAGTCCTGTGATCATCAAGCGGCTGTCTCATCGCTTGCCTGCGGATACAGTCTT 240

```

```

DB 181 CGCAAGTCCTGTGATCATCAAGCGGCTGTCTCATCGCTTGCCTGCGGATACAGTCTT 240
QY 241 CTCTCTCCCGGAGAACTGAAGTCAAGTTCATCATGCTGTGCAACACCCCTCTTTGTA 300
DB 241 CTCTCTCCCGGAGAACTGAAGTCAAGTTCATCATGCTGTGCAACACCCCTCTTTGTA 300
QY 301 CGGCGCAAGGCCCCAAGAAAGGGGAAAGTTGCTGCGGCTTCANSCATGCTCCGCAC 360
DB 301 CGGCGCAAGGCCCCAAGAAAGGGGAAAGTTGCTGCGGCTTCANSCATGCTCCGCAC 360
QY 361 CACCATCT 369
DB 361 CACCATCT 369

```

```

RESULT 2
US-09-656-668-199
; Sequence 199, Application US/09656668
; GENERAL INFORMATION:

```

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C3
; CURRENT APPLICATION NUMBER: US/09/656,668
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-656-668-199

```

Query Match 100.0%; Score 369; DB 25; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.1e-188; Mismatches 0; Indels 0; Gaps 0;

```

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATTCAGTGTACCA 60
DB 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATTCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGCAAGACGACGCTCCGCCGAGTTTCATTTGTAATGCAC 120
DB 61 GTGTGAAGATTCAGCTGCAAGACGACGCTCCGCCGAGTTTCATTTGTAATGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTAGATGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTAGATGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CGCAAGTCCTGTGATCATCAAGCGGCTGTCTCATCGCTTGCCTGCGGATACAGTCTT 240
DB 181 CGCAAGTCCTGTGATCATCAAGCGGCTGTCTCATCGCTTGCCTGCGGATACAGTCTT 240
QY 241 CTCTCTCCCGGAGAACTGAAGTTCATCATGCTGTGCAACACCCCTCTTTGTA 300
DB 241 CTCTCTCCCGGAGAACTGAAGTTCATCATGCTGTGCAACACCCCTCTTTGTA 300
QY 301 CGGCGCAAGGCCCCAAGAAAGGGGAAAGTTGCTGCGGCTTCANSCATGCTCCGCAC 360
DB 301 CGGCGCAAGGCCCCAAGAAAGGGGAAAGTTGCTGCGGCTTCANSCATGCTCCGCAC 360
QY 361 CACCATCT 369
DB 361 CACCATCT 369

```

RESULT 3

```

US-09-713-550-199
; Sequence 199, Application US/09713550
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-199

```

```

Query Match          100.0%; Score 369; DB 28; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACACAGACAGCTGCTCCCGGAGTTCATTTGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACACAGACAGCTGCTCCCGGAGTTCATTTGTAATTCAC 120
QY 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGAGTGTGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGAGTGTGACAAAGTCCGGGATCATGTA 180
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACACGATCCTT 240
DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACACGATCCTT 240
QY 241 CTGCTCCCCAGGAAACTGAACTCACTTTGTCATCAGCTGCTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCCAGGAAACTGAACTCACTTTGTCATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCCAAGAAAGGGAGTCTGCTCGGCGCTCANGCCATGCTCCGCAC 360
DB 301 CGGGCCAAAGGCCCCAAGAAAGGGAGTCTGCTCGGCGCTCANGCCATGCTCCGCAC 360
QY 361 CACCATCCT 369
DB 361 CACCATCCT 369

```

```

RESULT 4
US-09-825-294-199
; Sequence 199, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Steven P.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

```

Query Match          100.0%; Score 369; DB 31; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACACAGACAGCTGCTCCCGGAGTTCATTTGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACACAGACAGCTGCTCCCGGAGTTCATTTGTAATTCAC 120
QY 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGAGTGTGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACCTTCAAGACATGTGTCAAGAAAGAGTGTGACAAAGTCCGGGATCATGTA 180
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACACGATCCTT 240
DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACACGATCCTT 240
QY 241 CTGCTCCCCAGGAAACTGAACTCACTTTGTCATCAGCTGCTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCCAGGAAACTGAACTCACTTTGTCATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCCAAGAAAGGGAGTCTGCTCGGCGCTCANGCCATGCTCCGCAC 360
DB 301 CGGGCCAAAGGCCCCAAGAAAGGGAGTCTGCTCGGCGCTCANGCCATGCTCCGCAC 360
QY 361 CACCATCCT 369
DB 361 CACCATCCT 369

```

```

RESULT 5
US-09-970-966-199
; Sequence 199, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 29, 345
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-199

```

```

Query Match          100.0%; Score 369; DB 36; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGCGATTTGCTTCTTCAGGCTTGGCGTCAATCCAGTCTACCA 60

```



```

; Sequence 340, Application US/10235954
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM002C1N
; CURRENT APPLICATION NUMBER: US/10/235,954
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/757,034
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 1440
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 340
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (367)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (443)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-235-954-340

```

```

Query Match      85.9%; Score 317; DB 42; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-160;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 89
DB 52 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 111
QY 90 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 112 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 171
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 172 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 231
QY 210 GTCATCATGCTTCGCGGGTACAGTCCTTGTGTCGCCCGAGGAACTGAACACTAGTTT 269
DB 232 GTCATCATGCTTCGCGGGTACAGTCCTTGTGTCGCCCGAGGAACTGAACACTAGTTT 291
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAAGTT 329
DB 292 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAAGTT 351
QY 330 CTGCTTCGGCGCTCANG 346
DB 352 CTGCTTCGGCGCTCANG 368

```

```

RESULT 9
US-10-212-677-283
; Sequence 283, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Panger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

```

```

; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-283

```

```

Query Match      85.4%; Score 315; DB 42; Length 414;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 89
DB 38 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 97
QY 90 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 98 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 157
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 158 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 217
QY 210 GTCATCATGCTTCGCGGGTACAGTCCTTGTGTCGCCCGAGGAACTGAACACTAGTTT 269
DB 218 GTCATCATGCTTCGCGGGTACAGTCCTTGTGTCGCCCGAGGAACTGAACACTAGTTT 277
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAAGTT 329
DB 278 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAAGTT 337
QY 330 CTGCTTCGGCGCTCANG 344
DB 338 CTGCTTCGGCGCTCANG 352

```

```

RESULT 10
US-09-234-611-18421
; Sequence 18421, Application US/09234611
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/234,611
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18421
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)---(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-611-18421

```

```

Query Match      85.4%; Score 315; DB 16; Length 488;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 89
DB 79 CAGGCTTTCGGCGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGCACT 138
QY 90 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 139 GCTCCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGTGAGAAAG 198

```

```

QY 150 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 11
US-09-277-227-6100

```

; Sequence 6100, Application US/09277227
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-766
; CURRENT APPLICATION NUMBER: US/09/277,227
; CURRENT FILING DATE: 1999-03-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6100
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-277-227-6100

```

Query Match
Best Local Similarity 100.0%; Score 315; DB 16; Length 488;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGACAGAGACT 89
    |||||||
Db 79 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGACAGAGACT 138
QY 90 GCTCCTCCCGGAGTTCATTTGTAAGGGAAGTTCAGGTAAGTGTGCAAGAA 149
    |||||||
Db 139 GCTCCTCCCGGAGTTCATTTGTAAGGGAAGTTCAGGTAAGTGTGCAAGAA 198
QY 150 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 12
US-09-904-809-18421
; Sequence 18421, Application US/09904809
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/904,809
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18421
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-18421

```

Query Match
Best Local Similarity 100.0%; Score 315; DB 34; Length 488;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGACAGAGACT 89
    |||||||
Db 79 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGACAGAGACT 138
QY 90 GCTCCTCCCGGAGTTCATTTGTAAGGGAAGTTCAGGTAAGTGTGCAAGAA 149
    |||||||
Db 139 GCTCCTCCCGGAGTTCATTTGTAAGGGAAGTTCAGGTAAGTGTGCAAGAA 198
QY 150 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGATCATGTACCGCAAGTCTCTGATCATCAGGCGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGCTCCCAAGGGAAGTCACTGTTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACGGGGCCCAAGGCCCAAGAAAGGGAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 13
US-09-909-627-6100
; Sequence 6100, Application US/09909627
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-766
; CURRENT APPLICATION NUMBER: US/09/909,627
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/277,227
; PRIOR FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 23680
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6100
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-909-627-6100

Query Match	85.4%	Score 315	DB 34	Length 488
Best Local Similarity	100.0%	Pred. No. 2e-159		
Matches 315	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	30	CAGGCTTTGCAGCTGCAAAATCCAGTGTCTACCACTGTGAAGAATTTCCAGCTGAACAACGACT	89	
Db	79	CAGGTTTGGCGGTGCAAAATCCAGTGTCTACCACTGTGAAGAATTTCCAGCTGAACAACGACT	138	
QY	90	GCTCTCTCCCCGAGTTTCATTTGGAATTTGACGGGTGAACCTTCAAGCATATGTGTCAAGAAG	149	
Db	139	GCTCTCTCCCCGAGTTTCATTTGGAATTTGACGGGTGAACCTTCAAGCATATGTGTCAAGAAG	198	
QY	150	AAGTATGAGCAAAAGTGGCGGGATTCATTACCGCAAGTCTGTGATATCAGCGGCT	209	
Db	199	AAGTATGAGCAAAAGTGGCGGGATTCATTACCGCAAGTCTGTGATATCAGCGGCT	258	
QY	210	GTCATCATGGCCTCTGTCCGGGTACCAAGTCTTGTCTTCCCAAGGAAATCGAATCTAGTTT	269	
Db	259	GTCATCATGGCCTCTGTCCGGGTACCAAGTCTTGTCTTCCCAAGGAAATCGAATCTAGTTT	318	
QY	270	GCATCAGCTGCTGCAACACCCCTCTTTTGTAAAGGGCCAGGCCCAAGAAAAGGGGAAGTT	329	
Db	319	GCATCAGCTGCTGCAACACCCCTCTTTTGTAAAGGGCCCAAGGCCCAAGAAAAGGGGAAGTT	378	
QY	330	CTGCCCTGGGCTCTCA 344		
Db	379	CTGCCCTGGGCTCTCA 393		

```

RESULT 14
US-10-119-480-15
; Sequence 15, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10-119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-15

Query Match      85.4%; Score 315; DB 40; Length 1524;
Best Local Similarity 100.0%; Pred. NO. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Query Match	85.4%	Score 315	DB 40	Length 1524
Best Local Similarity	100.0%	Pred. No. 2e-159		
Matches 315	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	30	CAGGCTTTGGCGTGCAAATTCAGTGTACCAAGTGTAGAGAAATTCAGCTGGAACACGACT	89	
Db	170	CAGGCTTTGGCGTGCAAATTCAGTGTACCAAGTGTAGAGAAATTCAGCTGGAACACGACT	229	
Qy	90	GCCTCCCTCCCGAGTTCATGTCAATTGCAGCGGTGAACGTTCAAGACATGTGCACGAAG	149	
Db	230	GCCTCCCTCCCGAGTTCATGTCAATTGCAGCGGTGAACGTTCAAGACATGTGCACGAAG	289	
Qy	150	AATGTATGAGCAAAAGTGC CGGATCATGTACCGCAAGTCTTGATCATCATAGCGGCTT	209	
Db	290	AATGTATGAGCAAAAGTGC CGGATCATGTACCGCAAGTCTTGATCATCATAGCGGCTT	349	
Qy	210	GCTTCATCGCCTTGCCGGGTACCAAGTCTTTCGCTCCCAAGGAAACTCAACTCACTT	269	

Accession	Sequence	Position
Db	GTCTATCATGCGCTTCAGCGGGGTACAGTCTCTTCCTCCAGGGAACTAACTCAGTTT	409
Qy	270 GCATCAGTGTGTGCAACACCCCTTTTGTATACGGGCCCAAGGCCAAGAAAGGGAGTT	329
Dd	410 GCATAGGTGTGTGCAACACCCCTCTTGTATACGGGCCCAAGGCCAAGAAAGGGAGTT	469
Qy	330 CTGACCTCGGCCCTCA	344
Dd	470 CTGACCTCGGCCCTCA	484

```

RESULT 15
US-10-216-159A-15
: Sequence 15, Application US/10216159A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gunney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P16
: CURRENT APPLICATION NUMBER: US/10/216.159A
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining prior application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-216-159A-15

```

	Query Match	Best Local Similarity	85.4%;	Score 315;	DB 42;	Length 1524;
	Matches 315;	Conservative	0;	Mismatches	0;	Indels
						Gaps
Qy	30	CAGGCTTTGGCGCTGCACAAATCCAGTGTCTACCAATGTGAAGAAATTCACGTGACACAGACT	89			
Db	170	CAGGCTTTGGCGCTGCACAAATCCAGTGTCTACCAATGTGAAGAAATTCACGTGACACAGACT	228			
Qy	90	GCTCTCTCCCCCGAGTTCATTGTGAATTGACAGCGTGAACGTTCAAGACATGTGTCAAGAAG	149			
Db	230	GCTCTCTCCCCCGAGTTCATTGTGAATTGACAGCGTGAACGTTCAAGACATGTGTCAAGAAG	288			
Qy	150	AATGATGAGGACAAATGCGCGGGAGTCATGTACCGCAATCCTGTGACATCAGCGGCT	209			

Accession	Sequence	Length
Db	290 AAGTGAATGAGACAAAGTGTCCGGGATCAATGATCCGACAGTCTGTGCAATCAATCAGGGCCT	349
Qy	210 GTMCATATGCGCTCTGCCGGGTACAGATCTCTGCTCCCGAAGAAATCTAATCATGTTT	269
Db	350 GTCTATATGCTCTGCGGGGTACAGATCTCTGCTCCCGAAGAAATCTAATCATGTTT	409
Qy	270 GCATATGCTGCTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAAAGGGGAATT	329
Db	410 GCATATGCTGCTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAAAGGGGAATT	469
Qy	330 CTMGCTGGGGCCCTCA	344
Db	470 CTGGCTTGGGGCCCTCA	484

```

RESULT 16
US-10-216-160-15
: Sequence 15, Application US/10216160
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: ACIDS AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530PIC8
: CURRENT APPLICATION NUMBER: US/10/216,160
: CURRENT FILING DATE: 2002-08-09
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-216-160-15

```

Query Match	85.4%;	Score 315;	DB 42;	Length 1524;
Best Local Similarity	100.0%;	Pred. No. 2e-159;		
Matches 315;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	30	CAGGTTTGCCCTGCAATTCAGTGTACCAAGTGTGAAGAAATTCACCTGTAACAGACT	89
Db	170	CAGGCTTTGGCCCTGCAATTCAGTGTACCAAGTGTGAAGAAATTCACCTGTAACAGACT	229
Oy	90	GCTCTCTCCCCGAGTTCATTGTGATTTGCAAGGTGAAGCTTCAAGACATGTGTGAGAAAG	149
Db	230	GCTCTCTCCCCGAGTTCATTGTGATTTGCAAGGTGAAGCTTCAAGACATGTGTGAGAAAG	289
Oy	150	AAGTATGATGACCAAGTGTCCGGAGTCATGTACCGCAAGTCTGTGTCATCATACGGGCTT	209
Db	290	AAGTATGATGACCAAGTGTCCGGAGTCATGTACCGCAAGTCTGTGTCATCATACGGGCTT	349
Oy	210	GTTTCATGCTCTTGCCGGGGTACCAAGTTCCTTTCTGCTTCCCAAGGAAATCAACTCAGTTT	269
Db	350	GTTTCATGCTCTTGCCGGGGTACCAAGTTCCTTTCTGCTTCCCAAGGAAATCAACTCAGTTT	409
Oy	270	GCATCAGCTGTGTGAACAACCCCTTTTGTAAAGGGGCCCAAGGAAAGGGAAGTT	329
Db	410	GCATCAGCTGTGTGAACAACCCCTTTTGTAAAGGGGCCCAAGGAAAGGGAAGTT	469
Oy	330	CTGCTCTGGGCCCTCA	344
Db	470	CTGCTCTGGGCCCTCA	484

```

RESULT 17
US-10-216-162-15
Sequence 15, Application US/10216162
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C2
CURRENT APPLICATION NUMBER: US/10/216.162
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/068873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-162-15

```

Query Match	85.4%	Score 315;	DB 42;	Length 1524;
Best Local Similarity	100.0%;	Pred. No. 2e-159;		
Matches 315; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	30	CAGGCTTTCGCGTGAATTCGAGTCTCCAGATGTGAAGAAATTCAGGCTGAACAGCACT	89
Db	170	CAGGCTTTCGCGTGAATTCGAGTCTCCAGATGTGAAGAAATTCAGGCTGAACAGCACT	22
OY	90	GCTCTCCCCGAGTTCATGTGAATTGCAGCGTGAACGTTCAAGACATGTGTCAGAAG	14
Db	230	GCTCTCCCCGAGTTCATGTGAATTGCAGCGTGAACGTTCAAGACATGTGTCAGAAG	28
OY	150	AAGTATGTGAGCAAAAGTCCGGGATCATGTACCCGAAGCTGTGCATCATCAGCGACT	20
Db	290	AAGTATGTGAGCAAAAGTCCGGGATCATGTACCCGAAGCTGTGTGATCATCATAGCGGCT	34
OY	210	GTCATCATGCGCTCTGCCGGGTACAGTCCCTTGTCTCCCGAGGAAACTGAATCACTATT	26
Db	350	GTCATCATGCGCTCTGCCGGGTACAGTCCCTTGTCTCCCGAGGAAACTGAATCACTATT	40
OY	270	GCATCAGCTGCGCAACACCCCTCTTGTGAACGGGCCCAAGGCCCAAGAAAAGGGAAGTT	32
Db	410	GCATCAGCTGCGCAACACCCCTCTTGTGAAGGGGCCCAAGGCCCAAGAAAAGGGAAGTT	46
OY	330	CTGCCTCGGCCCCCA 344	

Db 350 GTCATCGCTGCGGGGTACAGTCTTGTGCTCCAGGAAACTCACTCACTTT 409
|||||
QY 270 GCATGAGCTCTGCAACACCCCTTTTGTAAACGGCCAGGCCCAAGAAAGGGAGTT 329
|||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGTAAACGGCCAGGCCCAAGAAAGGGAGTT 469
|||||
QY 330 CTGCTCGGCGCTCA 344
|||||
Db 470 CTGCTCGGCGCTCA 484

RESULT 20

US-10-216-165-15
; Sequence 15, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephen, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P350P1C7
; CURRENT APPLICATION NUMBER: US/10/216.165
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-165-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCTGCAATCACTGCTACCAAGTGTGAAGAATTCCAGCTGAACAGACT 89
|||||
Db 170 CAGCCTTGGCTGCAATCACTGCTACCAAGTGTGAAGAATTCCAGCTGAACAGACT 229
|||||
QY 90 GCTCCTCCCGGAGTGTGTAATGCAAGGTTCAAGAGCTTCAAGACATGTGTGAGAAG 149
|||||
Db 230 GCTCCTCCCGGAGTGTGTAATGCAAGGTTCAAGAGCTTCAAGACATGTGTGAGAAG 289
|||||
QY 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATACGGGCTT 209

Db 290 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATACGGGCT 349
|||||
QY 210 GTCATCGCTGCGGGGTACAGTCTTGTGCTCCAGGAAACTCACTCACTTT 269
|||||
Db 350 GTCATCGCTGCGGGGTACAGTCTTGTGCTCCAGGAAACTCACTCACTTT 409
|||||
QY 270 GCATGAGCTCTGCAACACCCCTTTTGTAAACGGCCAGGCCCAAGAAAGGGAGTT 329
|||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGTAAACGGCCAGGCCCAAGAAAGGGAGTT 469
|||||
QY 330 CTGCTCGGCGCTCA 344
|||||
Db 470 CTGCTCGGCGCTCA 484

RESULT 21

US-10-216-166-15
; Sequence 15, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephen, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C9
; CURRENT APPLICATION NUMBER: US/10/216.166
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-166-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCTGCAATCACTGCTACCAAGTGTGAAGAATTCCAGCTGAACAGACT 89
|||||
Db 170 CAGCCTTGGCTGCAATCACTGCTACCAAGTGTGAAGAATTCCAGCTGAACAGACT 229
|||||
QY 90 GCTCCTCCCGGAGTGTGTAATGCAAGGTTCAAGAGCTTCAAGACATGTGTGAGAAG 149

|||||
Db 230 GCTCTCCCCCAGTTTCATTGTGAATTCACGGTGAACGTTCAAGACATGTGTGAGAAG 289
Oy 150 AAGTATGAGCAAAAGTGGCGGGATCATGTACCGCAAGCTCTGTGATCAGCGGCT 209
Db 290 AAGTATGAGCAAAAGTGGCGGGATCATGTACCGCAAGCTCTGTGATCAGCGGCT 349
Oy 210 GTCTATCGCCTCTGCGGGGTACAGTCTCTTGTCTCCCGAGGGAACAGTCACTAGTTT 269
Db 350 GTCTATCGCCTCTGCGGGGTACAGTCTCTTGTCTCCCGAGGGAACAGTCACTAGTTT 409
Oy 270 GCATAGCTGTGCAACACACCCCTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
Db 410 GCATAGCTGTGCAACACACCCCTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469
Oy 330 CTGCTCGGCGCTCA 344
Db 470 CTGCTCGGCGCTCA 484

RESULT 22
US-10-216-167-15
Sequence 15, Application US/10216167

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC4
CURRENT APPLICATION NUMBER: US/10/216,167
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-167-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 CAGGCTTTGGCTGCAAAATCAGTGTACCAAGTGTGAAGATTCCAGCTGAACAACGACT 89

|||||
Db 170 CAGGCTTTGGCTGCAAAATCAGTGTACCAAGTGTGAAGATTCCAGCTGAACAACGACT 229
Oy 90 GCTCTCCCCCAGTTTCATTGTGAATTCACGGTGAACGTTTCAGACATGTGTGAGAAG 149
Db 230 GCTCTCCCCCAGTTTCATTGTGAATTCACGGTGAACGTTTCAGACATGTGTGAGAAG 289
Oy 150 AAGTATGAGCAAAAGTGGCGGGATCATGTACCGCAAGCTCTGTGATCAGCGGCT 209
Db 290 AAGTATGAGCAAAAGTGGCGGGATCATGTACCGCAAGCTCTGTGATCAGCGGCT 349
Oy 210 GTCTATCGCCTCTGCGGGGTACAGTCTCTTGTCTCCCGAGGGAACAGTCACTAGTTT 269
Db 350 GTCTATCGCCTCTGCGGGGTACAGTCTCTTGTCTCCCGAGGGAACAGTCACTAGTTT 409
Oy 270 GCATAGCTGTGCAACACACCCCTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
Db 410 GCATAGCTGTGCAACACACCCCTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469
Oy 330 CTGCTCGGCGCTCA 344
Db 470 CTGCTCGGCGCTCA 484

RESULT 23
US-10-216-168-15
Sequence 15, Application US/10216168

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC10
CURRENT APPLICATION NUMBER: US/10/216,168
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-168-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 CAGGCTTTGGCTGCAAAATCAGTGTACCAAGTGTGAAGATTCCAGCTGAACAACGACT 89

Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGCGTGAACAGACT 89
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGCGTGAACAGACT 229
OY 90 GCTCTCCGCCGAGTTCATTGTGAATTCAGCGTGAAGATTCAGCGTGAACAGACT 149
DB 230 GCTCTCCGCCGAGTTCATTGTGAATTCAGCGTGAAGATTCAGCGTGAACAGACT 289
OY 150 AAGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 209
DB 290 AAGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 349
OY 210 GTCCTATCCGCTCTGCGGGGTACAGTCTCTGCTGCCAGGAAATGACTCAGTTT 269
DB 350 GTCCTATCCGCTCTGCGGGGTACAGTCTCTGCTGCCAGGAAATGACTCAGTTT 409
OY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAGGGAAGTT 469
OY 330 CTGCTCTGGGCTCTCA 344
DB 470 CTGCTCTGGGCTCTCA 484
```

RESULT 24
US-10-218-612-15

Sequence 15, Application US/10218612

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Geritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530PIC21

CURRENT APPLICATION NUMBER: US/10/218,612

PRIOR FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 15

LENGTH: 1524

TYPE: DNA

ORGANISM: Homo Sapien
US-10-218-612-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGCGTGAACAGACT 89
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGCGTGAACAGACT 229
OY 90 GCTCTCCGCCGAGTTCATTGTGAATTCAGCGTGAAGATTCAGCGTGAACAGACT 149
DB 230 GCTCTCCGCCGAGTTCATTGTGAATTCAGCGTGAAGATTCAGCGTGAACAGACT 289
OY 150 AAGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 209
DB 290 AAGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 349
OY 210 GTCCTATCCGCTCTGCGGGGTACAGTCTCTGCTGCCAGGAAATGACTCAGTTT 269
DB 350 GTCCTATCCGCTCTGCGGGGTACAGTCTCTGCTGCCAGGAAATGACTCAGTTT 409
OY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAGGGAAGTT 469
OY 330 CTGCTCTGGGCTCTCA 344
DB 470 CTGCTCTGGGCTCTCA 484
```

RESULT 25
US-10-218-631-15

Sequence 15, Application US/10218631

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Geritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530PIC14

CURRENT APPLICATION NUMBER: US/10/218,631

PRIOR FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-218-631-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30 CAGCGTTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 89
170 CAGCGTTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 229
90 GCTCCCTCCCGGAGTTCATTTGTAATTCACGAGTGAACGTTTCAAGAATGTGTAGAAAG 149
230 GCTCCCTCCCGGAGTTCATTTGTAATTCACGAGTGAACGTTTCAAGAATGTGTAGAAAG 289
150 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
290 AAGTGTAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 349
210 GTCTCATGCGCTCTGCGCGGATCATGTCTGTCTCCCGGAGAACTGACATCAGTTT 269
350 GTCTCATGCGCTCTGCGCGGATCATGTCTGTCTCCCGGAGAACTGACATCAGTTT 409
270 GCATGCGCTGCTGCAACACCCCTTTGTACGGGCGCAAGGCGCAAGAAAGGGAAGTT 329
410 GCATGCGCTGCTGCAACACCCCTTTGTACGGGCGCAAGGCGCAAGAAAGGGAAGTT 469
330 CTGCTCTGCGGCTCTCA 344
470 CTGCTCTGCGGCTCTCA 484

RESULT 26
US-10-218-765-15
Sequence 15, Application US/10218765
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218, 765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119, 480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23

PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222

PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 28-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCTGCAATCCAGTCTACCGAGTGTGAAGAATTCAGCTGACAAACGACT 89
DB 170 CAGGCTTTGGCTGCAATCCAGTCTACCGAGTGTGAAGAATTCAGCTGACAAACGACT 229

QY 90 GCTCTCTCCCGAGTATTGTGAATTCACAGGTTGAACGTTCAAGACATGTGTCAAGAAG 149
DB 230 GCTCTCTCCCGAGTATTGTGAATTCACAGGTTGAACGTTCAAGACATGTGTCAAGAAG 289

QY 150 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCATACGGGCT 209
DB 290 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCATACGGGCT 349

QY 210 GCTCATGCGCTCTGCGGGTACCATGCTCTGTCTCCCGAGGAACTGACTGACTT 269
DB 350 GCTCATGCGCTCTGCGGGTACCATGCTCTGTCTCCCGAGGAACTGACTGACTT 409

QY 270 GCATCAGCTGCTGCAACCCCTTTGTAAAGGCGCAAGGCCAAGAAAGGGAAGT 329
DB 410 GCATCAGCTGCTGCAACCCCTTTGTAAAGGCGCAAGGCCAAGAAAGGGAAGT 469

QY 330 CTGCTCGGCGCTCA 344
DB 470 CTGCTCGGCGCTCA 484

RESULT 27
US-10-218-784-15
; Sequence 15, Application US/10218784
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1018
; CURRENT APPLICATION NUMBER: US/10/218,784
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038

PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28

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; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

```

```

Query Match          85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCGCTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
Db 170 CAGGCTTTGGCGCTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229
    |||||||
QY 90 GCTCCTCCCCCGAGTTTGAATGTAATGCAAGTGAAGCTTCAAGACATGTGTAGAAG 149
    |||||||
Db 230 GCTCCTCCCCCGAGTTTGAATGTAATGCAAGTGAAGCTTCAAGACATGTGTAGAAG 289
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
Db 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||
QY 210 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACCTCAGTTT 269
    |||||||
Db 350 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACCTCAGTTT 409
    |||||||
QY 270 GCATCAGCTCTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAAGGGGAAGTT 329
    |||||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAAGGGGAAGTT 469
    |||||||
QY 330 CTGCTCTGGGCTCTCA 344
    |||||||
Db 470 CTGCTCTGGGCTCTCA 484

```

```

RESULT 28
US-10-218-849-15
; Sequence 15, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/218.849
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-849-15

```

```

Query Match          85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCGCTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
Db 170 CAGGCTTTGGCGCTGCAAAATCCAGTCTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229
    |||||||
QY 90 GCTCCTCCCCCGAGTTTGAATGTAATGCAAGTGAAGCTTCAAGACATGTGTAGAAG 149
    |||||||
Db 230 GCTCCTCCCCCGAGTTTGAATGTAATGCAAGTGAAGCTTCAAGACATGTGTAGAAG 289
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
Db 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||
QY 210 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACCTCAGTTT 269
    |||||||
Db 350 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACCTCAGTTT 409
    |||||||
QY 270 GCATCAGCTCTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAAGGGGAAGTT 329
    |||||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGAACGGGCAAGGCCCAAGAAAAGGGGAAGTT 469
    |||||||
QY 330 CTGCTCTGGGCTCTCA 344
    |||||||
Db 470 CTGCTCTGGGCTCTCA 484

```

```

RESULT 29
US-10-218-930-15
; Sequence 15, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC13
; CURRENT APPLICATION NUMBER: US/10/218.930
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-930-15

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Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGGCGCAATCAGGCTACCGTGAAGAAATTCAGCTGCAACGACT 89
DB 170 CAGGCTTTGGGCGCAATCAGGCTACCGTGAAGAAATTCAGCTGCAACGACT 229
QY 90 GCTCTCTCCCGGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGCAAGAA 149
DB 230 GCTCTCTCCCGGAGTTCATTGTGAATTGACGGTGAACGTTCAAGACATGTGCAAGAA 289
QY 150 AAGTGAATGAGCAAGAGCCGGGATCATGTACCCGAGTCTCTGTCATCATCAGGGGCT 209
DB 290 AAGTGAATGAGCAAGAGCCGGGATCATGTACCCGAGTCTCTGTCATCATCAGGGGCT 349
QY 210 GTCCTACGCTCTGCGGGGTACAGTCTCTGCTCCCGGAAACTGAACACTGATT 269
DB 350 GTCCTACGCTCTGCGGGGTACAGTCTCTGCTCCCGGAAACTGAACACTGATT 409
QY 270 GCATCAGCTCTGCAACACCCCTTTGTGAACGGGCCAAGGCCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTCTGCAACACCCCTTTGTGAACGGGCCAAGGCCCAAGAAAGGGAAGTT 469
QY 330 CTGGCTCGGCCCTCA 344
DB 470 CTGGCTCGGCCCTCA 484

RESULT 30
US-10-218-956-15
Sequence 15: Application US/10218956
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C15
CURRENT APPLICATION NUMBER: US/10/218,956
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638

PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 CAGGCTTGGCGTGCAGATCCAGTGTACAGTGTGAGAAATCCAGCTGAACAGCACT 89
Db 170 CAGGCTTGGCGTGCAGATCCAGTGTACAGTGTGAGAAATCCAGCTGAACAGCACT 229
Oy 90 GCTCCTCCCGAGTTCATTGTGAATTCACGAGTGAAGCTTCAGACATGTGTGAGAAG 149
Db 230 GCTCCTCCCGAGTTCATTGTGAATTCACGAGTGAAGCTTCAGACATGTGTGAGAAG 289
Oy 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAATCTCTGTGATCATCAGCGCCT 209
Db 290 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAATCTCTGTGATCATCAGCGCCT 349
Oy 210 GTCTCATGCGCTGCGGATACAGTCTCTGCTCCCGAGGAAATGAACTCAGTTT 269
Db 350 GTCTCATGCGCTGCGGATACAGTCTCTGCTCCCGAGGAAATGAACTCAGTTT 409
Oy 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAGGGAAGTT 329
Db 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAGGGAAGTT 469
Oy 330 CTGCTCGGCGCTCA 344
Db 470 CTGCTCGGCGCTCA 484

RESULT 31
US-10-219-003-15
Sequence 15: Application US/10219003
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P9530P1C12
CURRENT APPLICATION NUMBER: US/10/219, 003
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119, 480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079656
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/084441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086392
 PRIOR FILING DATE: 1998-05-22
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 PRIOR APPLICATION NUMBER: 60/089538
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 PRIOR APPLICATION NUMBER: 60/089905
 PRIOR FILING DATE: 1998-06-18
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090691
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/095302
 PRIOR FILING DATE: 1998-08-04
 PRIOR APPLICATION NUMBER: 60/095318
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 PRIOR APPLICATION NUMBER: 60/096146
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 PRIOR APPLICATION NUMBER: 60/096791
 PRIOR FILING DATE: 1998-08-17
 PRIOR APPLICATION NUMBER: 60/097986
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/098544
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 PRIOR FILING DATE: 1998-09-11
 PRIOR APPLICATION NUMBER: 60/100385
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: 60/100390
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: 60/100627

PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: 60/100848
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/100919
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: 60/101477
 PRIOR FILING DATE: 1998-09-23
 PRIOR APPLICATION NUMBER: 60/101738
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 60/101741
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 PRIOR FILING DATE: 1998-11-17
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 PRIOR APPLICATION NUMBER: 60/115565
 PRIOR FILING DATE: 1999-01-12
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 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/119549
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 PRIOR APPLICATION NUMBER: 60/130232
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 60/131022
 PRIOR FILING DATE: 1999-04-26
 PRIOR APPLICATION NUMBER: 60/131270
 PRIOR FILING DATE: 1999-04-27
 PRIOR APPLICATION NUMBER: 60/131291
 PRIOR FILING DATE: 1999-04-27
 PRIOR APPLICATION NUMBER: 60/131445
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 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 60/140650
 PRIOR FILING DATE: 1999-06-22
 PRIOR APPLICATION NUMBER: 60/140723
 PRIOR FILING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
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PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
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PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
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PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTCCGCGCAATCCAGTGTACAGTGAAGATCCAGTGAACAGACT 89
DB 170 CAGGCTTCCGCGCAATCCAGTGTACAGTGAAGATCCAGTGAACAGACT 229
QY 90 GCTCTCCCGCCAGTTCATTGTGAATTGCAAGGTTGCAAGCTTCAAGACATGTGTGAGAAG 149
DB 230 GCTCTCCCGCCAGTTCATTGTGAATTGCAAGGTTGCAAGCTTCAAGACATGTGTGAGAAG 289
QY 150 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTGTGATCATCGCGGCT 209
DB 290 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTGTGATCATCGCGGCT 349
QY 210 GTCATCAGCTCTGCGCGGATCACTCTCTGCTCCCGAGGGAAGTCACTGATT 269
DB 350 GTCATCAGCTCTGCGCGGATCACTCTCTGCTCCCGAGGGAAGTCACTGATT 409
QY 270 GCATCAGCTCTGCAACACCCCTCTTTGTACGGGCCCAAGGCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTCTGCAACACCCCTCTTTGTACGGGCCCAAGGCCAAGAAAGGGAAGTT 469
QY 330 CTGCGTCCGCGCTCA 344
DB 470 CTGCGTCCGCGCTCA 484

RESULT 32
US-10-219-010-15

Sequence 15, Application US/10219010
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Godard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530PIC20
CURRENT APPLICATION NUMBER: US/10/219,010
PRIOR APPLICATION DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
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PRIOR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/089538
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/09786
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022

PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAAGACT 89
DB 170 CAGGCTTGGCGCTCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAAGACT 229
QY 90 GCTCCTCCCGGAGTTGATTTGAATTCAGGCTGAAGCTTCAAGCATGTGTCAAGAA 149
DB 230 GCTCCTCCCGGAGTTGATTTGAATTCAGGCTGAAGCTTCAAGCATGTGTCAAGAA 289
QY 150 AAGTATGAGCAAGTCCCGGAGTATGATACCGAAGTCTGTGATCATCAGCGCT 209
DB 290 AAGTATGAGCAAGTCCCGGAGTATGATACCGAAGTCTGTGATCATCAGCGCT 349
QY 210 GTCTCATGCGCTGTGCGCGGATACAGTCTTGTGCTCCCGAAGAAATGAATCAAGTT 269
DB 350 GTCTCATGCGCTGTGCGCGGATACAGTCTTGTGCTCCCGAAGAAATGAATCAAGTT 409
QY 270 GCATCAGTCTGTGCAACACCCCTTTTGAAGGGGCAAGCCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGTCTGTGCAACACCCCTTTTGAAGGGGCAAGCCCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
DB 470 CTGCTCGGCGCTCA 484

RESULT 33
US-10-219-060-15
Sequence 15, Application US/10219060
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltzen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC22
CURRENT APPLICATION NUMBER: US/10/219,060
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146

PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
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PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-10-28
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PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
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PRIOR APPLICATION NUMBER: 60/113296
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PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
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PRIOR APPLICATION NUMBER: 60/115558
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10

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PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
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PRIOR FILING DATE: 1999-04-05
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

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Query Match 85.4%; Score 315; DB 42; Length 1524;
 Best Local Similarity 100.0%; Pred. No. 2e-159;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTCCGCTGCAAAATCCAGTGTACAGGTGAAGAATTCACCTGTAACAAGACT 89
DB 170 CAGGCTTTCCGCTGCAAAATCCAGTGTACAGGTGAAGAATTCACCTGTAACAAGACT 229
QY 90 GCTCCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAA 149
DB 230 GCTCCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAA 289
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 290 AAGTATGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 349
QY 210 GTCATATCGCTGCGCGGATACAGTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 269
DB 350 GTCATATCGCTGCGCGGATACAGTCTTCTGCTCCCGAGGAAACTGAACTCAGTTT 409

```

```

QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
DB 470 CTGCTCGGCGCTCA 484

```

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RESULT 34
US-10-219-061-15
; Sequence 15, Application US/10219061
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC16
; CURRENT APPLICATION NUMBER: US/10/219,061
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-061-15

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Query Match 85.4%; Score 315; DB 42; Length 1524;
 Best Local Similarity 100.0%; Pred. No. 2e-159;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTCCGCTGCAAAATCCAGTGTACAGGTGAAGAATTCACCTGTAACAAGACT 89
DB 170 CAGGCTTTCCGCTGCAAAATCCAGTGTACAGGTGAAGAATTCACCTGTAACAAGACT 229
QY 90 GCTCCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAA 149
DB 230 GCTCCTCCCCGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAA 289
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 290 AAGTATGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 349

```


QY	90	GCTCCTCCCCGAGTTCATTTGTAATTGCACGGTGAACGTTCAAGACATGTCAGAAAG	1.49
Dp	230	GCTCCTCCCCGAGTTCATTTGTAATTGCACGGTGAACGTTCAAGACATGTCAGAAAG	28.88
QY	150	AAGTGAATGAGCAAAAGTCCGGGATCATGTACGCCAAGTCTGTGCATCATCAGCGGCT	20.9
Dp	290	AAGTGAATGAGCAAAAGTCCGGGATCATGTACGCCAAGTCTGTGCATCATCAGCGGCT	34.9
QY	210	GTCATCATGGCCTTGCCGGGTACCAAGTCCTTCCTCCCAAGGAAACTGAACATCATTT	26.5
Dp	350	GTCATCATGGCCTTGCCGGGTACCAAGTCCTTCCTCCCAAGGAAACTGAACATCATTT	40.9
QY	270	GCATCAAGCTGTGCACAACCCCTCTTTGTAAAGGGCCCAAGGCCCAAAAAAGGGGAATT	32.9
Dp	410	GCATCAAGCTGTGCACAACCCCTCTTTGTAAAGGGCCCAAGGCCCAAAAAAGGGGAATT	46.9
QY	330	CTGGCTGGGCCCTCA 344	
Dp	470	CTGGCTGGGCCCTCA 484	

RESULT 37
US-10-219-064-15

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? Sequence 15, Application US/10219064
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Gerritsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaud, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Philippe F.
? APPLICANT: Watanabe, Colin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P3530P1C44
? CURRENT APPLICATION NUMBER: US/10/219,064
? CURRENT FILING DATE: 2002-08-13
? PRIOR APPLICATION NUMBER: 10/119,480
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? Remaining prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 246
? SEQ ID NO 15
? LENGTH: 1524
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-219-064-15

```

Query Match	85.48;	Score 315;	DB 42;	Length 1524;
Best Local Similarity	100.0%;	Pred. NO. 2e-159;		
Matches 315; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	30	CAGGCTTTGGCCCTCAAAATCCAGAGCTACAGTGTGAAGAAATTCACGTGAACAACAGCT	89
Db	170	CAGGCTTTGGCCCTGCAATTCAGAGCTACAGTGTGAAGAAATTCACGTGAACAACAGCT	228
QY	90	GCTCTCTCCCCGAGTTCAATTGTGAATTGACAGGTGAAGCTTCAAGACATGTTCAGAAG	148
Db	230	GCTCTCTCCCCGAGTTCAATTGTGAATTGACAGGTGAAGCTTCAAGACATGTTCAGAAG	288
QY	150	AAGTGAATGAGACAAAGTCCCGGAGTCAATGTACCGCAAGTCCGTGCATCAACAGCGGCT	208
Db	290	AAGTGAATGAGACAAAGTCCCGGAGTCAATGTACCGCAAGTCCGTGCATCAACAGCGGCT	348
QY	210	GTTTCATCGCTCTTGCCGGGTACAGTCTTCTGCTCCCAAGGAAACTGAATCACTTT	268
Db	350	GTTTCATCGCTCTTGCCGGGTACAGTCTTCTGCTCCCAAGGAAACTGAATCACTTT	408
QY	270	GCAATCAGCTGTGCAACACCCCTTTTGTAAAGGAGCCCAAGGCCCAAAAAAGGGAGATT	328
Db	410	GCAATCAGCTGTGCAACACCCCTTTTGTAAAGGAGCCCAAGGCCCAAAAAAGGGAGATT	468
QY	330	CTGGCTCGGCGCCCTCA 344	
Db	470	CTGGCTCGGCGCCCTCA 484	

RESULT 38
US-10-219-065-15

```

Sequence 15, Application US/10219065
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC39
CURRENT APPLICATION NUMBER: US/10/219,065
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15

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; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-219-065-15

```

```
Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGCGGTGCAAAATCCAGTGTACAGTGTGAAGAATTCAGTGAACAAGACT 89
    |||||||
DB 170 CAGGCTTTGCGGTGCAAAATCCAGTGTACAGTGTGAAGAATTCAGTGAACAAGACT 229
    |||||||

QY 90 GCTCTCTCCCGGAGTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 149
    |||||||
DB 230 GCTCTCTCCCGGAGTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 289
    |||||||

QY 150 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
DB 230 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||

QY 210 GTCATATGCGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAACCTGAGTTT 269
    |||||||
DB 350 GTCATATGCGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAACCTGAGTTT 409
    |||||||

QY 270 GCATAGCTGCTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAGTT 329
    |||||||
DB 410 GCATAGCTGCTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAGTT 469
    |||||||

QY 330 CTGCCTCGGCCCTCA 344
    |||||||
DB 470 CTGCCTCGGCCCTCA 484
    |||||||

RESULT 39
US-10-219-066-15
: Sequence 15, Application US/10219066
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530PIC27
: CURRENT APPLICATION NUMBER: US/10/219,066
: PRIOR FILING DATE: 2002-08-13
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
```

```
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-219-066-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGCGGTGCAAAATCCAGTGTACAGTGTGAAGAATTCAGTGAACAAGACT 89
    |||||||
DB 170 CAGGCTTTGCGGTGCAAAATCCAGTGTACAGTGTGAAGAATTCAGTGAACAAGACT 229
    |||||||

QY 90 GCTCTCTCCCGGAGTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 149
    |||||||
DB 230 GCTCTCTCCCGGAGTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 289
    |||||||

QY 150 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
DB 290 AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||

QY 210 GTCATATGCGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAACCTGAGTTT 269
    |||||||
DB 350 GTCATATGCGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAACCTGAGTTT 409
    |||||||

QY 270 GCATAGCTGCTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAGTT 329
    |||||||
DB 410 GCATAGCTGCTGCAACACCCCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAGTT 469
    |||||||

QY 330 CTGCCTCGGCCCTCA 344
    |||||||
DB 470 CTGCCTCGGCCCTCA 484
    |||||||

RESULT 40
US-10-219-067-15
: Sequence 15, Application US/10219067
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530PIC51
: CURRENT APPLICATION NUMBER: US/10/219,067
: PRIOR FILING DATE: 2002-08-14
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
```

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGCTGAACAGCACT 89
DB 170 CAGGCTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGCTGAACAGCACT 229
QY 90 GCTCCCTCCCGAGTTCATTGTGAATTGCAAGGTTGCAAGACATGTGTAGAAAG 149
DB 230 GCTCCCTCCCGAGTTCATTGTGAATTGCAAGGTTGCAAGACATGTGTAGAAAG 289
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGATCATCAGCGGCT 209
DB 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGATCATCAGCGGCT 349
QY 210 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 269
DB 350 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 409
QY 270 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAATT 329
DB 410 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAATT 469
QY 330 CTGCTCTGCGGCTCTCA 344
DB 470 CTGCTCTGCGGCTCTCA 484

RESULT 41
US-10-219-068-15

; Sequence 15, Application US/10219068
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C31
; CURRENT APPLICATION NUMBER: US/10/219,068
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-15

Query Match 85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGCTGAACAGCACT 89
DB 170 CAGGCTTCCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGCTGAACAGCACT 229
QY 90 GCTCCCTCCCGAGTTCATTGTGAATTGCAAGGTTGCAAGACATGTGTAGAAAG 149
DB 230 GCTCCCTCCCGAGTTCATTGTGAATTGCAAGGTTGCAAGACATGTGTAGAAAG 289
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGATCATCAGCGGCT 209
DB 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGATCATCAGCGGCT 349
QY 210 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 269
DB 350 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 409
QY 270 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAATT 329
DB 410 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAATT 469
QY 330 CTGCTCTGCGGCTCTCA 344
DB 470 CTGCTCTGCGGCTCTCA 484

RESULT 42
US-10-219-069-15

; Sequence 15, Application US/10219069
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17

```

; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-069-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 89
DB 170 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 229
QY 90 GCTCTCCGCCGAGTTCATTGTGAATTGACAGGTTCAGACATGTGTCAAGAAG 149
DB 230 GCTCTCCGCCGAGTTCATTGTGAATTGACAGGTTCAGACATGTGTCAAGAAG 289
QY 150 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCAGGGCCT 209
DB 290 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCAGGGCCT 349
QY 210 GTCATCAGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAATGAACTCAGTTT 269
DB 350 GTCATCAGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAATGAACTCAGTTT 409
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 329
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 469
QY 330 CTGCTCGGCCCTCA 344
DB 470 CTGCTCGGCCCTCA 484

RESULT 43
US-10-219-070-15
; Sequence 15, Application US/10219070
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC42
; CURRENT APPLICATION NUMBER: US/10/219,070
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
```

```

; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-070-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 89
DB 170 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 229
QY 90 GCTCTCCGCCGAGTTCATTGTGAATTGACAGGTTCAGACATGTGTCAAGAAG 149
DB 230 GCTCTCCGCCGAGTTCATTGTGAATTGACAGGTTCAGACATGTGTCAAGAAG 289
QY 150 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCAGGGCCT 209
DB 290 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCAGGGCCT 349
QY 210 GTCATCAGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAATGAACTCAGTTT 269
DB 350 GTCATCAGCTCTGCGGGGTACAGTCTTGTCTGCCAGGGAATGAACTCAGTTT 409
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 329
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 469
QY 330 CTGCTCGGCCCTCA 344
DB 470 CTGCTCGGCCCTCA 484

RESULT 44
US-10-219-071-15
; Sequence 15, Application US/10219071
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC46
; CURRENT APPLICATION NUMBER: US/10/219,071
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
```



```

; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-071-15

```

```

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCTGCAATATCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
DB 170 CAGGCTTTGGCTGCAATATCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229
QY 90 GCTCCTCCCGGAGTTCATTGTGAATTCACAGGTTCAAGACGTTCAAGACATGTGTCAAGAA 149
    |||||||
DB 230 GCTCCTCCCGGAGTTCATTGTGAATTCACAGGTTCAAGACGTTCAAGACATGTGTCAAGAA 289
QY 150 AAGTATGAGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
DB 290 AAGTATGAGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
QY 210 GTCTCATGCGCTTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 269
    |||||||
DB 350 GTCTCATGCGCTTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 409
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
    |||||||
DB 470 CTGCTCGGCGCTCA 484

```

```

RESULT 45
US-10-219-072-15
; Sequence 15. Application us/10219072
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C45
; CURRENT FILING DATE: 2002-08-13

```

```

; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-072-15

```

```

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCTGCAATATCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
DB 170 CAGGCTTTGGCTGCAATATCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229
QY 90 GCTCCTCCCGGAGTTCATTGTGAATTCACAGGTTCAAGACGTTCAAGACATGTGTCAAGAA 149
    |||||||
DB 230 GCTCCTCCCGGAGTTCATTGTGAATTCACAGGTTCAAGACGTTCAAGACATGTGTCAAGAA 289
QY 150 AAGTATGAGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
DB 290 AAGTATGAGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
QY 210 GTCTCATGCGCTTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 269
    |||||||
DB 350 GTCTCATGCGCTTGCAGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 409
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCGCTCA 344
    |||||||
DB 470 CTGCTCGGCGCTCA 484

```

```

Search completed: November 8, 2002, 01:59:07
Job time : 834.445 secs

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```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C45
; CURRENT FILING DATE: 2002-08-13

```


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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 : Search time 10.3091 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggaacttttgcggattgt.....tgcctccgaccaccatcct 369

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size: 10

Total number of hits satisfying chosen parameters: 25490

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Pending_Patents_NA.New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	85.4	1524	6	US-10-230-437-15
2	18	4.9	1587	6	US-10-092-411A-1425
3	18	4.9	1586	6	US-10-092-411A-2083
4	17	4.6	393	6	US-10-092-411A-263
5	16	4.3	311	5	US-09-513-999C-36268
6	16	4.3	397	6	US-10-266-131-144
7	16	4.3	433	5	US-09-513-999C-28601
8	16	4.3	577	5	US-09-513-999C-37773
9	15	4.1	455	5	US-09-513-999C-1336
10	15	4.1	460	5	US-09-513-999C-14500
11	15	4.1	481	5	US-09-513-999C-14500
12	15	4.1	579	6	US-10-240-425-140
13	15	4.1	686	6	US-10-240-425-710
14	15	4.1	940	1	PCT-US02-3203-35
15	15	4.1	1292	6	US-10-264-237-1045
16	15	4.1	1542	6	US-10-264-237-315
17	15	4.1	1733	6	US-10-264-237-315
18	15	4.1	1773	6	US-10-125-923A-555
19	15	4.1	1913	6	US-10-264-237-1252
20	15	4.1	3513	6	US-10-240-851-69
21	15	4.1	25020	6	US-10-192-280-1
22	15	4.1	36534	6	US-10-240-425-1461
23	15	4.1	74822	6	US-10-240-425-1121
24	14	3.8	25	7	US-60-417-190-48787
25	14	3.8	25	7	US-60-417-190-48788
26	14	3.8	25	7	US-60-417-190-48789

C 27	14	3.8	25	7	US-60-417-190-48790	Sequence 48790, A
C 28	14	3.8	25	7	US-60-417-190-48791	Sequence 48791, A
C 29	14	3.8	25	7	US-60-417-190-48792	Sequence 48792, A
C 30	14	3.8	25	7	US-60-417-190-48793	Sequence 48793, A
C 31	14	3.8	25	7	US-60-417-190-48794	Sequence 48794, A
C 32	14	3.8	25	7	US-60-417-190-48795	Sequence 48795, A
C 33	14	3.8	25	7	US-60-417-190-48796	Sequence 48796, A
C 34	14	3.8	25	7	US-60-417-190-48797	Sequence 48797, A
C 35	14	3.8	25	7	US-60-417-190-48798	Sequence 48798, A
C 36	14	3.8	25	7	US-60-417-190-48799	Sequence 48799, A
C 37	14	3.8	25	7	US-60-417-190-48800	Sequence 48800, A
C 38	14	3.8	25	7	US-60-417-190-48801	Sequence 48801, A
C 39	14	3.8	25	7	US-60-417-190-48802	Sequence 48802, A
C 40	14	3.8	25	7	US-60-417-190-48803	Sequence 48803, A
C 41	14	3.8	25	7	US-60-417-190-48804	Sequence 48804, A
C 42	14	3.8	25	7	US-60-417-190-48805	Sequence 48805, A
C 43	14	3.8	25	7	US-60-417-190-48806	Sequence 48806, A
C 44	14	3.8	25	7	US-60-417-190-48807	Sequence 48807, A
C 45	14	3.8	25	7	US-60-417-190-48808	Sequence 48808, A

ALIGNMENTS

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C94
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 85.4%; Score 315; DB 6; Length 1524;

Best Local Similarity 100.0%; Pred. No. 8.4e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGCAATCCAGTGCACAGTGTGAAGATTCACAGTCAACAGCT 89
170 CAGGCTTTGGCGCAATCCAGTGTGAAGATTCACAGTCAACAGCT 229

QY 90 GCTCCCTCCCGAGTTCATGTGAATTCACAGGTAACAGTTCAGACATGTTCAGAAAG 149
230 GCTCCCTCCCGAGTTCATGTGAATTCACAGGTAACAGTTCAGACATGTTCAGAAAG 289

QY 150 AAGTGAATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
290 AAGTGAATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349

QY 210 GTCATCAGCCTGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 269
350 GTCATCAGCCTGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 409

QY 270 GCATCAGCTGTGCACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAGTT 329
410 GCATCAGCTGTGCACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGGAGTT 469

QY 330 CTGGCTGGGCCCCCA 344
470 CTGGCTGGGCCCCCA 484

RESULT 2

US-10-092-411A-1425

; Sequence 1425, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 1425
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-1425

Query Match 4.9%; Score 18; DB 6; Length 1587;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 AATTCACGCTGAACAAG 86
567 AATTCACGCTGAACAAG 584

RESULT 3

US-10-092-411A-2083/C

; Sequence 2083, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 2083
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-2083

Query Match 4.9%; Score 18; DB 6; Length 1596;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGATCAGCTGTGCAC 286
1308 TGATCAGCTGTGCAC 1291

RESULT 4

US-10-092-411A-263/C

; Sequence 263, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 263
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-263

Query Match 4.6%; Score 17; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 TCATGTGATTCGACG 121
389 TCATGTGATTCGACG 373

RESULT 5

US-09-513-999C-36268/C

; Sequence 36268, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 36268
; LENGTH: 111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-36268

Query Match 4.3%; Score 16; DB 5; Length 111;

Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 TGAAGTCACTTTCAT 273
|||||
DB 70 TGAAGTCACTTTCAT 55

RESULT 6

US-10-266-131-144/c
; Sequence 144, Application US/10266131
; GENERAL INFORMATION:
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
; TITLE OF INVENTION: Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0030-USA
; CURRENT APPLICATION NUMBER: US/10/266,131
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/617,675
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/143,878
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2908
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-266-131-144

Query Match
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TCTGCTCCCGAGGAA 255
|||||
DB 247 TCTGCTCCCGAGGAA 232

RESULT 7

US-09-513-999C-28601/c
; Sequence 28601, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28601
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 275
; OTHER INFORMATION: n-a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 309
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 310
; OTHER INFORMATION: r-a or g

Query Match
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGGATCA 176
|||||
DB 305 CAAAGTCCCGGATCA 290

RESULT 8

US-09-513-999C-3777/c
; Sequence 3777, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3777
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..474
; NAME/KEY: sig_peptide
; LOCATION: 73..123
; OTHER INFORMATION: score 9.3
US-09-513-999C-3777

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGATCAGCTGCTGCA 284
|||||
DB 335 TGATCAGCTGCTGCA 320

RESULT 9

US-09-513-999C-24773/c
; Sequence 24773, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 24773
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 182
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature

LOCATION: 183
OTHER INFORMATION: k=g or t
US-09-513-999C-24773

Query Match
Best Local Similarity 4.1%; Score 15; DB 5; Length 250;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GCTGCAATTCAGTG 54
Db 39 GCTGCAATTCAGTG 25

RESULT 10
US-09-513-999C-1336

Sequence 1336, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Duclert, A.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 1336
LENGTH: 466
TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS

LOCATION: 141..464
FEATURE:

NAME/KEY: misc_feature
LOCATION: 194
OTHER INFORMATION: m=a or c

FEATURE:
NAME/KEY: misc_feature
LOCATION: 197
OTHER INFORMATION: m=a or c

FEATURE:
NAME/KEY: misc_feature
LOCATION: 198
OTHER INFORMATION: n=a, g, c or t

FEATURE:
NAME/KEY: UNSURE
LOCATION: 19
OTHER INFORMATION: Xaa=Lys or Asn

FEATURE:
NAME/KEY: UNSURE
LOCATION: 20
OTHER INFORMATION: Xaa=Phe or Ile or Leu or Val

US-09-513-999C-1336

Query Match
Best Local Similarity 4.1%; Score 15; DB 5; Length 466;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 TGAGAATTCAGCT 78
Db 281 TGAGAATTCAGCT 295

RESULT 11
US-09-513-999C-14500/c

Sequence 14500, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14500
LENGTH: 481
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 133
OTHER INFORMATION: y=c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 325
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 326
OTHER INFORMATION: w=a or t

US-09-513-999C-14500

Query Match
Best Local Similarity 4.1%; Score 15; DB 5; Length 481;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 AGTTCTGCTCGGCC 340
Db 388 AGTTCTGCTCGGCC 374

RESULT 12
US-10-240-425-140

Sequence 140, Application US/10240425
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Schert, Uwe
APPLICANT: Vockley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentlin Ver. 2.1
SEQ ID NO 140
LENGTH: 579
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19
OTHER INFORMATION: Xaa=Lys or Asn

US-10-240-425-140

Query Match
Best Local Similarity 4.1%; Score 15; DB 6; Length 579;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GCCAAGCCCAAGAA 318
Db 81 GCCAAGCCCAAGAA 95

```
RESULT 13
US-10-240-425-710
; Sequence 710, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 710
; LENGTH: 686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF634580
; NAME/KEY: unsure
; LOCATION: (1)..(686)
; OTHER INFORMATION: n = a or c or g or t
US-10-240-425-710

Query Match
Best Local Similarity 100.0%; Score 15; DB 6; Length 686;
Pred. No. 33;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GTCGAGAAGAGTGA 155
DB 554 GTCGAGAAGAGTGA 568

RESULT 14
PCT-US02-32032-35/C
; Sequence 35, Application PC/TUS0232032
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: WARREN, Bridget A.
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: TRAN,uyen K.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: YANG, Junming
; APPLICANT: XU, Yuming
; APPLICANT: TANG, Y. Tom
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: BECHA, Shanya D.
; APPLICANT: YAO, Monique G.
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: LAL, Preeti G.
; APPLICANT: ZEBARJADIAN, Yeganeh
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jeyalakmi
; APPLICANT: GORVAD, Ann E.
; APPLICANT: KABLE, Amy E.
; APPLICANT: LU, Dyung Alina M.
```

```
APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PF-1217 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/32032
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,945
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US 60/343,718
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/343,980
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/332,426
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7340485CB1
PCT-US02-32032-35

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 940;
Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 TGTGAGATTCACG 76
DB 303 TGTGAGATTCACG 289

RESULT 15
US-10-264-237-561/C
; Sequence 561, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P431PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patent Ver. 3.1
; SEQ ID NO 561
; LENGTH: 1292
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (534)..(534)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-561

Query Match
Best Local Similarity 100.0%; Score 15; DB 6; Length 1292;
Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGCCCAAGAA 318
DB 434 GCCAAGCCCAAGAA 420

RESULT 16
US-10-264-237-1045
; Sequence 1045, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

FILE REFERENCE: PAL31PI
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1045
LENGTH: 1542
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1471)..(1471)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1045

Query Match 4.1%; Score 15; DB 6; Length 1542;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 CAGGCTTGGCTGC 44
DB 310 CAGGCTTGGCTGC 324

RESULT 17
US-10-264-237-315/C
Sequence 315, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Blise et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAL31PI
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 315
LENGTH: 1733
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1459)..(1459)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1509)..(1509)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-315

Query Match 4.1%; Score 15; DB 6; Length 1733;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 GTGTGAAGATTCCA 75
DB 1051 GTGTGAAGATTCCA 1037

RESULT 18
US-10-125-923A-555/C
Sequence 555, Application US/10125923A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P94301C79
CURRENT APPLICATION NUMBER: US/10/125,923A
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 555
LENGTH: 1773
TYPE: DNA
ORGANISM: Homo sapien
US-10-125-923A-555

Query Match 4.1%; Score 15; DB 6; Length 1773;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 TCAGCTGCTGCACACA 287
DB 1008 TCAGCTGCTGCACACA 994

RESULT 19
US-10-264-237-1252
Sequence 1252, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Blise et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAL31PI
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1252
LENGTH: 1913
TYPE: DNA
ORGANISM: Homo sapiens
US-10-264-237-1252

Query Match 4.1%; Score 15; DB 6; Length 1913;
Best Local Similarity 100.0%; Pred. No. 35;

Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGCCCCAGAA 318
|||||

Db 136 GCCAAGCCCCAGAA 150

RESULT 20

US-10-240-851-69/C

; Sequence 69, Application US/10240851

; GENERAL INFORMATION:

; APPLICANT: John P. Carulli et al.

; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3

; FILE REFERENCE: 032796-021

; CURRENT APPLICATION NUMBER: US/10/240,851

; PRIOR FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: US 09/544,398

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 09/543,771

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 09/229,319

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 60/071,449

; PRIOR FILING DATE: 1998-01-13

; PRIOR APPLICATION NUMBER: US 60/105,511

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 109

; SEQ ID NO 69

; LENGTH: 3513

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-240-851-69

Query Match 4.1%; Score 15; DB 6; Length 3513;
Best Local Similarity 100.0%; Pred. No. 36;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 CAGCTGCTGCAACAC 288
|||||

Db 944 CAGCTGCTGCAACAC 930

RESULT 21

US-10-192-280-1

; Sequence 1, Application US/10192280

; GENERAL INFORMATION:

; APPLICANT: Dattagupta, Nanibhushan

; APPLICANT: Shah, Ketan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING

; TITLE OF INVENTION: STREPTOCOCCUS AGALACTIAE CAPSULAR POLYSACCHARIDE SYNTHESIS

; FILE REFERENCE: 475412001300

; CURRENT APPLICATION NUMBER: US/10/192,280

; PRIOR FILING DATE: 2002-07-09

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 25020

; TYPE: DNA

; ORGANISM: Streptococcus agalactiae

US-10-192-280-1

Query Match 4.1%; Score 15; DB 6; Length 25020;
Best Local Similarity 100.0%; Pred. No. 39;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAAGTGTGAGC 161
|||||

Db 10941 AAGAAGTGTGAGC 10955

RESULT 22

US-10-240-425-1461

; Sequence 1461, Application US/10240425

; GENERAL INFORMATION:

; APPLICANT: Williams, Amanda

; APPLICANT: Boland, Joseph F.

; APPLICANT: Lord, Reginald V.

; APPLICANT: Alvarez, Chris

; APPLICANT: Wetzel, Jon C.

; APPLICANT: Scherf, Uwe

; APPLICANT: Vockley, Joseph G.

; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

; FILE REFERENCE: 44921-5026

; CURRENT APPLICATION NUMBER: US/10/240,425

; PRIOR FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: PCT/US01/09847

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 60/193,446

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 1588

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1461

; LENGTH: 36534

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-240-425-1461

Query Match 4.1%; Score 15; DB 6; Length 36534;
Best Local Similarity 100.0%; Pred. No. 39;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CTGACTCAGTTTGC 271
|||||

Db 23250 CTGACTCAGTTTGC 23264

RESULT 23

US-10-240-425-1121

; Sequence 1121, Application US/10240425

; GENERAL INFORMATION:

; APPLICANT: Williams, Amanda

; APPLICANT: Boland, Joseph F.

; APPLICANT: Lord, Reginald V.

; APPLICANT: Alvarez, Chris

; APPLICANT: Wetzel, Jon C.

; APPLICANT: Scherf, Uwe

; APPLICANT: Vockley, Joseph G.

; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

; FILE REFERENCE: 44921-5026

; CURRENT APPLICATION NUMBER: US/10/240,425

; PRIOR FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: PCT/US01/09847

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 60/193,446

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 1588

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1121

; LENGTH: 74822

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-240-425-1121

Query Match 4.1%; Score 15; DB 6; Length 74822;
Best Local Similarity 100.0%; Pred. No. 40;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ATGTCTCAGAAAGAA 151
|||||

Db 70056 ATGTCTCAGAAAGAA 70070

```

RESULT 24
US-60-417-190-48787/c
; Sequence 48787, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48787

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 23 AAGATTCCAGCTG 10
|||||

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; ORGANISM: Homo sapien
US-60-417-190-48789

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 20 AAGATTCCAGCTG 7
|||||

RESULT 27
US-60-417-190-48790/c
; Sequence 48790, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48790

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 19 AAGATTCCAGCTG 6
|||||

RESULT 28
US-60-417-190-48791/c
; Sequence 48791, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48791

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 18 AAGATTCCAGCTG 5
|||||

RESULT 29
US-60-417-190-48792/c
; Sequence 48792, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy

```

```

; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48792

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 AAGATTCCAGCTG 79
    |||||||
Db 16 AAGATTCCAGCTG 3

RESULT 30
US-60-417-190-48793/C
; Sequence 48793, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48793
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48793

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 AAGATTCCAGCTG 79
    |||||||
Db 15 AAGATTCCAGCTG 2

RESULT 31
US-60-417-190-94484/C
; Sequence 94484, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94484

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 143 CAGAAAGAGTGAT 156
    |||||||
Db 25 CAGAAAGAGTGAT 12

RESULT 32
US-60-417-190-94485/C
; Sequence 94485, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94485
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94485

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGAT 156
    |||||||
Db 24 CAGAAAGAGTGAT 11

RESULT 33
US-60-417-190-94486/C
; Sequence 94486, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94486
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94486

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGAT 156
    |||||||
Db 23 CAGAAAGAGTGAT 10

RESULT 34
US-60-417-190-94487/C
; Sequence 94487, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
```

NUMBER OF SEQ ID NOS: 122930
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 94487
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-417-190-94487

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGAT 156
|||||
DB 22 CAGAAAGAGTGAT 9

RESULT 35
US-60-417-190-94488/C
Sequence 94488, Application US/60417190
GENERAL INFORMATION:
APPLICANT: Giulia Kennedy
APPLICANT: Hajime Matsuzaki
APPLICANT: Mei-Mei Shen

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522
CURRENT APPLICATION NUMBER: US/60/417,190
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 122930
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 94488
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-417-190-94488

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGAT 156
|||||
DB 20 CAGAAAGAGTGAT 7

RESULT 36
US-60-417-190-94489/C
Sequence 94489, Application US/60417190
GENERAL INFORMATION:
APPLICANT: Giulia Kennedy
APPLICANT: Hajime Matsuzaki
APPLICANT: Mei-Mei Shen
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REFERENCE: 3522
CURRENT APPLICATION NUMBER: US/60/417,190
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 122930
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 94489
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-417-190-94489

Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGAT 156
|||||
DB 19 CAGAAAGAGTGAT 6

RESULT 37
US-09-513-999C-16171/C
Sequence 16171, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 16171
LENGTH: 80
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-16171

Query Match
Best Local Similarity 100.0%; Score 14; DB 5; Length 80;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 93 CCTCCCCGAGTTC 106
|||||
DB 26 CCTCCCCGAGTTC 13

RESULT 38
US-09-513-999C-17785
Sequence 17785, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 17785
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 69
OTHER INFORMATION: h-a or c or t
US-09-513-999C-17785

Query Match
Best Local Similarity 100.0%; Score 14; DB 5; Length 100;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGCGAT 174
|||||
DB 43 CAAAGTCCGCGAT 56

RESULT 39
US-09-513-999C-19578
Sequence 19578, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO: 19578
LENGTH: 109
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-19578

Query Match 3.8%; Score 14; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174
DB 87 CAAAGTCCGGGAT 100

RESULT 40
US-09-513-999C-23316
Sequence 23316, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO: 23316
LENGTH: 112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-23316

Query Match 3.8%; Score 14; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174
DB 83 CAAAGTCCGGGAT 96

RESULT 41
US-09-513-999C-18596/C
Sequence 18596, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO: 18596
LENGTH: 116
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-18596

Query Match 3.8%; Score 14; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174
DB 95 CAAAGTCCGGGAT 82

RESULT 42
US-09-513-999C-14544/C
Sequence 14544, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO: 14544
LENGTH: 125
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-14544

Query Match 3.8%; Score 14; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CGCCTCTGCCGGGT 230
DB 109 CGCCTCTGCCGGGT 96

RESULT 43
US-09-513-999C-18527/C
Sequence 18527, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO: 18527
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-18527

Query Match 3.8%; Score 14; DB 5; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174
DB 55 CAAAGTCCGGGAT 42

RESULT 44
US-09-513-999C-28218
Sequence 28218, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 28218
 ; LENGTH: 138
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-513-999C-28218

Query Match 3.8%; Score 14; DB 5; Length 138;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 TTCATTGTGAATTG 117
 |||||
 Db 20 TTCATTGTGAATTG 33

RESULT 45
 US-09-513-999C-25794
 ; Sequence 25794, Application US/09513999C
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 25794
 ; LENGTH: 142
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-513-999C-25794

Query Match 3.8%; Score 14; DB 5; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 ACATGTGTGAGAAA 148
 |||||
 Db 39 ACATGTGTGAGAAA 52

Search completed: November 8, 2002, 02:02:17
 Job time : 69.3091 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 494.427 Seconds
(without alignments)
12086.984 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggcgaacttttgcggtgtgt.....tggtccgcacacacacact 369

Scoring table: OLIGO_NUC
Gapop 60.0 ; Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5082808

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	315	85.4	704	BI919074 603180881
2	315	85.4	707	BI913989 603180565
3	315	85.4	920	AL538562 AL538562
4	314	85.1	593	BE386060 601276753
5	307	83.2	747	BI917149 603181571
6	295	79.9	987	BQ68420 AGENCOURT

7	284	77.0	690	13	BI669845
8	283	76.7	340	14	H06756
9	271	73.4	1010	12	BF345141
10	263	71.3	573	10	BE395206
11	262	71.0	548	10	B0882838
12	258	69.9	704	13	BI823714
13	237	64.2	570	13	BI831919
14	235	63.7	352	9	AA349894
15	224	60.7	670	12	BE753617
16	205	55.6	654	12	BE746601
17	196	53.1	698	13	BI554034
18	190	51.5	540	10	AW954549
19	175	47.4	433	9	AA582576
20	175	47.4	522	9	AI767459
21	175	47.4	541	14	BM974798
22	175	47.4	651	10	AV717094
23	175	47.4	652	14	BM980701
24	175	47.4	738	14	BM981455
25	174	47.2	890	12	BF125425
26	173	46.9	449	9	AI140655
27	167	45.3	878	12	BF125664
28	166	45.0	395	14	R20352
29	166	45.0	429	14	HI7189
30	151	40.9	434	9	AI299246
31	148	40.1	424	9	AI138793
32	145	39.3	435	10	AW014802
33	143	38.8	516	9	AA776783
34	143	38.8	794	12	BE731003
35	143	38.8	1134	12	BE730800
36	141	38.2	350	12	BE213586
37	141	38.2	484	12	BE184021
38	140	37.9	781	12	BE193459
39	140	37.7	424	12	BE188218
40	139	37.7	323	12	BE192926
41	139	37.7	323	12	BE210457
42	139	37.7	324	12	BE215210
43	139	37.7	330	12	BE200048
44	139	37.7	331	12	BE181955
45	139	37.7	331	12	BE204666

ALIGNMENTS

RESULT 1
BI919074 704 bp mRNA linear EST 16-OCT-2001
603180881.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5',
LOCUS
DEFINITION
mRNA sequence.
ACCESSION
BI919074
VERSION
BI919074.1 GI:16200128
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 704)
AUTHORS
NIH-MGC http://mgc.ncl.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM1618 row: a column: 21
High quality sequence start: 4
High quality sequence stop: 702.
Location/Qualifiers

FEATURES

source

1. 704
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5244956"
/clone_1lb="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 132 a 237 c 204 g 131 t

ORIGIN

Query Match 85.4%; Score 315; DB 13; Length 704;
Best Local Similarity 100.0%; Pred. No. 1.7e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTCTACAGTGTGAAGATTCCAGTGAACAAGACT 89
DB 347 CAGGCTTGGCGCTGCAATCCAGTCTACAGTGTGAAGATTCCAGTGAACAAGACT 406
QY 90 GCTCTCTCCCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 149
DB 407 GCTCTCTCCCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 466
QY 150 AAGTATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTGTGCATCATCAGCGGCT 209
DB 467 AAGTATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTGTGCATCATCAGCGGCT 526
QY 210 GTCTCATGCGCTGTGCGGGATACAGTCTGTGCTCCCGAGGAAATGTAACATCAGTTT 269
DB 527 GTCTCATGCGCTGTGCGGGATACAGTCTGTGCTCCCGAGGAAATGTAACATCAGTTT 586
QY 270 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
DB 587 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 646
QY 330 CTGCTCGGGCCCTCA 344
DB 647 CTGCTCGGGCCCTCA 661

RESULT 2 707 bp mRNA linear EST 16-OCT-2001
BI913989
LOCUS 603180565F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244569 5',
DEFINITION mRNA sequence.
ACCESSION BI913989
VERSION BI913989.1 GI:16178286
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 707)
NIH-MGC http://imgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Plate: L1AM11617 row: a column: 18
High quality sequence stop: 698.
Location/Qualifiers
1. 707
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5244569"
/clone_1lb="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t

ORIGIN

Query Match 85.4%; Score 315; DB 13; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.7e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTCTACAGTGTGAAGATTCCAGTGAACAAGACT 89
DB 315 CAGGCTTGGCGCTGCAATCCAGTCTACAGTGTGAAGATTCCAGTGAACAAGACT 374
QY 90 GCTCTCTCCCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 149
DB 375 GCTCTCTCCCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 434
QY 150 AAGTATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTGTGCATCATCAGCGGCT 209
DB 435 AAGTATGAGACAAAGTCCCGGATCATGTACCCCAAGTCTGTGCATCATCAGCGGCT 494
QY 210 GTCTCATGCGCTGTGCGGGATACAGTCTGTGCTCCCGAGGAAATGTAACATCAGTTT 269
DB 495 GTCTCATGCGCTGTGCGGGATACAGTCTGTGCTCCCGAGGAAATGTAACATCAGTTT 554
QY 270 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
DB 555 GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 614
QY 330 CTGCTCGGGCCCTCA 344
DB 615 CTGCTCGGGCCCTCA 629

RESULT 3 920 bp mRNA linear EST 16-FEB-2001
AL538562
LOCUS AL538562 L11_F1013.FBn1 Homo sapiens cDNA clone CSODF024Y004 5
DEFINITION Prime, mRNA sequence.
ACCESSION AL538562
VERSION AL538562.1 GI:12866967
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 920)
LI, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 920

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DF0241004"
 /clone_11b="LTI_FL013_FBrn1"
 /dev_stage="pooled tissue from post conception fetuses (20
 week, 24 week and 26 week)"
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dt) primer. Five prime
 end and enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by life
 technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 172 a 285 c 257 g 199 t 7 others
 ORIGIN

Query Match 85.4%; Score 315; DB 9; Length 920;
 Best Local Similarity 100.0%; Pred. No. 1.8e-166;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAAGCACT 89
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 DB 308 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAAGCACT 367
 |||||||
 QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGCACGCGTGAACGTTCAAGACATGTGTCAAGAA 149
 |||||||
 DB 368 GCTCTCTCCCGAGTTCATTGTGAATTGCACGCGTGAACGTTCAAGACATGTGTCAAGAA 427
 |||||||
 QY 150 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCT 209
 |||||||
 DB 428 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCT 487
 |||||||
 QY 210 GTCTCATGCGCTTGCAGGATGACAGTCTTCTGCTCCCAAGGAACTGAACATCAGTTT 269
 |||||||
 DB 488 GTCTCATGCGCTTGCAGGATGACAGTCTTCTGCTCCCAAGGAACTGAACATCAGTTT 547
 |||||||
 QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTATACGGGGCCCAAGGAAAGGGGAAGTT 329
 |||||||
 DB 548 GCATCAGCTGTGCAACACCCCTCTTTGTATACGGGGCCCAAGGAAAGGGGAAGTT 607
 |||||||
 QY 330 CTGCTCGGGCCCTCA 344
 |||||||
 DB 608 CTGCTCGGGCCCTCA 622

RESULT 4
 BE386060 593 bp mRNA linear EST 21-JUL-2000
 LOCUS BE386060
 DEFINITION 601276753.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617749 5',
 mRNA sequence.
 ACCESSION BE386060
 VERSION BE386060.1 GI:9331425
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 593)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Plate: L1CM285 row: 1 column: 14
 High quality sequence stop: 593.
 Location/Qualifiers
 1..593
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3617749"
 /clone_11b="NIH_MGC_20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin. Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 139 a 166 c 183 g 105 t
 ORIGIN

Query Match 85.1%; Score 314; DB 10; Length 593;
 Best Local Similarity 100.0%; Pred. No. 5.9e-166;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAAGCACTG 90
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 DB 246 AGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAAGCACTG 305
 |||||||
 QY 91 CTCCTCTCCCGAGTTCATTGTGAATTGCACGCGTGAACGTTCAAGACATGTGTCAAGAA 150
 |||||||
 DB 306 CTCCTCTCCCGAGTTCATTGTGAATTGCACGCGTGAACGTTCAAGACATGTGTCAAGAA 365
 |||||||
 QY 151 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCTG 210
 |||||||
 DB 366 AAGTGTGAGCAAGAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGGCTG 425
 |||||||
 QY 211 TCTCATGCGCTTGCAGGATGACAGTCTTCTGCTCCCAAGGAACTGAACATCAGTTT 270
 |||||||
 DB 426 TCTCATGCGCTTGCAGGATGACAGTCTTCTGCTCCCAAGGAACTGAACATCAGTTT 485
 |||||||
 QY 271 CATCAGCTGTGCAACACCCCTCTTTGTATACGGGGCCCAAGGAAAGGGGAAGTTT 330
 |||||||
 DB 486 CATCAGCTGTGCAACACCCCTCTTTGTATACGGGGCCCAAGGAAAGGGGAAGTTT 545
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 QY 331 TGCCTCGGGCCCTCA 344
 |||||||
 DB 546 TGCCTCGGGCCCTCA 559

RESULT 5
 BI917149 747 bp mRNA linear EST 16-OCT-2001
 LOCUS BI917149
 DEFINITION 603181571.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245648 5',
 mRNA sequence.
 ACCESSION BI917149
 VERSION BI917149.1 GI:16181111
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 747)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Found through the I.M.A.G.E. Consortium/LLNL at:
 http://lmlm1619.gov
 Plate: LMLM1619 row: n column: 17
 High quality sequence stop: 737.

FEATURES
 source
 1. 747
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5245648"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t
 ORIGIN

Query Match 83.28; Score 307; DB 13; Length 747;
 Best Local Similarity 100.0%; Pred. No. 5.7e-162;
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCGCTCAATCCAGTGCATGCAAGTGAAGATTCACCTGACACAGACT 89
 |||||||
 Db 354 CAGCCTTGGCGCTCAATCCAGTGCATGCAAGTGAAGATTCACCTGACACAGACT 413
 QY 90 GCTCCCTCCCGAGATTCATGTAATGCAAGTGAAGTTCAGACATGTGCAGAAAG 149
 |||||||
 Db 414 GCTCCCTCCCGAGATTCATGTAATGCAAGTGAAGTTCAGACATGTGCAGAAAG 473
 QY 150 AAGTGAAGGAGCAAGGCGGGGATCATGTACGCAAGTCCCTGTGCATCATCAGCGGCT 209
 |||||||
 Db 474 AAGTGAAGGAGCAAGGCGGGGATCATGTACGCAAGTCCCTGTGCATCATCAGCGGCT 533
 QY 210 GTCTCATCGGCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTCAACTCAGTTT 269
 |||||||
 Db 534 GTCTCATCGGCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTCAACTCAGTTT 593
 QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAGCGGCGCCCAAGAAAAAGGGAAGTT 329
 |||||||
 Db 594 GCATCAGCTGCTGCAACACCCCTCTTTGTAAGCGGCGCCCAAGAAAAAGGGAAGTT 653
 QY 330 CTGCTCTC 336
 |||||||
 Db 654 CTGCTCTC 660

RESULT 6
 B0668420 987 bp mRNA linear EST 15-JUL-2002
 LOCUS B0668420
 DEFINITION AGENCOURT_8301981 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5275121
 5' mRNA sequence.
 ACCESSION B0668420
 VERSION B0668420.1 GI:21778667
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgc.ncl.nih.gov/ (bases 1 to 987)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://lmlm1619.gov
 Plate: LLM2457 row: m column: 10
 High quality sequence stop: 583.

FEATURES
 source
 1. 987
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5275121"
 /clone_lib="NIH_MGC_102"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 196 a 314 c 285 g 191 t 1 others
 ORIGIN

Query Match 79.98; Score 295; DB 14; Length 987;
 Best Local Similarity 100.0%; Pred. No. 3.7e-155;
 Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCGCTCAATCCAGTGCATGCAAGTGAAGATTCACCTGACACAGACT 89
 |||||||
 Db 301 CAGCCTTGGCGCTCAATCCAGTGCATGCAAGTGAAGATTCACCTGACACAGACT 360
 QY 90 GCTCCCTCCCGAGATTCATGTAATGCAAGTGAAGTTCAGACATGTGCAGAAAG 149
 |||||||
 Db 361 GCTCCCTCCCGAGATTCATGTAATGCAAGTGAAGTTCAGACATGTGCAGAAAG 420
 QY 150 AAGTGAAGGAGCAAGGCGGGGATCATGTACGCAAGTCCCTGTGCATCATCAGCGGCT 209
 |||||||
 Db 421 AAGTGAAGGAGCAAGGCGGGGATCATGTACGCAAGTCCCTGTGCATCATCAGCGGCT 480
 QY 210 GTCTCATCGGCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTCAACTCAGTTT 269
 |||||||
 Db 481 GTCTCATCGGCTGCGGGGTACAGTCTTGTGCTCCCGAGGAACTCAACTCAGTTT 540
 QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAGCGGCGCCCAAGAAAAAGG 324
 |||||||
 Db 541 GCATCAGCTGCTGCAACACCCCTCTTTGTAAGCGGCGCCCAAGAAAAAGG 595

RESULT 7
 B1669845 690 bp mRNA linear EST 12-SEP-2001
 LOCUS B1669845
 DEFINITION 603293440F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312889 5',
 mRNA sequence.
 ACCESSION B1669845
 VERSION B1669845.1 GI:15584078
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgc.ncl.nih.gov/ (bases 1 to 690)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
 Toshitsuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

FEATURES

source

Location/Qualifiers
1. 1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4153684"
/issue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."
266 a 344 c 254 g 146 t

BASE COUNT
ORIGIN

Query Match 73.4%; Score 271; DB 12; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1.3e-141;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGCGTTGCGCTGCAATCCAGTGTACAGTGAAGATTCAGGTGAACAACGACTG 90
DB 258 AGCGTTGCGCTGCAATCCAGTGTACAGTGAAGATTCAGGTGAACAACGACTG 317
QY 91 CTGCTCCCGGAGTCTATTGTGAATTCACAGGTGAACGATGTTGTCAGAAAGA 150
DB 318 CTGCTCCCGGAGTCTATTGTGAATTCACAGGTGAACGATGTTGTCAGAAAGA 377
QY 151 AGTATGAGACAAAGTCCGGGATCATGTACCCCAAGTCTGTGATCATCAGGGGCTG 210
DB 378 AGTATGAGACAAAGTCCGGGATCATGTACCCCAAGTCTGTGATCATCAGGGGCTG 437
QY 211 TCTCATGCGCTTGCAGGATGATCAGTCTCTCCCAAGGAACTGAAGTCAAGTTTG 270
DB 438 TCTCATGCGCTTGCAGGATGATCAGTCTCTCCCAAGGAACTGAAGTCAAGTTTG 497
QY 271 CATCAGTCTGTCACACACCCCTTTGTATAC 301
DB 498 CATCAGTCTGTCACACACCCCTTTGTATAC 528

RESULT 10
BE395206 573 bp mRNA linear EST 21-JUL-2000
LOCUS 60130955881 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631047 5',
DEFINITION mRNA sequence.
ACCESSION BE395206
VERSION BE395206.1 GI:9340571
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC <http://mgi.nci.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory

FEATURES

source

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LICM320 row: c column: 16
High quality sequence stop: 573.
Location/Qualifiers
1. 573
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3631047"
/issue_type="NIH-MGC_44"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
119 a 192 c 154 g 108 t

BASE COUNT
ORIGIN

Query Match 71.3%; Score 263; DB 10; Length 573;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAAGACTGCTCCCTCCCGGATTCATTGTAATGACGGTGAACGTTCAAGCATGTG 141
DB 1 CAAGACTGCTCCCTCCCGGATTCATTGTAATGACGGTGAACGTTCAAGCATGTG 60
QY 142 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATACCGCAAGTCTGTGATCATC 201
DB 61 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATACCGCAAGTCTGTGATCATC 120
QY 202 AGCGGCTGTCTATCCTCTGCGGATGACAGTCTCTGCTCCCAAGGAACTGAA 261
DB 121 AGCGGCTGTCTATCCTCTGCGGATGACAGTCTCTGCTCCCAAGGAACTGAA 180
QY 262 CTCAGTTGATCATGCTGTGCAACACCCCTTTGTATACGGGCAAGGCCAAGAAAG 321
DB 181 CTCAGTTGATCATGCTGTGCAACACCCCTTTGTATACGGGCAAGGCCAAGAAAG 240
QY 322 GGGAGTTCTGCTCCGCGGCTCA 344
DB 241 GGGAGTTCTGCTCCGCGGCTCA 263

RESULT 11
B0882838 948 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT_8627686 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6291960
DEFINITION 5', mRNA sequence.
ACCESSION B0882838
VERSION B0882838.1 GI:22274846
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC <http://mgi.nci.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM2492 row: k column: 01
 High quality sequence stop: 533.
 Location/Qualifiers

FEATURES

source

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1. '948
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_43"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: eye; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(g). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

```

BASE COUNT 183 a 288 c 286 g 190 t 1 others
 ORIGIN

Query Match 71.0%; Score 262; DB 14; Length 948;
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 30 CAGGCTTGGCGTCAAAATCCAGTGTACGATGGAAGAATTCAGCTGAACAACGACT 89
DB 298 CAGGCTTGGCGTCAAAATCCAGTGTACGATGGAAGAATTCAGCTGAACAACGACT 357
QY 90 GCTCCCTCCCGAGTTCATTGTGAATTGACAGGTGAACATGATGTGCAAGAAG 149
DB 358 GCTCCCTCCCGAGTTCATTGTGAATTGACAGGTGAACATGATGTGCAAGAAG 417
QY 150 AAGTATGAGACAAAGTCCGGGATCATGACCAAGTCTGTGCATCATCAGCGGCT 209
DB 418 AAGTATGAGACAAAGTCCGGGATCATGACCAAGTCTGTGCATCATCAGCGGCT 477
QY 210 GTCTCATCGCTTCGCCGGGTACCAAGTCTGTGCCCAAGGAAGCAACTGATT 269
DB 478 GTCTCATCGCTTCGCCGGGTACCAAGTCTGTGCCCAAGGAAGCAACTGATT 537
QY 270 GCATCAGCTGCTGCAACACCC 291
DB 538 GCATCAGCTGCTGCAACACCC 559
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RESULT 12
 BI823714 704 bp mRNA linear EST 04-OCT-2001
 LOCUS 603040833F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181585 5',
 DEFINITION mRNA sequence.
 ACCESSION BI823714
 VERSION BI823714.1 GI:15935264
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 704)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Plate: LLM11453 row: a column: 10
 High quality sequence stop: 692.
 Location/Qualifiers

FEATURES

source

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1. '704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_115"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B"
/Note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research genetics tracking code
021. Note: this is a NIH_MGC library."

```

BASE COUNT 135 a 227 c 205 g 137 t
 ORIGIN

Query Match 69.9%; Score 258; DB 13; Length 704;
 Best Local Similarity 100.0%; Pred. No. 2.7e-134;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 30 CAGGCTTGGCGTCAAAATCCAGTGTACGATGGAAGAATTCAGCTGAACAACGACT 89
DB 309 CAGGCTTGGCGTCAAAATCCAGTGTACGATGGAAGAATTCAGCTGAACAACGACT 368
QY 90 GCTCCCTCCCGAGTTCATTGTGAATTGACAGGTGAACATGATGTGCAAGAAG 149
DB 369 GCTCCCTCCCGAGTTCATTGTGAATTGACAGGTGAACATGATGTGCAAGAAG 428
QY 150 AAGTATGAGACAAAGTCCGGGATCATGACCAAGTCTGTGCATCATCAGCGGCT 209
DB 429 AAGTATGAGACAAAGTCCGGGATCATGACCAAGTCTGTGCATCATCAGCGGCT 488
QY 210 GTCTCATCGCTTCGCCGGGTACCAAGTCTGTGCCCAAGGAAGCAACTGATT 269
DB 489 GTCTCATCGCTTCGCCGGGTACCAAGTCTGTGCCCAAGGAAGCAACTGATT 548
QY 270 GCATCAGCTGCTGCAACA 287
DB 549 GCATCAGCTGCTGCAACA 566
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RESULT 13
 BI831919 570 bp mRNA linear EST 04-OCT-2001
 LOCUS 603078792F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170606 5',
 DEFINITION mRNA sequence.
 ACCESSION BI831919
 VERSION BI831919.1 GI:15943469
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 570)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Plate: LLM11424 row: g column: 23

High quality sequence stop: 566.
Location/Qualifiers

FEATURES
source

1..570
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5170606"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
BASE COUNT 130 a 170 c 137 g 133 t
ORIGIN

Query Match 64.2%; Score 237; DB 13; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.9e-122; Mismatches 0; Indels 0; Gaps 0;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CACGACTGCTCTCCGCCGAGTTCATTTGTAATGCAAGGTAAGTCAAGACATGTG 141
DB 1 CACGACTGCTCTCTCCGCCGAGTTCATTTGTAATGCAAGGTAAGACATGTG 60
QY 142 TCAGAAAGAGTATGAGGCAAGGCGGAGTATCTATGACCGCAAGTCTGTGCATCATC 201
DB 61 TCAGAAAGAGTATGAGGCAAGGCGGAGTATCTATGACCGCAAGTCTGTGCATCATC 120
QY 202 AGCGGCTGTCTATCCCTCTGCGGAGTACAGTCTTGTGTCGCCAGGAAACGTGA 261
DB 121 AGCGGCTGTCTATCCCTCTGCGGAGTACAGTCTTGTGTCGCCAGGAAACGTGA 180
QY 262 CTCAGTTGATCAGCTGCTCAACACCCCTCTTTGTAACGGGCCCAAGGCCAAGAA 318
DB 181 CTCAGTTGATCAGCTGCTCAACACCCCTCTTTGTAACGGGCCCAAGGCCAAGAA 237

RESULT 14
AA349894 352 bp mRNA linear EST 21-APR-1997
LOCUS
DEFINITION EST56849 Infant brain Homo sapiens CDNA 5' end, mRNA sequence.
ACCESSION AA349894
VERSION AA349894.1 GI:2002213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 352)
TITLE Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3,400 expressed sequence tags identify diversity of transcripts
from human brain
JOURNAL Nat. Genet. 4, 256-267 (1993)
MEDLINE 93364420
COMMENT Other-ESTs: EST56848 THC106611
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1..352

FEATURES
source

/organism="Homo sapiens"
/db_xref="ATCC (Inhost):150796"
/db_xref="taxon:9606"
/clone_lib="Infant brain"
/sex="female"
/dev stage="Infant"
/note="Organ: brain; Vector: lafmd BA; Site_1: HindIII; Site_2: NotI"
BASE COUNT 76 a 111 c 85 g 77 t 3 others
ORIGIN

Query Match 63.7%; Score 235; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.2e-121; Mismatches 0; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GTGAATTGCAGCGGTGAACCTTCAGACATGTGTCAGAAAGAGTATGAGCAAGTGC 169
DB 1 GTGAATTGCAGCGGTGAACCTTCAGACATGTGTCAGAAAGAGTATGAGCAAGTGC 60
QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTGCGCGG 229
DB 61 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTGCGCGG 120
QY 230 TACAGTCTCTGCTCCCGAGGAACGACAGTTCATGATCAGCTGCGCAACAC 289
DB 121 TACAGTCTCTGCTCCCGAGGAACGACAGTTCATGATCAGCTGCGCAACAC 180
QY 290 CCTCTTTGTAACGGGCGCAAGGCCCAAGAAAGGGAGTTCGCTCGGCGCTCA 344
DB 181 CCTCTTTGTAACGGGCGCAAGGCCCAAGAAAGGGAGTTCGCTCGGCGCTCA 235

RESULT 15
BG753617 670 bp mRNA linear EST 15-MAY-2001
LOCUS
DEFINITION 602732803F1 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:4876392 5',
RNA sequence.
ACCESSION BG753617
VERSION BG753617.1 GI:14064270
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 670)
TITLE NIH-MGC <http://mgc.ncl.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: LNCM1759 row: e column: 01
High quality sequence stop: 585.
Location/Qualifiers
1..670

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4876392"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).
 Note: This is a NIH-MGC Library. I"

BASE COUNT 144 a 198 c 165 g 163 t
 ORIGIN

Query Match 60.7%; Score 224; DB 12; Length 670;
 Best Local Similarity 100.0%; Pred. No. 4,3e-115;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30 CAGGCTTTCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGTGAACAGACT 89
 DB 61 CAGGCTTTCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCCAGTGAACAGACT 120
 QY 90 GCTCTCCCGGAGTTCATTTGTAATGACGAGTGAACGTTCAAGACATGTGCAAGAAG 149
 DB 121 GCTCTCCCGGAGTTCATTTGTAATGACGAGTGAACGTTCAAGACATGTGCAAGAAG 180
 QY 150 AAGTATGAGCAAAAGTCCGCGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 209
 DB 181 AAGTATGAGCAAAAGTCCGCGGATCATGTACGCAAGTCTGTGATCATCAGCGGCT 240
 QY 210 GTCTCATCCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGG 253
 DB 241 GTCTCATCCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGG 284

RESULT 16
 BE746601 654 bp mRNA linear EST 15-SEP-2000
 LOCUS 601580186f1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928868 5',
 DEFINITION mRNA sequence.
 ACCESSION BE746601
 VERSION BE746601.1 GI:10160593
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 654)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Ling Hong/Rubin laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L1CM760 row: 1 column: 21
 High quality sequence stop: 651.
 Location/Qualifiers

FEATURES
 source
 1..654
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3928868"
 /clone_1db="NIH_MGC_9"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: ovary; Vector: pOTB7; Site:1: XhoI; Site:2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 121 a 219 c 187 g 126 t
 ORIGIN

Query Match 55.6%; Score 205; DB 12; Length 654;
 Best Local Similarity 100.0%; Pred. No. 2.3e-104;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TCCATGCTACACAGTGTGAAGATTCCAGTGAACAGACTGCTCTCCCGAGTTCA 107
 DB 303 TCCAGTGTACACAGTGTGAAGATTCCAGTGAACAGACTGCTCTCCCGAGTTCA 362
 QY 108 TTGTAATGTCACGCTGTAACGTTCAAGACATGTGTGCAAGAAGTATGAGCAAGTG 167
 DB 363 TTGTAATGTCACGCTGTAACGTTCAAGACATGTGTGCAAGAAGTATGAGCAAGTG 422
 QY 168 CCGGATCATGTATCCGCAAGTCTGTGATCATCAGCGGCTGTTCATGCTCTGCGC 227
 DB 423 CCGGATCATGTATCCGCAAGTCTGTGATCATCAGCGGCTGTTCATGCTCTGCGC 482
 QY 228 GGTACAGTCTTCTGCTCCCGAG 252
 DB 483 GGTACAGTCTTCTGCTCCCGAG 507

RESULT 17
 B1554034 698 bp mRNA linear EST 05-SEP-2001
 LOCUS 603235426f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:309527
 DEFINITION 5', mRNA sequence.
 ACCESSION B1554034
 VERSION B1554034.1 GI:15441348
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 698)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L1AM1784 row: d column: 08
 High quality sequence stop: 687.
 Location/Qualifiers

FEATURES
 source
 1..698
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:309527"
 /clone_1db="NCI_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-Sport6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 131 a 231 c 204 g 132 t
 ORIGIN

Query Match 53.1%; Score 196; DB 13; Length 698;
 Best Local Similarity 100.0%; Pred. No. 2.8e-99;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GAAGTATGAGCAAAAGTCCGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGCC 208
 DB 427 GAAGTATGAGCAAAAGTCCGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGCC 486
 QY 209 TGTCTCATCCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAAACTGACTCAGTT 268
 DB 487 TGTCTCATCCGCTCTGCCGGGTACCACTCTTCTGCTCCCAAGGAAACTGACTCAGTT 546

Qy	Db	Qy	Db
269	547	329	607
TGCATCAGCTGCTCAGCACCCTCTTTGTAAAGGGCCAAAGAAAGGGAGT	TGCATCAGCTGCTCAGCACCCTCTTTGTAAAGGGCCAAAGAAAGGGAGT	TCTGCTTCGGCCCTCTCA	TCTGCTTCGGCCCTCTCA
328	606	344	622

RESULT 18
AM954549

LOCUS	AW954549	540 bp	mRNA	linear	EST 01-JUN-2000
DEFINITION	EST366619	MAGE	resequences,	MAQC	Homo sapiens CDNA, mRNA sequence.
ACCESSION	AW954549				
VERSION	AW954549.1	GI:8144232			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
Hegde, P., Ql, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holtz
1 (bases 1 to 540)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 3528
Fax: 301 838 0208
Email: johngeth@igf.org
plate: 65
Seq primer: Reverse.

FEATURES	Location/Qualifiers
source	1. .540

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE_resesquences_MAGC"
/note="Vector: pBluescriptSkM"
BASE COUNT      122 a      150 c      134 g      134 t
ORIGIN

```

Query Match	51.5%	Score 190;	DB 10;	Length 540;
Best Local Similarity	100.0%	Pred. No. 6.5e-96;		
Matches 190;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

155 ATGAGACAAAGTCCGGGATCATGTACCCAGTCTCTGTGCATCATACAGCGGCTGTCTC 214
 56 ATGAGACAAAGTCCGGGATCATGTACCCAGTCTCTGTGCATCATACAGCGGCTGTCTC 115

QY 215 ATCGCTCTGCGGGTACCACTCTCTGTGCTCCACGGAACTGAACACTAGTTGCATC 274

07 AGCTGCTGCAACACCCCTCTTTGTAAAGGCGCAAGGCCAAGAAAAGGGAGTTCTGCC 334

Db 176 AGCTGCTGCACACCCCTCTTTGTAAAGGGGCCAAGGCCCAAGAAAAAGGGGAAGTCTGCC 235

Oy 335 TCGGGCCCTCA 344

Db 236 TCGGGCCCTCA 245

RESULT 19
AA582576
AA582576
LOCUS 433 bp
EBNA1 1:10000
ECM 36 500 1000

ACCESSION	mRNA sequence.
VERSION	AA582576
	AA582576.1
	GI:2359936

KEYWORDS	EST.
SOURCE	human.

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 433)
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.	1 (bases 1 to 433)

AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
DOI Tumor Gene Index
ISSN Published (1997)

CONTACT: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-1@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R Emmert-Buck, M.D., Ph.D.
CDM Library Description: Cholesterol T-

CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LEWU at:
www-bio.llnl.gov/bdipr/image/image.html
Insert length: 904 Std Error: 0.00
Seq primer: -40m13 fwd. 5' from Amersham
High quality sequence. stop: 407.

```

FEATURES
source
1. .433

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1087804"
/clone_lib="NCI_CGAP_kid6"
/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SOLR (Kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
GATTCGCGACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

```

Query Match	47.48	Score 175	DB 9	Length 433
Best Local Similarity	100.0%	Pred. No. 1.8e-87		
Matches 175, Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTCTCGCGGG 229
|||||
D0 258 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTCTCGCGGG 3171

230 TACAGTCCCTTCTGCTCCCGAGGAACTGAACTCAGTTTGCATCAGCTGCTGCAACACC 289

290 CCTCTTTGTACGGGGCCAGAGGCCCAAGAAAGGGAAGTTCTGCGCTCGGCCCTCA 344

Db 378 CCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGGAAGTTCGCTCGGCCCTCA 432

	RESOL 20	
A1767459		
LOCUS	522 bp	mRNA linear EST 20-DEC-1999
A1767459		

[illegible]

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 522)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.linnl.gov/dbp/image/image.html
 Insert length: 877 Std Error: 0.00
 Seq primer: -40UP from Glibco
 High quality sequence stop: 470.

FEATURES

source

Location/Qualifiers
 1..522
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2381909"
 /clone_1ib="NCI CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

113 a 141 c 116 g 152 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 175; DB 9; Length 522;
 Pred. No. 1.9e-87;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 GGATCATGATACCGCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCCGGG 229
 DB 286 GGGATCATGATACCGCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCCGGG 345

OY 230 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGATGCTGTCGAACACC 289
 DB 346 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGATGCTGTCGAACACC 405

OY 290 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCCCTCA 344
 DB 406 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCCCTCA 460

RESULT 21 541 bp mRNA linear EST 21-MAR-2002
 LOCUS BM974798

DEFINITION UI-CF-EC1-acd-1-10-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
 ACCESSION BM974798
 VERSION BM974798.1 GI:19592389

KEYWORDS

EST.

SOURCE

human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 541)
 Bernaldo,M.F., Lennon,G. and Soares,M.B.

AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

CONTACT: McCreay, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

FEATURES

source

Location/Qualifiers
 1..541
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-EC1-acd-1-10-0-UI"
 /clone_1ib="UI-CF-EC1"
 /issue_type="Lung"
 /dev_stage="Adult and Fetal"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTCTTAC.

BASE COUNT 119 a 142 c 120 g 160 t
 ORIGIN TAG-LIB-UI-CF-EC1
 TAG-TISSUE-Normal Lung Epithelial Cells Tissue nos 369-371
 and 380-383
 TAG-SEO-AAGTCTTAC"

Query Match 47.4%; Score 175; DB 14; Length 541;
 Best Local Similarity 100.0%; Pred. No. 1.9e-87;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 GGATCATGATACCGCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCCGGG 229
 DB 296 GGGATCATGATACCGCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCCGGG 355

OY 230 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGATGCTGTCGAACACC 289
 DB 356 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGATGCTGTCGAACACC 415

OY 290 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCCCTCA 344
 DB 416 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCCCTCA 470

RESULT 22 651 bp mRNA linear EST 16-OCT-2000
 LOCUS AV171094

DEFINITION AV171094 DCB Homo sapiens cDNA clone DCBAZD04 5', mRNA sequence.
 ACCESSION AV171094
 VERSION AV171094.1 GI:10814246

KEYWORDS

EST.

SOURCE

human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 651)
 Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,

Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., and Han, Z.
 Homo sapiens CDNA DCB clones
 Unpublished (2000)
 CONTACT: Zeyuan Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzye@chgc.sh.cn

FEATURES
 source
 Location/Qualifiers
 1..651
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="DCB" /clone="DCB.DCB04"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25.8"
 /note="Vector: pTRIPlex2; Site_1: sf11A; Site_2: sf11B"
 This clone is available at CHGC in Shanghai.

BASE COUNT 171 a 156 c 178 g 146 t
 ORIGIN

Query Match 47.4%; Score 175; DB 10; Length 651;
 Best Local Similarity 100.0%; Pred. No. 2e-87;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGCGCGG 229
 Db 279 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGCGCGG 220
 OY 230 TACCAGTCT 289
 Db 219 TACCAGTCT 160
 OY 290 CCTCTTTGTACGGGCCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCA 344
 Db 159 CCTCTTTGTACGGGCCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCA 105

RESULT 23
 LOCUS BM980701 652 bp mRNA linear EST 21-MAR-2002
 DEFINITION UI-CF-EN1-add-j-04-0-0-UI-s1 UI-CF-EN1 Homo sapiens CDNA clone
 ACCESSION BM980701
 VERSION UI-CF-EN1-add-j-04-0-0-UI 3', mRNA sequence.
 KEYWORDS EST.
 SOURCE BM980701.1 GI:19602430
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 652)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL discovery
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 COMMENT 97044477
 Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).

FEATURES
 source
 Location/Qualifiers
 1..652
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UI-CF-EN1-add-j-04-0-UI"
 /clone="UI-CF-EN1"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pTR73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-CF-EN1 is a normalized CDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand CDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 CDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pTR73-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand CDNA contains a library tag sequence that is
 located between the Not I site and the (drr)18 tail. The
 sequence tag for this library is CTGCTCAGGT.
 TAG-LIB=UI-CF-EN1
 TAG-TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG-SEQ=CTGCTCAGGT"

BASE COUNT 135 a 183 c 142 g 192 t
 ORIGIN

Query Match 47.4%; Score 175; DB 14; Length 652;
 Best Local Similarity 100.0%; Pred. No. 2e-87;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGCGCGG 229
 Db 292 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGCGCGG 351
 OY 230 TACCAGTCT 289
 Db 352 TACCAGTCT 411
 OY 290 CCTCTTTGTACGGGCCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCA 344
 Db 412 CCTCTTTGTACGGGCCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCA 466

RESULT 24
 LOCUS BM981455 738 bp mRNA linear EST 21-MAR-2002
 DEFINITION UI-CF-EN1-add-b-10-0-0-UI-s1 UI-CF-EN1 Homo sapiens CDNA clone
 ACCESSION BM981455
 VERSION UI-CF-EN1-add-b-10-0-0-UI 3', mRNA sequence.
 KEYWORDS EST.
 SOURCE BM981455.1 GI:19603962
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 738)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL discovery
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 COMMENT 97044477
 Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).

Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Genetix (www.resgen.com).
 Seq primer: M13 FORWARD
 POLY-A=yes.

FEATURES

source Location/Qualifiers
 1..738
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-adh-b-10-0-UI"
 /clone_lib="UI-CF-EN1"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; ui-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
 TAG LIB=UI-CF-EN1
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 hmr to LPS 24h
 TAG_SEQ=CTGCTCAGGT"
 151 a 199 c 164 g 221 t 3 others
 BASE COUNT
 ORIGIN

Query Match 47.4%; Score 175; DB 14; Length 738;
 Best Local Similarity 100.0%; Pred No. 2.1e-87;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGTACCGCAAGTCTGTGATCATACGCGCTGTCTCATCGCTTCCGGG 229
 |||||||
 DB 290 GGGATCATGTACCGCAAGTCTGTGATCATACGCGCTGTCTCATCGCTTCCGGG 349
 |||||||
 QY 230 TACCACTCTCTTGTCTCCAGGAACTGAACTGATTCATCAGCTGCTGCAACAC 289
 |||||||
 DB 350 TACCACTCTCTTGTCTCCAGGAACTGAACTGATTCATCAGCTGCTGCAACAC 409
 |||||||
 QY 290 CCTCTTGTACGGGCAAGGCAAGGGAAGTCTGCTCGGCCCTCA 344
 |||||||
 DB 410 CCTCTTGTACGGGCAAGGCAAGGGAAGTCTGCTCGGCCCTCA 464
 |||||||

RESULT 25
 LOCUS BF125425 890 bp mRNA linear EST 24-OCT-2000
 DEFINITION 601763551f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026252 5',
 mRNA sequence.
 ACCESSION BF125425
 VERSION BF125425.1 GI:10964465
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 890)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC/DCID/DRP
 CDNA library preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
 Plate: LNC856 row: F column: 13
 High quality sequence stop: 553.
 Location/Qualifiers
 1..890

FEATURES

source Location/Qualifiers
 1..890
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4026252"
 /clone_lib="NIH_MGC_20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 232 a 258 c 239 g 161 t
 ORIGIN

Query Match 47.2%; Score 174; DB 12; Length 890;
 Best Local Similarity 100.0%; Pred No. 8.2e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGCGTTGGCTGCAAAATCAGTGTACCAAGTGAAGATTCACAGTGAACAAGCACTG 90
 |||||||
 DB 249 AGCGTTGGCTGCAAAATCAGTGTACCAAGTGAAGATTCACAGTGAACAAGCACTG 308
 |||||||
 QY 91 CTCCTCCCGGAGTTGATGTGAAATGCAAGGCAAGCTCAAGATCTGTGAGAAAGA 150
 |||||||
 DB 309 CTCCTCCCGGAGTTGATGTGAAATGCAAGGCAAGCTCAAGATCTGTGAGAAAGA 368
 |||||||
 QY 151 AGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGC 204
 |||||||
 DB 369 AGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGC 422
 |||||||

RESULT 26
 LOCUS A1140655 449 bp mRNA linear EST 29-OCT-1998
 DEFINITION qe22c09.x1 Soares-fetal_lung_NH19W Homo sapiens cDNA clone
 IMAGE:1739728 3', mRNA sequence.
 ACCESSION A1140655
 VERSION A1140655.1 GI:3648112
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 449)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 896 Std Error: 0.00
 Seg primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 429.
 Location/Qualifiers
 1..449

FEATURES

source Location/Qualifiers
 1..449

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1739728"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/organism="Homo sapiens"
/vector="pRT30 (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCTGAGTGGAGCGCGCAATTTTCTTTTCTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT30 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldi. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

BASE COUNT      101 a      115 c      104 g      129 t
ORIGIN
Query Match      46.98; Score 173; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 2,5e-86;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 170 GGATCATGATACCGGAGTCCGTGATCATGAGCGGCGCTGATGCGCTTCCGGG 229
|||||
Db 277 GGGATCATGATACCGGAGTCCGTGATCATGAGCGGCGCTGATGCGCTTCCGGG 336
|||||

Oy 220 TACCAAGCTCTCTGCTCCCGGAGAACTGACTGATTTGCATGAGTGTGACAC 289
|||||
Db 337 TACCAAGCTCTCTGCTCCCGGAGAACTGACTGATTTGCATGAGTGTGACAC 396
|||||

Oy 290 CCTCTTTGTAAAGGCGCCCAAGGCGGGAAGTTCGCTCGGCGCT 342
|||||
Db 397 CCTCTTTGTAAAGGCGCCCAAGGCGGGAAGTTCGCTCGGCGCT 449
|||||

RESULT 27
BF125664      878 bp      mRNA      linear      EST 24-OCT-2000
LOCUS      601763237F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026320 5',
DEFINITION      mRNA sequence.
ACCESSION      BF125664.1 GI:10964704
VERSION      EST.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 878)
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LCM856 row: 1 column: 09
High quality sequence stop: 598.
Location/Qualifiers
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4026320"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/organism="Homo sapiens"
/vector="pRT30 (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCTGAGTGGAGCGCGCAATTTTCTTTTCTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT30 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldi. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4026320"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/organism="Homo sapiens"
/vector="pRT30 (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCTGAGTGGAGCGCGCAATTTTCTTTTCTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT30 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldi. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

BASE COUNT      278 a      194 c      251 g      155 t
ORIGIN
Query Match      45.3%; Score 167; DB 12; Length 878;
Best Local Similarity 100.0%; Pred. No. 7.3e-83;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 GACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 145
|||||
Db 300 GACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 359
|||||

Oy 146 AAGAAGTATGATGAGCAAGTCCCGGATCATGATACCGCAAGTCTCTGATCATCAGCG 205
|||||
Db 360 AAGAAGTATGATGAGCAAGTCCCGGATCATGATACCGCAAGTCTCTGATCATCAGCG 419
|||||

Oy 206 GCTCTCTCATGCGCTCTGCGGATCAGTACAGTCTCTCTCTCTCTCTCTCTCTCTCT 252
|||||
Db 420 GCTCTCTCATGCGCTCTGCGGATCAGTACAGTCTCTCTCTCTCTCTCTCTCTCTCT 466
|||||

RESULT 28
R20352      395 bp      mRNA      linear      EST 17-APR-1995
LOCUS      y920f09.x1 Soares infant brain INIB Homo sapiens cDNA clone
DEFINITION      IMAGE:32715 5', mRNA sequence.
ACCESSION      R20352.1 GI:774986
VERSION      EST.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 395)
REFERENCE      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
AUTHORS      M., Hulman, M., Kuwaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston,
R., Williamson, A., Woldmann, P., and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL      Contact: Wilson R.
COMMENT      Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert size: 1628
High quality sequence stop: 326.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 1628 Std Error: 0.00
Seq primer: M13R1
High quality sequence stop: 326.
Location/Qualifiers
1..395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:32715"
/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/organism="Homo sapiens"
/vector="pRT30 (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGTACCAATCTGAGTGGAGCGCGCAATTTTCTTTTCTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT30 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldi. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

```

double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the lacMid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 73 a 126 c 103 g 92 t 1 others

Query Match 45.0%; Score 166; DB 14; Length 395;
Best Local Similarity 100.0%; Pred. No. 2, 1e-82;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 206
DB 1 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 60
QY 207 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 266
DB 61 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 120
QY 267 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 312
DB 121 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 166

RESULT 29 H17189 429 bp mRNA linear EST 29-JUN-1995

LOCUS H17189 ym37f07.r1 Soares infant brain INIB Homo sapiens cDNA clone

DEFINITION IMAGE:50205 5', mRNA sequence.

ACCESSION H17189 H17189.1 GI:883429

VERSION EST.

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 429)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, R., Williams, M., Kuchta, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Insert Size: 1633

High quality sequence stops: 287

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert length: 1633 Std Error: 0.00

Seq primer: M3Rpi

High quality sequence stop: 287.

Location/Qualifiers

1..429

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:50205"

/clone_lib="Soares infant brain INIB"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: lacMid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I-oligo(dT) primer [5',

AACGTGAGAAATTCGCGCCGCAAGATTTTTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

BASE COUNT 100 a 108 c 99 g 127 t

ORIGIN

Query Match 45.0%; Score 166; DB 14; Length 429;

Best Local Similarity 100.0%; Pred. No. 2, 2e-82;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 206

DB 1 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 60

QY 207 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 266

DB 61 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 120

QY 267 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 312

DB 121 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 166

RESULT 30 A1299246 434 bp mRNA linear EST 01-FEB-1999

LOCUS A1299246 gn33g10.x1 NCL_CGAP_Kids Homo sapiens cDNA clone IMAGE:190098 3',

DEFINITION mRNA sequence.

ACCESSION A1299246 A1299246.1 GI:3958900

VERSION EST.

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 434)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA library Preparation: M. Bento Soares, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnl.gov/bnpr/image/image.html

Insert length: 787 Std Error: 0.00

Seq primer: -40up from Gibco

High quality sequence stop: 433.

Location/Qualifiers

1..434

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:190098"

/clone_lib="NCI-CGAP_Kids"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I-oligo(dT) primer [5',

AACGTGAGAAATTCGCGCCGCAAGATTTTTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 100 a 108 c 99 g 127 t

ORIGIN

Query Match 45.0%; Score 166; DB 14; Length 429;

Best Local Similarity 100.0%; Pred. No. 2, 2e-82;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 206

DB 1 AAGAGTATGAGCAAAAGTCCGGGATCATGTACCCAGTCTGTGCATCATCAGCGG 60

QY 207 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 266

DB 61 CCTGTCTCATCGCTCTGCGGGATCACAGTCTGTCTCTCCAGGAACTGAACTCAG 120

QY 267 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 312

DB 121 TTTGCATCAGCTCTGCAACACCCCTTTGTAAAGGCGCAAGGCC 166

RESULT 30 A1299246 434 bp mRNA linear EST 01-FEB-1999

LOCUS A1299246 gn33g10.x1 NCL_CGAP_Kids Homo sapiens cDNA clone IMAGE:190098 3',

DEFINITION mRNA sequence.

ACCESSION A1299246 A1299246.1 GI:3958900

VERSION EST.

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 434)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA library Preparation: M. Bento Soares, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnl.gov/bnpr/image/image.html

Insert length: 787 Std Error: 0.00

Seq primer: -40up from Gibco

High quality sequence stop: 433.

Location/Qualifiers

1..434

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:190098"

/clone_lib="NCI-CGAP_Kids"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I-oligo(dT) primer [5',

AACGTGAGAAATTCGCGCCGCAAGATTTTTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 100 a 108 c 99 g 127 t

ORIGIN

Query Match 40.9%; Score 151; DB 9; Length 434;

Best Local Similarity 100.0%; Pred. No. 6.6e-74;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTGCGCGG 229

280 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTGCGCGG 339

230 TACGAGTCTTCTGCTCCCGGAGAACTGAATCAGTTTCATCAGCTGCTGCACACC 289

340 TACGAGTCTTCTGCTCCCGGAGAACTGAATCAGTTTCATCAGCTGCTGCACACC 399

290 CCTCTTTGTAACGGGCCAAGGCCCAAGAAA 320

400 CCTCTTTGTAACGGGCCAAGGCCCAAGAAA 430

RESULT 31 424 bp mRNA linear EST 28-OCT-1998

LOCUS A1138793 q998e07.x1 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1737540

DEFINITION 3', mRNA sequence.

ACCESSION A1138793

VERSION A1138793.1 GI:3644765

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 424)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/dbtrp/image/image.html

Insert length: 960 std Error: 0.00

Seq primer: -40m13 fwd. RT from Amersham

High quality sequence stop: 420.

Location/Qualifiers

1. 424

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1737540"

/clone_1lb="Soares_testis_NHT"

/sex="male"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

Inc. and primed with a Not I - oligo(dT) primer [5']

TGTTACATCTGAAGTGGAGCGGCGCCCAATTTTCTTTTCTTTT 3'.

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 96 a 108 c 96 g 124 t

ORIGIN

Query Match 40.1%; Score 148; DB 9; Length 424;

Best Local Similarity 100.0%; Pred. No. 3.2e-72;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTGCGCGG 229

DB 277 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTGCGCGG 336

QY 230 TACGAGTCTTCTGCTCCCGGAGAACTGAATCAGTTTCATCAGCTGCTGCACACC 289

DB 337 TACGAGTCTTCTGCTCCCGGAGAACTGAATCAGTTTCATCAGCTGCTGCACACC 396

QY 290 CCTCTTTGTAACGGGCCAAGGCCCAAGAAA 317

DB 397 CCTCTTTGTAACGGGCCAAGGCCCAAGAAA 424

RESULT 32 435 bp mRNA linear EST 10-SEP-1999

LOCUS AM014802 UI-H-B10-aag-b-04-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens CDNA clone

DEFINITION IMAGE:2709078 3', mRNA sequence.

ACCESSION AM014802

VERSION AM014802.1 GI:5863559

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 435)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. CDNA library preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the

I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/dbtrp/image/image.html

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. 435

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2709078"

/clone_1lb="NCI_CGAP_Sub1"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; The

NCI_CGAP_Sub1 library is a subtracted library derived from

BI. BI constitutes a mixture of 21 normalized or

subtracted NCI_CGAP libraries: NCI_CGAP_C04,

NCI_CGAP_Pt22, NCI_CGAP_Pt28, NCI_CGAP_C010, NCI_CGAP_C016

, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3,

NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_P08,

NCI_CGAP_C011, NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_C08,

, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_G04, NCI_CGAP_G06

, NCI_CGAP_Brn25. These 21 libraries were pooled and a

single-stranded DNA preparation of the resulting mixture

was used as a tracer in a subtractive hybridization with a

driver whose composition is detailed below: NCI_CGAP_Kid3

pool 1 LHAM 3334-3337, 3682-3683, 3798-3803 (IMAGE

cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855

) NCI_CGAP_Kid5 pool 1 LHAM 3338-3342, 3722-3723,

3776-3778 (IMAGE cloneids 1323912-1325831,

1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 LHAM

3575-3582, 3851-3854 (IMAGE cloneids 1414920-1417991,

1520904-1522439) NCI_CGAP_C04 pool 1 LHAM 3164-3167,

3716-3720, 3733-3735 (IMAGE cloneids 1257056-1258631,

1469064-1470983, 1475592-1476743) NCI_CGAP_Pt22 pool 1

LHAM 2457-2459, 2758-2759, 3062-3068 (IMAGE cloneids

985608-986759, 1101192-1101959, 1217928-1220615)

NCI_CGAP_C010 pool 1 LHAM 2644-2653, 2871-2872 (IMAGE

CloneIDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 530,000 recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. genome research 6, 791-806].

Research 6, 791-806
TAG-LIB-NCL-CGAP_K1d5
TAG-TISSUE-Kidney
TAG_SEQ-ATTC"

BASE COUNT 95 a 109 c 95 g 136 t

Query Match 39.3%; Score 145; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.6e-70;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGGCTCTTCATCGCTTCGCCGG 229

DB 291 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGGCTCTTCATCGCTTCGCCGG 350

QY 230 TACCACTCCTTCCTGCTCCCGAGGAACCTGACACTGATTTGCATCAGCTGCTGCACACC 289

DB 351 TACCACTCCTTCCTGCTCCCGAGGAACCTGACACTGATTTGCATCAGCTGCTGCACACC 410

QY 290 CCTCTTTGTACGCGGCCAAGGCCA 314

DB 411 CCTCTTTGTACGCGGCCAAGGCCA 435

RESULT 33

LOCUS

AA776783 516 bp mRNA linear EST 12-JAN-1999

DEFINITION ah36904.s1 Soares-testis_NHT Homo sapiens cDNA clone 1276662 3',

ACCESSION AA776783 mRNA sequence.

VERSION AA776783.1 GI:2836117

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Unpublished (1997)

JOURNAL Tumor Gene Index

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnlnl.gov/dbirp/image/image.html

Insert Length: 941 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amersham

High quality sequence stop: 510.

Location/Qualifiers

1, 516

FEATURES

source

and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

Research 6, 791-806
TAG-LIB-NCL-CGAP_K1d5
TAG-TISSUE-Kidney
TAG_SEQ-ATTC"

BASE COUNT 117 a 139 c 121 g 139 t

Query Match 38.8%; Score 143; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.3e-69;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGGCTCTTCATCGCTTCGCCGG 229

DB 268 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGGCTCTTCATCGCTTCGCCGG 327

QY 230 TACCACTCCTTCCTGCTCCCGAGGAACCTGACACTGATTTGCATCAGCTGCTGCACACC 289

DB 328 TACCACTCCTTCCTGCTCCCGAGGAACCTGACACTGATTTGCATCAGCTGCTGCACACC 387

QY 290 CCTCTTTGTACGCGGCCAAGGCC 312

DB 388 CCTCTTTGTACGCGGCCAAGGCC 410

RESULT 34

LOCUS

BE731003 794 bp mRNA linear EST 15-SEP-2000

DEFINITION 601570968F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845440 5',

ACCESSION BE731003 mRNA sequence.

VERSION BE731003.1 GI:10144995

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://imgc.ncbi.nlm.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Tissue Procurement: ATCC

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: Ling Hong/Rubin Laboratory

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.lnlnl.gov

Plate: L1CM543 row: h column: 17

High quality sequence stop: 642.

Location/Qualifiers

1, 794

FEATURES

source

1, 794

FEATURES

source

and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

Research 6, 791-806
TAG-LIB-NCL-CGAP_K1d5
TAG-TISSUE-Kidney
TAG_SEQ-ATTC"

BASE COUNT 195 a 227 c 217 g 155 t

Query Match 38.8%; Score 143; DB 12; Length 794;
Best Local Similarity 100.0%; Pred. No. 2.6e-69;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCMAATCCAGTGTACCACTGTAAGAAATTCACGTCGACACACT 89


```

DB 284 CAGGCTTTCGGCTCAATCAATCAGTGTACAGTGTGAAGATTCCAGCTGACAGCAACGACT 343
|||||
QY 90 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 149
|||||
DB 344 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 403
|||||
QY 150 AAGTATGGAGCAAGTCCCGG 172
|||||
DB 404 AAGTATGGAGCAAGTCCCGG 426
|||||

RESULT 35
BE730800 1134 bp mRNA linear EST 15-SEP-2000
LOCUS 601570755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845557 5',
DEFINITION mRNA sequence.
ACCESSION BE730800
VERSION BE730800.1 GI:10144792
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1134)
NHL-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rs99b@nsl.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at: Image.lnl.gov
Plate: L10M543 row: m column: 14
High quality sequence stop: 640.

FEATURES
Source
Location/Qualifiers
1..1134
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming,
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 329 a 320 c 308 g 177 t
ORIGIN
```

```

Query Match 38.8%; Score 143; DB 12; Length 1134;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 30 CAGGCTTTCGGCTCAATCAATCAGTGTACAGTGTGAAGATTCCAGCTGACAGCAACGACT 89
|||||
DB 284 CAGGCTTTCGGCTCAATCAATCAGTGTACAGTGTGAAGATTCCAGCTGACAGCAACGACT 343
|||||
QY 90 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 149
|||||
DB 344 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 403
|||||
QY 150 AAGTATGGAGCAAGTCCCGG 172
|||||
DB 404 AAGTATGGAGCAAGTCCCGG 426
|||||
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```

RESULT 36
BG213596 350 bp mRNA linear EST 21-APR-2001
LOCUS BG213596
DEFINITION R533211 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG213596
VERSION BG213596.1 GI:13735283
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 350)
Harrington,J.,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kilka,A., Hess,J., Colthen,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL MEDLINE
TITLE Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 350.

FEATURES
Source
Location/Qualifiers
1..350
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology', in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
```

```

BASE COUNT 98 a 93 c 84 g 75 t
ORIGIN
```

```

Query Match 38.2%; Score 141; DB 12; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.8e-68;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 30 CAGGCTTTCGGCTCAATCAATCAGTGTACAGTGTGAAGATTCCAGCTGACAGCAACGACT 89
|||||
DB 19 CAGGCTTTCGGCTCAATCAATCAGTGTACAGTGTGAAGATTCCAGCTGACAGCAACGACT 78
|||||
QY 90 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 149
|||||
DB 79 GCTCCCTCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 138
|||||
```

```

QY 150 AAGTATGGAGCAAGTCCCG 170
|||||
DB 139 AAGTATGGAGCAAGTCCCG 159
|||||
```

```

RESULT 37
BG184021 484 bp mRNA linear EST 21-APR-2001
LOCUS BG184021
DEFINITION R572936 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG184021
VERSION BG184021.1 GI:13705708
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 484)
```


AUTHORS
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Harrington, J.,
Lerner, L., Costanzo, D., McElligott, K., Boozar, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL MEDLINE
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 482.

FEATURES
source
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 137 a 122 c 107 g 118 t
ORIGIN

Query Match
Best Local Similarity 38.2%; Score 141; DB 12; Length 484;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACT 89
|||||
DB 5 CAGGCTTGGCGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACT 64
|||||

QY 90 GCTCTCTCCCGGAGTTCATTGTGAATTCAGCGTGAACGTTCAAGACATGTGTGCAAGAAG 149
|||||
DB 65 GCTCTCTCCCGGAGTTCATTGTGAATTCAGCGTGAACGTTCAAGACATGTGTGCAAGAAG 124
|||||

QY 150 AAGTGATGGAGCAAAAGTCCG 170
|||||
DB 125 AAGTGATGGAGCAAAAGTCCG 145
|||||

RESULT 38
BG193459 781 bp mRNA linear EST 21-APR-2001
LOCUS
RST12532 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG193459
VERSION
BG193459.1 GI:13715146
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 781)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Harrington, J.,
Lerner, L., Costanzo, D., McElligott, K., Boozar, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900

JOURNAL MEDLINE
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900

FEATURES
source
1..781
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 187 a 180 c 193 g 221 t
ORIGIN

Query Match
Best Local Similarity 38.2%; Score 141; DB 12; Length 781;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACT 89
|||||
DB 37 CAGGCTTGGCGCTGCAAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACT 96
|||||

QY 90 GCTCTCTCCCGGAGTTCATTGTGAATTCAGCGTGAACGTTCAAGACATGTGTGCAAGAAG 149
|||||
DB 97 GCTCTCTCCCGGAGTTCATTGTGAATTCAGCGTGAACGTTCAAGACATGTGTGCAAGAAG 156
|||||

QY 150 AAGTGATGGAGCAAAAGTCCG 170
|||||
DB 157 AAGTGATGGAGCAAAAGTCCG 177
|||||

RESULT 39
BG188218 424 bp mRNA linear EST 21-APR-2001
LOCUS
RST7232 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG188218
VERSION
BG188218.1 GI:13709905
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 424)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Harrington, J.,
Lerner, L., Costanzo, D., McElligott, K., Boozar, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 424.
Location/Qualifiers
1..424
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match 37.9%; Score 140; DB 12; Length 424;

Best Local Similarity 100.0%; Pred. No. 1,1e-67;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT 121 a 102 c 99 g 101 t 1 others

ORIGIN

33 GCCTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCT 92
 |||||||
 39 GCCTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCT 98
 |||||||
 93 CTTCCCGGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAG 152
 |||||||
 99 CTTCCCGGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAG 158
 |||||||
 153 TGATGAGCAAAAGTCCGGG 172
 |||||||
 159 TGATGAGCAAAAGTCCGGG 178

RESULT 40
 BG192926 323 bp mRNA linear EST 21-APR-2001
 LOCUS
 DEFINITION RST12050 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG192926
 VERSION BG192926.1 GI:13714613
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 323)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
 ,E., Veloso,N., Kilkha,A., Hess,J., Cothren,K., Lo,K., Offenbacher
 ,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Scott J. Cain
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scaine@atersys.com
 High quality sequence stop: 323.

FEATURES
 source
 1..323
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 90 a 84 c 78 g 71 t

Query Match 37.7%; Score 139; DB 12; Length 323;
 Best Local Similarity 100.0%; Pred. No. 3,6e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

34 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCTC 93
 |||||||
 1 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCTC 60

ORIGIN

94 CTCCTCCGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAGT 153
 |||||||
 61 CTCCTCCGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAGT 120
 |||||||
 154 GATGAGCAAAAGTCCGGG 172
 |||||||
 121 GATGAGCAAAAGTCCGGG 139

RESULT 41
 BG210457 323 bp mRNA linear EST 21-APR-2001
 LOCUS
 DEFINITION RST30002 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG210457
 VERSION BG210457.1 GI:13732144
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 323)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
 ,E., Veloso,N., Kilkha,A., Hess,J., Cothren,K., Lo,K., Offenbacher
 ,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 Contact: Scott J. Cain
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scaine@atersys.com
 High quality sequence stop: 323.

FEATURES
 source
 1..323
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 90 a 83 c 78 g 72 t

Query Match 37.7%; Score 139; DB 12; Length 323;
 Best Local Similarity 100.0%; Pred. No. 3,6e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

34 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCTC 93
 |||||||
 1 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGCTGACAGCTGCTC 60
 |||||||
 94 CTTCCCGGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAGT 153
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 61 CTTCCCGGAGTTCATTGTGAATTCGACGGTGAACGTTCAAGACATGTGTCAAGAAAGT 120
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 154 GATGAGCAAAAGTCCGGG 172
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 121 GATGAGCAAAAGTCCGGG 139

RESULT 42
 BG215210 324 bp mRNA linear EST 21-APR-2001
 LOCUS
 DEFINITION RST34874 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG215210
 VERSION BG215210.1 GI:13741231
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
 J., Danzig, J., and Ducar, M.
 TITLE Creation of genome-wide protein expression libraries using random
 activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scalin@athersys.com
 High quality sequence stop: 324.
 Location/Qualifiers
 1..324
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."
 BASE COUNT 90 a 83 c 79 g 72 t
 ORIGIN
 Query Match 37.7%; Score 139; DB 12; Length 324;
 Best Local Similarity 100.0%; Pred. No. 3.6e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACCTGCTC 93
 Db 1 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACCTGCTC 60
 QY 94 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 133
 Db 61 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 120
 QY 154 GATGAGCAAAAGTCCGGG 172
 Db 121 GATGAGCAAAAGTCCGGG 139
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 BG200048/c 330 bp mRNA linear EST 21-APR-2001
 LOCUS RS1919350 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG200048
 ACCESSION BG200048
 VERSION BG200048.1 GI:13721735
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
 J., Danzig, J., and Ducar, M.

TITLE Creation of genome-wide protein expression libraries using random
 activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scalin@athersys.com
 High quality sequence stop: 330.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
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 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
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 expressed in HT1080 under normal circumstances."
 BASE COUNT 71 a 80 c 86 g 93 t
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 Query Match 37.7%; Score 139; DB 12; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACCTGCTC 93
 Db 330 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGACACGACCTGCTC 271
 QY 94 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 153
 Db 270 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 211
 QY 154 GATGAGCAAAAGTCCGGG 172
 Db 210 GATGAGCAAAAGTCCGGG 192
 RESULT 44
 BG181955/c 331 bp mRNA linear EST 21-APR-2001
 LOCUS RS181955 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG181955
 ACCESSION BG181955
 VERSION BG181955.1 GI:13703642
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 331)
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
 J., Danzig, J., and Ducar, M.
 TITLE Creation of genome-wide protein expression libraries using random
 activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scalin@athersys.com
 High quality sequence stop: 331.
 Location/Qualifiers
 1..331

/organism="Homo sapiens"
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 /clone_lib="Athersys RAGE Library"
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 /note="See 'Creation of Genome-wide Protein Expression
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 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."
 BASE COUNT 74 a 81 c 87 g 89 t

Query Match 37.7%; Score 139; DB 12; Length 331;
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CTTTGGCGTCAATCCAGTCTACCGAGTGTGAAGATTCCAGCTGAACAGACTGCTC 93
 DB 331 CTTTGGCGTCAATCCAGTCTACCGAGTGTGAAGATTCCAGCTGAACAGACTGCTC 272
 QY 94 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGT 153
 DB 271 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGT 212
 QY 154 GATGGAGCAAAAGTCCGGG 172
 DB 211 GATGGAGCAAAAGTCCGGG 193

RESULT 45
 LOCUS BG204666/c 331 bp mRNA linear EST 21-Apr-2001

DEFINITION RST24065 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG204666
 VERSION BG204666.1 GI:13726337
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 331)
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
 Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
 E., Veloso, N., Klika, A., Hess, J., Coltrien, K., Lo, K., Offenbacher,
 J., Danzig, J. and Ducar, M.

TITLE Creation of genome-wide protein expression libraries using random
 activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com

FEATURES
 source
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 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."
 High quality sequence stop: 331.

BASE COUNT 73 a 81 c 86 g 91 t
 ORIGIN

Query Match 37.7%; Score 139; DB 12; Length 331;
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CTTTGGCGTCAATCCAGTCTACCGAGTGTGAAGATTCCAGCTGAACAGACTGCTC 93
 DB 331 CTTTGGCGTCAATCCAGTCTACCGAGTGTGAAGATTCCAGCTGAACAGACTGCTC 272
 QY 94 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGT 153
 DB 271 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGT 212
 QY 154 GATGGAGCAAAAGTCCGGG 172
 DB 211 GATGGAGCAAAAGTCCGGG 193

Search completed: November 7, 2002, 23:07:28
 Job time : 503.427 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 938.618 Seconds
(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggcgaacttttcgcgattgt.....tggctcgcacacacacatcct 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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10: gb_ro: *
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13: gb_un: *
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22: em_ov: *
23: em_pat: *
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25: em_pl: *
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27: em_sts: *
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32: em_htg_other: *
33: em_htg_mus: *
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41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	99.5	369	6	AX093381
2	365.4	99.0	466	6	AX093381
3	365.4	99.0	1524	6	BC017318
4	365.4	99.0	1524	6	AX358762
5	365.4	99.0	1832	6	AX362255
6	365.4	99.0	1832	6	AX094501
7	363.4	93.1	1990	6	AX136281
8	336.4	91.2	2528	6	AX093191
9	305.2	82.7	1797	10	AX319944
10	284	77.0	591	6	AB041649
11	198.2	53.7	129676	9	AX136556
12	159	43.1	209885	2	AC079773
13	145.6	39.5	147131	9	AC124493
14	80.2	21.7	136799	2	AC010974
15	80.2	21.7	190503	2	AC110334
16	38.4	10.4	90060	2	AC128363
17	37.2	10.1	150724	9	AC111928
18	37.2	10.1	180884	9	AP000550
19	36.8	10.0	177088	2	AC008018
20	36.4	9.9	235593	2	AC096395
21	36.4	9.9	293387	2	AL772296
22	36.2	9.8	3405	4	AL807802
23	36.2	9.8	3486	4	BTEAG1
24	36.2	9.8	168181	2	AC115890
25	36.2	9.8	191141	9	AC073424
26	36	9.8	44032	2	AC014006
27	36	9.8	160089	3	AC007813
28	36	9.8	255624	3	AE003723
29	35.8	9.7	157226	9	AC018902
30	35.8	9.7	163135	2	AC098218
31	35.8	9.7	184157	2	AC073438
32	35.6	9.6	36424	2	AL390015
33	35.6	9.6	168767	9	AC099562
34	35.2	9.5	65280	9	AC118549
35	35.2	9.5	179854	9	AC007437
36	35.2	9.5	188561	2	AC110739
37	35	9.5	38491	3	LMFL8138
38	35	9.5	40620	3	AF239995
39	34.8	9.4	164462	2	AC106546
40	34.6	9.4	169123	2	AC130865
41	34.6	9.4	199450	2	AC124918
42	34.6	9.4	204767	2	AC097561
43	34.4	9.3	187023	2	AC120749
44	34.2	9.3	2817	3	AF015539
45	34.2	9.3	64958	2	AC090905

ALIGNMENTS

RESULT 1
AX093381
LOCUS AX093381
DEFINITION Sequence 199 from Patent WO0118046.
ACCESSION AX093381
VERSION AX093381.1 GI:13509829
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 369)
Xu, J. and Stolk, J. A.
Ovarian tumor sequences and methods of use therefor
Patent: WO 0118046-A 199 15-MAR-2001;
JOURNAL

Pred. No. is the number of results predicted by chance to have a

FEATURES CORIXA CORPORATION (US)
Location/Qualifiers
source 1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 1. .369
/note="n = A,T,C or G"

BASE COUNT 82 a 109 c 90 g 86 t 2 others
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Best Local Similarity 100.0%; Pred. No. 3,7e-96;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCAACTTTTGGCGATGTTCTTCTTTCAGGCTTGGCGTGAATTCAGTGGTACCA 60
DB 1 GGCAACTTTTGGCGATGTTCTTCTTTCAGGCTTGGCGTGAATTCAGTGGTACCA 60
OY 61 GTGTGAAGATTTCCAGCTGACACAGACTGCTTCCCGAGTTCATTTGAAATTGCAC 120
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DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
OY 181 CCGCAAGTCTGTGTCATATGACGCGCTGTCTCATCTCCCTTCCGGGTACAGTCCCT 240
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OY 241 CTGCTCCCGAGGAAACAGACTGCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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OY 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTGCGCCCTTCAGCCATGGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTGCGCCCTTCAGCCATGGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

RESULT 2 946 bp mRNA linear PRI 09-NOV-2001
BC017318 Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.
LOCUS BC017318
DEFINITION BC017318
ACCESSION BC017318.1 GI:16878239
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 946)
Strausberg, R.
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nrl.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantirrop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 39 Row: b Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

FEATURES Location/Qualifiers
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/clone_lib="NIH-MGC_39"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
261. .686
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BASE COUNT 197 a 292 c 261 g 196 t
ORIGIN

Query Match 99.0%; Score 365.4; DB 9; Length 946;
Best Local Similarity 99.2%; Pred. No. 1.1e-95;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 281 GGCAACTTTTGGCGATGTTCTTCTTTCAGGCTTGGCGTGAATTCAGTGGTACCA 340
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OY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
DB 401 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 460
OY 181 CCGCAAGTCTGTGTCATATGACGCGCTGTCTCATCTCCCTTCCGGGTACAGTCCCT 240
DB 461 CCGCAAGTCTGTGTCATATGACGCGCTGTCTCATCTCCCTTCCGGGTACAGTCCCT 520
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DB 521 CTGCTCCCGAGGAAACAGACTGCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
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DB 581 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTGCGCCCTTCAGCCATGGCTCCGAC 640
OY 361 CACCATCTCT 369
DB 641 CACCATCTCT 649

RESULT 3 1524 bp DNA linear PAT 13-FEB-2002
AX358762
LOCUS AX358762
DEFINITION Sequence 15 from Patent W00193983.
ACCESSION AX358762
VERSION AX358762.1 GI:16675282
KEYWORDS

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.
 TITLES Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: WO 0193983-A 15 13-DEC-2001;
 Genentech Inc. (US)

FEATURES
 source
 Location/Qualifiers
 1..1524
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

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 Best Local Similarity 99.2%; Pred. No. 1,1e-95;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 DB 261 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTGGCGGATCATGTA 320
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 DB 321 CCGCAAGTCTGTGCTATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCAGTCTT 380
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 DB 381 CTGCTCCCGAGGAACTGAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
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 DB 441 CGGGCCAAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCGCTCCGCAC 500
 QY 361 CACCATCTCT 369
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 DB 501 CACCATCTCT 509

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 LOCUS Sequence 15 from Patent WO0208288.
 DEFINITION AX362255
 ACCESSION AX362255
 VERSION AX362255.1 GI:18694585
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.
 TITLES Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;
 Genentech, Inc. (US)

FEATURES
 source
 Location/Qualifiers
 1..1524

BASE COUNT 321 a 433 c 435 g 335 t

ORIGIN

Query Match 99.0%; Score 365.4; DB 6; Length 1524;
 Best Local Similarity 99.2%; Pred. No. 1,1e-95;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTCTTCTTNCAGGCTTTGGCTGCAATCCAGTGTACCA 60
 |||
 DB 141 GGCACATTTTGGGATGTTCTTCTTNCAGGCTTTGGCTGCAATCCAGTGTACCA 200
 QY 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCCGCCGAGTTCTTGTGAATTGCAC 120
 |||
 DB 201 GTGTGAAGAAATTCAGCTGAACACGACTGCTCCGCCGAGTTCTTGTGAATTGCAC 260
 QY 121 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTGGCGGATCATGTA 180
 |||
 DB 261 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTGGCGGATCATGTA 320
 QY 181 CCGCAAGTCTGTGCTATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCAGTCTT 240
 |||
 DB 321 CCGCAAGTCTGTGCTATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCAGTCTT 380
 QY 241 CTGCTCCCGAGGAACTGAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 |||
 DB 381 CTGCTCCCGAGGAACTGAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
 QY 301 CGGGCCAAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCGCTCCGCAC 360
 |||
 DB 441 CGGGCCAAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCGCTCCGCAC 500
 QY 361 CACCATCTCT 369
 |||
 DB 501 CACCATCTCT 509

RESULT 5
 AK094501 1832 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ37182 fls, clone BRAL22001350, weakly similar
 DEFINITION to Homo sapiens Gz-selective GTPase-activating protein (RGS20)
 mRNA.
 ACCESSION AK094501
 VERSION AK094501.1 GI:21753575
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone_11b:BRAL22
 clone:BRAL22001350.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Waga, S., Murakawa, K., Kanehori, K., Takahashi, Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Negahari, K., Masuno, Y., Nagai, K. and Isogai, T.
 TITLES NED0 human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1832)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team): 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NED0 human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan: cDNA full insert sequencing:
 Research Association for Biotechnology (RAB) (supported by Japan
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'-3'-end one pass sequencing: RAB.

HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

source

1. .1832

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="BRAL22001350"

/issue_type="alzheimer cortex"

/clone_11b="BRAL22"

/note="Cloning vector: pME18FL3"

215. .640

/note="unnamed protein product"

/codon_start=1

/protein_id="BAC04368.1"

/db_xref="GI:2173576"

/translation="MWVIGIAATFCGLFLPGLFALQIQCYOCSEFQLNNDSSPEFIV
NCTVAVDQCKEYMEQESAGIMYRKSASACLIASAGYOSFCSPGKLNISVCSCN
TPLCNGPMPKRGSSASALRPLRTTILFLKLALFSAHC"

CDS

BASE COUNT 411 a 501 c 513 g 407 t

Query Match 99.0%; Score 365.4; DB 9; Length 1832; Best Local Similarity 99.2%; Pred. No. 1.1e-95; Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGCTTCTTCAGAGCTTGGCGTCAAAATCCAGTCTACCA 60
DB 225 GGCACTTTTGGCGATTGCTTCTTCAGAGCTTGGCGTCAAAATCCAGTCTACCA 294
QY 61 GTGTGAAGAAATTCACGCTGAACACGAGTCTCTCCCGAGTTCATTGTGAATGGAC 120
DB 295 GTGTGAAGAAATTCACGCTGAACACGAGTCTCTCCCGAGTTCATTGTGAATGGAC 354
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGAAAGTGGCGGATCATGTA 180
DB 355 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGAAAGTGGCGGATCATGTA 414
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCCCGGATACAGTCTT 240
DB 415 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCCCGGATACAGTCTT 474
QY 241 CTGCTCCCGAGGAAATCACTAGTTTGATCATGCTGTGCAACACCCCTTTTGTAA 300
DB 475 CTGCTCCCGAGGAAATCACTAGTTTGATCATGCTGTGCAACACCCCTTTTGTAA 534
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAGTTCGCTCGGCTTCANGCATGCTCCGAC 360
DB 535 CGGGCCAAAGGCCCAAGAAAGGGAGTTCGCTCGGCTTCANGCATGCTCCGAC 594
QY 361 CACCATCCT 369
DB 595 CACCATCCT 603

RESULT 6 AX136281 1890 bp DNA linear PAT 30-MAY-2001

LOCUS AX136281 Sequence 203 from Patent EPI067182.

DEFINITION AX136281

ACCESSION AX136281 GI:14272687

VERSION AX136281.1

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1890)

AUTHORS Ota, T., Isozaki, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and

Hayashi, K.

Secretory protein or membrane protein

Patient: EP 1067182-A 203 10-JAN-2001;

Helix Research Institute (JP)

Location/Qualifiers

source

1. .1890

/organism="Homo sapiens"

/db_xref="taxon:9606"

274. .771

/note="unnamed protein product"

/codon_start=1

/protein_id="CAC39782.1"

/db_xref="GI:14272688"

/translation="MWVIGIAATFCGLFLPGLFALQIQCYOCSEFQLNNDSSPEFIV
NCTVAVDQCKEYMEQESAGIMYRKSASACLIASAGYOSFCSPGKLNISVCSCN
TPLCNGPMPKRGSSASALRPLRTTILFLKLASSRHIAELKEMPPALFRQSPPT
PHLPE"

CDS

BASE COUNT 419 a 528 c 533 g 410 t

Query Match 99.0%; Score 365.4; DB 6; Length 1890; Best Local Similarity 99.2%; Pred. No. 1.1e-95; Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGCTTCTTCAGAGCTTGGCGTCAAAATCCAGTCTACCA 60
DB 294 GGCACTTTTGGCGATTGCTTCTTCAGAGCTTGGCGTCAAAATCCAGTCTACCA 353
QY 61 GTGTGAAGAAATTCACGCTGAACACGAGTCTCTCCCGAGTTCATTGTGAATGGAC 120
DB 354 GTGTGAAGAAATTCACGCTGAACACGAGTCTCTCCCGAGTTCATTGTGAATGGAC 413
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGAAAGTGGCGGATCATGTA 180
DB 414 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGAAAGTGGCGGATCATGTA 473
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCCCGGATACAGTCTT 240
DB 474 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCCCGGATACAGTCTT 533
QY 241 CTGCTCCCGAGGAAATCACTAGTTTGATCATGCTGTGCAACACCCCTTTTGTAA 300
DB 534 CTGCTCCCGAGGAAATCACTAGTTTGATCATGCTGTGCAACACCCCTTTTGTAA 593
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAGTTCGCTCGGCTTCANGCATGCTCCGAC 360
DB 594 CGGGCCAAAGGCCCAAGAAAGGGAGTTCGCTCGGCTTCANGCATGCTCCGAC 653
QY 361 CACCATCCT 369
DB 654 CACCATCCT 662

RESULT 7 AX093191 396 bp DNA linear PAT 30-MAR-2001

LOCUS AX093191 Sequence 9 from Patent WO0118046.

DEFINITION AX093191

ACCESSION AX093191 GI:13509640

VERSION AX093191.1

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 396)

AUTHORS Xu, J., and Stolk, J. A.

Ovarian tumor sequences and methods of use therefor

Patient: WO 0118046-A 9 15-MAR-2001;

CORTIXA CORPORATION (US)

Location/Qualifiers

source 1. .396

/organism="Homo sapiens"

/db_xref="taxon:9606"

/note="n = A, T, C or G"

BASE COUNT 90 a 117 c 95 g 92 t 2 others

misc_feature 1. .396

ORIGIN

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPCR-11 human BAC library was made from the blood of one male donor, as described by Osoegwa, K., Moon, P. Y., Zhao, B., Frengen, E., Tateo, M., Cateneo, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-11122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-256B17; actual end is at base position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES	Location/Qualifiers
source	1. .129676

repeat_region	/rpt_family="MaLR"	17508. .17966
	/rpt_family="ERV1"	18190. .18453
repeat_region	/rpt_family="ERV1"	18434. .18801
repeat_region	/rpt_family="ERV1"	18933. .19074
repeat_region	/rpt_family="ERV1"	19144. .19250
repeat_region	/rpt_family="ERV1"	19260. .19628
repeat_region	/rpt_family="ERV1"	20104. .20145
repeat_region	/rpt_family="(TG)n"	20170. .20305
	/rpt_family="MER1_type"	20618. .20756
repeat_region	/rpt_family="MER1_type"	21300. .21325
repeat_region	/rpt_family="(A)n"	21428. .21796
misc_feature	/note="match to EST BF821779 (MID:g12161303)"	23084. .23228
repeat_region	/rpt_family="MIR"	23967. .24256
repeat_region	/rpt_family="Alu"	25108. .25208
repeat_region	/rpt_family="MIR"	23485. .23605
repeat_region	/rpt_family="MaLR"	26417. .26463
repeat_region	/rpt_family="ERV1"	26466. .26655
repeat_region	/rpt_family="MER2_type"	26656. .27047
repeat_region	/rpt_family="MaLR"	27048. .27149
repeat_region	/rpt_family="MER2_type"	27246. .27403
repeat_region	/rpt_family="(TA)n"	27309. .27380
repeat_region	/rpt_family="r1"	27403. .27671
repeat_region	/rpt_family="Alu"	27698. .27749
repeat_region	/rpt_family="MER2_type"	27750. .27904
repeat_region	/rpt_family="(TA)n"	27926. .28052
misc_feature	/rpt_family="L2"	28052. .28667
repeat_region	/note="match to EST BF736070 (MID:g12062744)"	28834. .28958
repeat_region	/rpt_family="MIR"	29414. .29696
repeat_region	/rpt_family="Alu"	29727. .30221
repeat_region	/rpt_family="MaLR"	30363. .30543
repeat_region	/rpt_family="MER1_type"	30738. .30919
repeat_region	/rpt_family="MER1_type"	31494. .31783
repeat_region	/rpt_family="Alu"	32028. .32488
repeat_region	/rpt_family="ERV1"	32053. .32080
repeat_region	/rpt_family="(GA)n"	32667. .32787
repeat_region	/rpt_family="MIR"	34079. .34164
repeat_region	/rpt_family="L2"	

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repeat_region      34271..34348
                    /rpl_family="MERL_type"
misc_feature       34409..34703
                    /note="match to EST BG956501 (NID:g14374672)"
repeat_region      35346..35374
                    /rpl_family="TTTTGn"
repeat_region      35361..35676
                    /rpl_family="Alu"

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Query Match      53.7%; Score 198.2; DB 9; Length 129676;
Best local Similarity 98.0%; Pred. No. 7.2e-47;
Matches 200; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 166 TGGCGGATGATGATGACGCAAGTCTGTGCATGATGACGCGCTGTCTCATCCCTCTGC 225
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Db 120745 TACAGGATGATGATGACGCAAGTCTGTGCATGATGACGCGCTGTCTCATCCCTCTGC 120686

QY 226 CGGGTACAGTCTCTTCTGCTGCCAGGAAAGTGAAGTCTGATGATGATGATGATGATG 285
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120685 CGGGTACAGTCTCTTCTGCTGCCAGGAAAGTGAAGTCTGATGATGATGATGATGATG 120626

QY 286 CACCCCTCTTGTATGAGGCGCAAGGCGCAAGGGAAGTCTGCTGCGGCGCTGCAN 345
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120625 CACCCCTCTTGTATGAGGCGCAAGGCGCAAGGGAAGTCTGCTGCGGCGCTGCAG 120566

QY 346 GCCATGCTCTCCGACACCATCTCT 369
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120565 GCCATGCTCTCCGACACCATCTCT 120542

```

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RESULT 12
AC124493/C 209885 bp DNA linear HTG 05-JUL-2002
LOCUS AC124493
DEFINITION Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
ACCESSION AC124493
VERSION AC124493.2 GI:21699722
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 209885)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 209885)
TITLE McPherson,J.D. and Waterston,R.H.
JOURNAL Direct Submission
AUTHORS 3 (bases 1 to 209885)
TITLE McPherson,J.D. and Waterston,R.H.
JOURNAL Direct Submission
AUTHORS Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
TITLE Parkway, St. Louis, MO 63108, USA
JOURNAL On Jul 5, 2002 this sequence version replaced g1:2142614.
COMMENT
      ----- Genome Center -----
      Center: Washington University Genome Sequencing Center
      Center code: WUGSC
      Web site: http://genome.wustl.edu/gsc/index.shtml
      Contact: submissions@wustl.wustl.edu
      Project Information
      Center project name: M_BA0462P13

```

```

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208464 bases at least Q40

```

```

Consensus quality: 208911 bases at least Q30
Consensus quality: 209285 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 212112; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; agarose-fp
Quality coverage: 11.62 in Q20 bases; sum-of-contigs

```

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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```

1 11331: contig of 11331 bp in length
* 11332 11431: gap of unknown length
* 11432 28617: contig of 17186 bp in length
* 28618 28717: gap of unknown length
* 28718 49454: contig of 20737 bp in length
* 49455 49554: gap of unknown length
* 49555 107384: contig of 57830 bp in length
* 107385 107484: gap of unknown length
* 107485 209885: contig of 102401 bp in length.
Location/Qualifiers
1. 209885

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FEATURES
source
1. 209885

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misc_feature
1. 11331
/note="assembly_name:Contig8"
11432..28617
/note="assembly_name:Contig9"
28718..49454
/note="assembly_name:Contig10"
49555..107384
/note="assembly_name:Contig11"
107485..209885
misc_feature
/note="assembly_name:Contig12"
59789 a 44784 c 46164 g 58745 t 403 others
ORIGIN

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Query Match      43.1%; Score 159; DB 2; Length 209885;
Best local Similarity 87.0%; Pred. No. 2e-35;
Matches 174; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATGACGGGCTGTCTCATGCCCTGCCGG 229
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Db 66382 GGGATCATGTACCGCAAGTCTGTGCATCATGACGGGCTGTCTCATGCCCTGCCGG 66323

QY 230 TACCATGCTCTTCTGCTGCCAGGAAAGTGAAGTCTGATGATGATGATGATGATGATG 289
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66322 TACCATGCTCTTCTGCTGCCAGGAAAGTGAAGTCTGATGATGATGATGATGATGATG 66263

QY 290 CCTCTTGTATGAGGCGCAAGGCGCAAGGGAAGTCTGCTGCGGCGCTGCAN 349
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66262 CCTCTTGTATGAGGCGCAAGGCGCAAGGGAAGTCTGCTGCGGCGCTGCAN 66203

QY 350 TGGCTCCGACACCATCTCT 369
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66202 TGGCTCCGACACCATCTCT 66183

```

```

RESULT 13
AC010974/C 147131 bp DNA linear PRI 01-MAR-2002
LOCUS AC010974
DEFINITION Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION AC010974
VERSION AC010974.9 GI:19033964
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

```

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 147131)
MEDLINE Toward a complete human genome sequence
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 147131)
AUTHORS Vanbrunt, A. and Stromwater, C.
TITLE The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 147131)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 147131)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 147131)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 1, 2002 this sequence version replaced g1:13435273.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplensew@wustl.edu

Summary Statistics
Center project name: H_NH0159N20

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the
clone sequenced to the right is RP11-258B17. Actual start of this
clone is at base position 1 of RP11-159N20; actual end is at base
position 147131 of RP11-159N20.

FEATURES

There are polymorphic base differences in the overlap between the
clone RP11-159N20 and RP11-258B17.

Source	Location/Qualifiers
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	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2"
	/clone="RP11-159N20"
	/clone_lib="RP11-11"
	21. 67
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	118. 1013
repeat_region	/rpt_family="L1"
	984. 1176
misc_feature	/note="match to EST BG200048 (NID:g13721735)"
	991. 1176
misc_feature	/note="match to EST BG184021 (NID:g13705708)"
	991. 1176
misc_feature	/note="match to EST BG187166 (NID:g13708853)"
	1035. 1200
repeat_region	/rpt_family="Alu"
	1525. 1552
repeat_region	/rpt_family="(TTTA)n"
	1526. 1814
repeat_region	/rpt_family="Alu"
	2299. 2596
repeat_region	/rpt_family="Alu"
	4890. 5129
repeat_region	/rpt_family="MALR"
	5738. 5757
repeat_region	/rpt_family="(TG)n"
	6131. 6178
repeat_region	/rpt_family="GA-rich"
	7310. 7364
misc_feature	/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
	7811. 7881
repeat_region	/rpt_family="MIR"
	8227. 8260
repeat_region	/rpt_family="(CATTC)n"
	8373. 8683
repeat_region	/rpt_family="L1"
	8640. 9120
misc_feature	/note="match to EST BF112212 (NID:g10941902)"
	8776. 8838
repeat_region	/rpt_family="MIR"
	8810. 9257
misc_feature	/note="match to EST AA434316 (NID:g2139230) zw24e08.r1"
	9348. 9395
repeat_region	/rpt_family="GA-rich"
	9731. 9895
misc_feature	/note="match to EST BF347279 (NID:g11294874)"
	9743. 9895
misc_feature	/note="match to EST BG184021 (NID:g13705708)"
	9743. 9895
misc_feature	/note="match to EST BG187166 (NID:g13708853)"
	10053. 10359
repeat_region	/rpt_family="Alu"
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	13456. 13776
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	13854. 13855
misc_feature	/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
	15183. 15321
misc_feature	/note="match to EST BE386060 (NID:g9331425)"
	15183. 15321
misc_feature	/note="match to EST BG704350 (NID:g13977603)"
	15183. 15321
misc_feature	/note="match to EST BG753617 (NID:g14064270)"

1	1231:	contlg of 1231	bp in length
1232	1231:	gap of unknown	length
1332	2411:	contlg of 1080	bp in length
2412	2511:	gap of unknown	length
2512	3709:	contlg of 1198	bp in length
3710	3809:	gap of unknown	length
3810	4935:	contlg of 1126	bp in length
4936	5035:	gap of unknown	length
5036	6214:	contlg of 1179	bp in length
6215	6314:	gap of unknown	length
6315	7337:	contlg of 1123	bp in length
7338	7537:	gap of unknown	length
7538	8808:	contlg of 1271	bp in length
8809	9808:	gap of unknown	length
10059	10058:	contlg of 1150	bp in length
10059	10158:	gap of unknown	length
10159	11422:	contlg of 1264	bp in length
11423	11522:	gap of unknown	length
11523	12687:	contlg of 1165	bp in length
12688	12787:	gap of unknown	length
12788	13983:	contlg of 1196	bp in length
13984	14083:	gap of unknown	length
14084	15533:	contlg of 1450	bp in length
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VERSION	AC128363.1
KEYWORDS	GI:21909012
SOURCE	HTG; HTGS_PHASE1.
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	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi

REFERENCE
AUTHORS

Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 190503)

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

COMMENT

Muny, D.M., Adams, C., Adio-Oduola, B., Ali-Usman, F.R., Allen, C.,
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Unpublished

2 (bases 1 to 190503)

Direct Submission

Submitted (19-JUL-2002)

Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GZCA

Center clone name: CH230-22808

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap version 0.990329

Consensus quality: 13119 bases at least Q40

Consensus quality: 136808 bases at least Q30

Consensus quality: 141839 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 69 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
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59756: gap of unknown length
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* 66407 68763: contig of 2357 bp in length
* 68764 71061: contig of 2198 bp in length
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* 77234 77333: gap of unknown length
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Best Local Similarity 87.1%: Pred. No. 2e-12; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 13;

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Oy 166 TCCCGGATCATGATCCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCCGCTCTGC 225
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Oy 226 CGGATACGATGCTCTGTCTCCCGAGGAACCTGACTCAG 266
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Db 170117 TGGATACCTGTCTCTGTCTCTGGGAACCTGACTCCG 170077
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Search completed: November 7, 2002, 13:25:36
Job time : 1186.87 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:50:02 ; Search time 72.6545 Seconds

(without alignments)
11437.514 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369
Sequence: 1 ggcacatttctgcgagatgt.....tggctccgcaccacatcct 369

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	99.5	369	AAF95007	Human ovarian carc
2	367	99.5	369	ABT03274	Human ovarian carc
3	367	99.5	369	ABL48956	Ovarian carcinoma
4	365.4	99.0	1524	ABR33543	CDNA encoding huma
5	365.4	99.0	1619	ABT03277	Human ovarian carc
6	365.4	99.0	1619	ABT03281	Human ovarian carc
7	365.4	99.0	1619	ABL40345	Ovarian carcinoma
8	365.4	99.0	1619	ABL40349	Ovarian carcinoma
9	365.4	99.0	1890	AAF93845	Human CDNA encodin

10	365.4	99.0	1897	24	ABT03284	Human ovarian carc
11	365.4	99.0	1897	24	ABL40352	Ovarian carcinoma
12	352.4	95.5	1953	21	AAF22400	Human secreted pro
13	352.4	95.5	1956	22	AAF64188	Human secreted pro
14	343.4	93.1	396	22	AAF94818	Human ovarian carc
15	343.4	93.1	396	24	ABT03085	Human ovarian carc
16	343.4	93.1	396	24	ABL48768	Ovarian carcinoma
17	341.8	92.6	1010	24	ABT03282	Human ovarian carc
18	341.8	92.6	1010	24	ABL40350	Ovarian carcinoma
19	336.4	91.2	2528	22	ABL16690	Human G protein co
20	284	77.0	591	22	AAF94044	Primer specific fo
21	196.8	53.3	480	24	ABT03283	Human ovarian carc
22	196.8	53.3	480	24	ABL40351	Ovarian carcinoma
23	174.2	47.2	1608	24	ABO54231	Human ovarian carc
24	86.4	23.4	430	24	ABL81273	Human ovarian carc
25	36	9.8	44242	23	ABL19930	Drosophila melano
26	35.4	9.6	5811	21	AACT5680	Human OREF ORF1435
27	33.8	9.2	3268	23	AAST7591	DNA encoding novel
28	33.8	9.2	5676	22	AA159341	Human polynucleoti
29	33.8	9.2	4403765	22	AA199683	Mycobacterium tube
30	33.6	9.1	20578	22	AB16515	Human nervous syst
31	33.2	9.0	2133	22	AAH64972	C glutamic codin
32	33.2	9.0	34980	22	AAH64966	C glutamic codin
33	33	8.9	445	22	AA190253	Human polynucleoti
34	33	8.9	7931	23	ABL25204	Drosophila melano
35	32.2	8.7	479	22	AA126045	Human breast cance
36	32.2	8.7	815	22	AA116843	Human breast cance
37	32.2	8.7	3343	20	AAH87179	Fibroblast growth
38	32.2	8.7	110608	24	ABR83572	Human CDNA differe
39	32	8.7	3496	24	ABR64744	Human benign prost
40	31.8	8.6	759	15	AAO66584	Sequence of rabbit
41	31.6	8.6	544	22	AAO66584	Human cancer agent
42	31.6	8.6	658	21	AAO51550	Arabidopsis thalia
43	31.6	8.6	674	21	AAO51571	Arabidopsis thalia
44	31.6	8.6	775	24	ABR99125	Arabidopsis thalia
45	31.6	8.6	924	22	AAK57408	Human Immune/Haema

ALIGNMENTS

RESULT 1	
AAF95007	
ID AAF95007 standard; DNA; 369 BP.	
XX AAF95007;	
AC	23-MAY-2001 (first entry)
XX	
DT	Human ovarian cancer associated coding sequence SEQ ID NO: 199.
XX	
DE	Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
XX	
KW	Human, sapiens.
XX	
OS	
XX	
PN	WO200118046-A2.
XX	
PD	15-MAR-2001.
XX	
PF	08-SEP-2000; 2000WO-US24827.
XX	
PR	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA.
XX	
DR	WPI; 2001-211395/21.
XX	
PT	Isolated polypeptides associated with ovarian carcinomas, and the

PT nucleic acids that encode them, useful for the prevention diagnosis and
 PT treatment of ovarian cancers -
 XX
 XX
 PS Claim 18; Page 189; 189pp; English.

XX The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences.

XX Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTTGGGCTGCAAAATCCAGTCAACCA 60
 DB 1 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTTGGGCTGCAAAATCCAGTCAACCA 60
 QY 61 GTGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 120
 DB 61 GTGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 120
 QY 121 GGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 180
 DB 121 GGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 180
 QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCCAGTCTT 240
 DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCCAGTCTT 240
 QY 241 CTGCTCCCGAGGAACTGACTGATCTTGCATCAGCTGTGTAACCCCTTTGTAA 300
 DB 241 CTGCTCCCGAGGAACTGACTGATCTTGCATCAGCTGTGTAACCCCTTTGTAA 300
 QY 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 DB 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 QY 361 CACCATCTT 369
 DB 361 CACCATCTT 369

RESULT 2

ABT03274

ID ABT03274 standard; cDNA; 369 BP.

XX ABT03274;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

KW Human: ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KM cytostatic; gene; ss.

XX Homo sapiens.

XX WO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
 XX
 XX WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Example 1; Page 187; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.

XX Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 24; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTTGGGCTGCAAAATCCAGTCAACCA 60
 DB 1 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTTGGGCTGCAAAATCCAGTCAACCA 60
 QY 61 GTGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 120
 DB 61 GTGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 120
 QY 121 GGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 180
 DB 121 GGTGAAGATTCACAGTCAACAGACGCTCTCCCGGAGTTGTAATTGCAC 180
 QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCCAGTCTT 240
 DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGCAGGATCCAGTCTT 240
 QY 241 CTGCTCCCGAGGAACTGACTGATCTTGCATCAGCTGTGTAACCCCTTTGTAA 300
 DB 241 CTGCTCCCGAGGAACTGACTGATCTTGCATCAGCTGTGTAACCCCTTTGTAA 300
 QY 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 DB 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 QY 361 CACCATCTT 369
 DB 361 CACCATCTT 369

RESULT 3

ABL48956

ID ABL48956 standard; cDNA; 369 BP.

XX ABL48956;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 57887.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KM ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALCA/) ALGATE P A.
 PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;
 XX
 DR WPI; 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially ovarian cancer.
 PS
 XX
 PS Claim 1a; Page 116; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The sequences
 CC given in records ABL48760-ABL48956 represent polynucleotides encoding
 CC ovarian carcinoma proteins.
 CC
 SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 24; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCACCTTTTGGGATGTTCTGCTTNCAGCTTGCCTGCAAAATCCAGTGTACCA 60
 DB 1 GGCACCTTTTGGGATGTTCTGCTTNCAGCTTGCCTGCAAAATCCAGTGTACCA 60
 OY 61 GTGTGAAGAAATTCAGCTGAACAAGACAGCTCTCTCCCGAGTTCAATGTGAATTGCAC 120
 DB 61 GTGTGAAGAAATTCAGCTGAACAAGACAGCTCTCTCCCGAGTTCAATGTGAATTGCAC 120
 OY 121 GGTGAACCTTCAAGACATGTGTCTGAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 DB 121 GGTGAACCTTCAAGACATGTGTCTGAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 OY 181 CGCAGATCTCTGATCATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGATCTCT 240
 DB 181 CGCAGATCTCTGATCATCATCAGCGGCTGTCTCATGCTCTGCGGGATCAGATCTCT 240
 OY 241 CTCTCTCCCGAGGAAATGAACTGATTTGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 CTCTCTCCCGAGGAAATGAACTGATTTGATGATGATGATGATGATGATGATGATGAT 300
 OY 301 CGGCGCAAGGCGCAAGGAAAGGAGGAGTCTGCTCGGCGCTCCATGCGATGCGGAC 360
 DB 301 CGGCGCAAGGCGCAAGGAAAGGAGGAGTCTGCTCGGCGCTCCATGCGATGCGGAC 360
 OY 361 CACCATCTCT 369
 DB 361 CACCATCTCT 369

RESULT 4

ABK33543
 ID ABK33543 standard; cDNA; 1524 BP.

XX AC ABK33543;

XX DT 08-MAY-2002 (first entry)

XX DE cDNA encoding human PRO protein, Seq ID No 15.

XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha; gene; ss.

XX OS Homo sapiens.

XX FM WO200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US21066.

XX PR 20-JUL-2000; 2000US-219556P.

XX PR 25-JUL-2000; 2000US-220585P.

XX PR 25-JUL-2000; 2000US-220605P.

XX PR 25-JUL-2000; 2000US-220607P.

XX PR 25-JUL-2000; 2000US-220624P.

XX PR 25-JUL-2000; 2000US-220638P.

XX PR 25-JUL-2000; 2000US-220664P.

XX PR 26-JUL-2000; 2000US-220893P.

XX PR 28-JUL-2000; 2000WO-US20710.

XX PR 23-AUG-2000; 2000WO-US23522.

XX PR 24-AUG-2000; 2000WO-US23328.

XX PR 15-SEP-2000; 2000US-000000P.

XX PR 10-NOV-2000; 2000WO-US30873.

XX PR 28-NOV-2000; 2000US-253646P.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 20-DEC-2000; 2000US-0747259.

XX PR 20-DEC-2000; 2000WO-US34956.

XX PR 28-FEB-2001; 2001WO-US06520.

XX PR 10-MAY-2001; 2001US-0854280.

XX PR 25-MAY-2001; 2001WO-US17092.

XX PA (GENE) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR P-PSDB: AAU83599.

XX WPI; 2002-172001/22.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -

XX Claim 2; Figure 15; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. ABK3356-ABK33657 represent human
CC PRO protein coding sequences of the invention.

SO Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1524;
Best Local Similarity 99.2%; Pred. No. 1.1e-109;

Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 GGCACTTTTGGGATGTTCTTGTCTNAGGCTTGGCCGTGCAATTCAGTCTACCA 60
    |||
Db 141 GGCACTTTTGGGATGTTCTTGTCTNAGGCTTGGCCGTGCAATTCAGTCTACCA 200
    |||
QY 61 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 120
    |||
Db 201 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 260
    |||
QY 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 180
    |||
Db 261 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 320
    |||
QY 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 240
    |||
Db 321 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 380
    |||
QY 241 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 300
    |||
Db 381 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 440
    |||
QY 301 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 360
    |||
Db 441 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 500
    |||
QY 361 CACCATCT 369
    |||
Db 501 CACCATCT 509
```

RESULT 5
ABT03277
ID ABT03277 standard; cDNA; 1619 BP.

AC ABT03277;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;

PI Novel ovarian cancer polypeptide and polynucleotide, useful for
PI detecting the presence of ovarian cancer in a patient, and in
PI pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PI

XX Claim 2; Page 189-190; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

SO Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;
Best Local Similarity 99.2%; Pred. No. 1.2e-109;

Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 GGCACTTTTGGGATGTTCTTGTCTNAGGCTTGGCCGTGCAATTCAGTCTACCA 60
    |||
Db 1 GGCACTTTTGGGATGTTCTTGTCTNAGGCTTGGCCGTGCAATTCAGTCTACCA 60
    |||
QY 61 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 120
    |||
Db 61 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 120
    |||
QY 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 180
    |||
Db 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCATTGTGAATTGCAC 180
    |||
QY 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 240
    |||
Db 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 240
    |||
QY 241 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 300
    |||
Db 241 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 300
    |||
QY 301 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 360
    |||
Db 301 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCAGTCTT 360
    |||
QY 361 CACCATCT 369
    |||
Db 361 CACCATCT 369
```

RESULT 6
ABT03281
ID ABT03281 standard; cDNA; 1619 BP.

AC ABT03281;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;

PI Novel ovarian cancer polypeptide and polynucleotide, useful for
PI detecting the presence of ovarian cancer in a patient, and in
PI pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PI

XX Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 XX
 PS Claim 2; Page 195; 197pp; English.
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATTGTTCTTTCAGGCTTTGCGTCAATTCAGTCTACCA 60
 |||||||
 DB 1 GGCACCTTTTGGCGATTGTTCTTTCAGGCTTTGCGTCAATTCAGTCTACCA 60
 QY 61 GTGGAAGAAATTCAGTGAACAGACAGCTGCTCCCGGAGTCAATTTGATGAC 120
 |||||||
 DB 61 GTGGAAGAAATTCAGTGAACAGACAGCTGCTCCCGGAGTCAATTTGATGAC 120
 QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 |||||||
 DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 QY 181 CCGGAGTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCACTCTT 240
 |||||||
 DB 181 CCGGAGTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCACTCTT 240
 QY 241 CTGCTCCCGGAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300
 |||||||
 DB 241 CTGCTCCCGGAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300
 QY 301 CCGGCGCAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 |||||||
 DB 301 CCGGCGCAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 QY 361 CACCATCTT 369
 |||||||
 DB 361 CACCATCTT 369

RESULT 7

ABLA0345
 ID ABLA0345 standard; cDNA; 1619 BP.

AC ABLA0345;
 XX

DT 28-JUN-2002 (first entry)
 XX

DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
 XX

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KM ss.
 XX

OS Homo sapiens.
 XX

PN US2002004491-A1.
 XX

PD 10-JAN-2002.
 XX

PF 03-APR-2001; 2001US-0825294.
 XX

PR 10-SEP-1999; 99US-0394374.
 XX

PR 01-MAY-2000; 2000US-0561778.
 XX

PR 15-AUG-2000; 2000US-0640173.
 XX

PR 07-SEP-2000; 2000US-0656668.
 XX

PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XUJ/) XU J.
 PA (STOLK/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 XX
 PI XU J, Stolk JA, Algate PA, Fling SP;
 DR WPI; 2002-171027/22.
 XX
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 XX prevention and/or treatment of cancer, especially ovarian cancer
 XX

Claim 1a; Page 119-120; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the extended cDNA sequence of ovarian carcinoma
 CC isolate 57887 given in record ABL48956.
 XX

SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATTGTTCTTTCAGGCTTTGCGTCAATTCAGTCTACCA 60
 |||||||
 DB 1 GGCACCTTTTGGCGATTGTTCTTTCAGGCTTTGCGTCAATTCAGTCTACCA 60
 QY 61 GTGGAAGAAATTCAGTGAACAGACAGCTGCTCCCGGAGTCAATTTGATGAC 120
 |||||||
 DB 61 GTGGAAGAAATTCAGTGAACAGACAGCTGCTCCCGGAGTCAATTTGATGAC 120
 QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 |||||||
 DB 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180
 QY 181 CCGGAGTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCACTCTT 240
 |||||||
 DB 181 CCGGAGTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCACTCTT 240
 QY 241 CTGCTCCCGGAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300
 |||||||
 DB 241 CTGCTCCCGGAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300
 QY 301 CCGGCGCAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 |||||||
 DB 301 CCGGCGCAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
 QY 361 CACCATCTT 369
 |||||||
 DB 361 CACCATCTT 369

RESULT 8

ABLA0349
 ID ABLA0349 standard; cDNA; 1619 BP.

AC ABL40349;
 XX 28-JUN-2002 (first entry)
 XX Ovarian carcinoma O591S nucleotide sequence.
 DE Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW ss.
 XX Homo sapiens.
 OS
 PN US2002004491-A1.
 PD 10-JAN-2002.
 XX 03-APR-2001; 2001US-0825294.
 PE
 XX 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656568.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XUJ/) XU J.
 PA (STOL/) STOLK J A.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PI Xu J, Stolk JA, Algate PA, Fling SP;
 DR WPI: 2002-171027/22.
 XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PT prevention and/or treatment of cancer, especially ovarian cancer.
 XX
 PS Claim 1a: Page 125-126; 131pp; English.
 XX
 XX The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma O591S nucleotide sequence.
 CC
 XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
 SQ
 Query Match 99.0%; Score 365.4; DB 24; Length 1619;
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 181 CCGCAAGTCCTGTGCATCATCAGCGGCTGTCTCATGCGCTCGCGGACACATCCTT 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 CTGCTCCCCAGGAAACTGAACCTCAGTTTGATCAGCTGCTGCAACACCCTCTTTGTA 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 CTGCTCCCCAGGAAACTGAACCTCAGTTTGATCAGCTGCTGCAACACCCTCTTTGTA 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTTGCCTCGGCGCTCAGGCCATGCTCCGCAC 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTTGCCTCGGCGCTCAGGCCATGCTCCGCAC 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 CACCATCCT 369
 |||||||||||
 DB 361 CACCATCCT 369
 |||||||||||
 RESULT 9
 AAF93845
 ID AAF93845 standard; CDNA; 1890 BP.
 XX
 AC AAF93845;
 XX 23-MAY-2001 (first entry)
 DT
 XX Human cDNA encoding a membrane or secretory protein clone PSEC0181.
 DE
 XX Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW Rheumatoid arthritis; diabetes; ss.
 XX
 OS Homo sapiens.
 XX
 PN Ep1067182-A2.
 XX 10-JAN-2001.
 PD
 XX 07-JUL-2000; 2000EP-0114090.
 PE
 XX 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR WPI: 2001-093989/11.
 PT P-PSDB; AAB88418.
 XX
 XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
 CC gene therapy or as candidate target molecules in drug development -
 CC
 XX Claim 1; SEQ ID 203; 609pp + CD ROM; English.
 CC
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

SO Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other:

Query Match 99.0%; Score 365.4; DB 22; Length 1890;
Best Local Similarity 99.2%; Pred. No. 1.2e-109;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGGATGTTCTTCTTCCTTNCAGGCTTTGCGTCAATTCAGTGTACCA 60
   |||||||
Db 294 GGCACCTTTTGGGATGTTCTTCTTCCTTNCAGGCTTTGCGTCAATTCAGTGTACCA 353
QY 61 GTGTGAAGAATTCAGCTGGAACAAGACTGCTCTCCCGAGTTCAATGTAATTCAC 120
   |||||||
Db 354 GTGTGAAGAATTCAGCTGGAACAAGACTGCTCTCCCGAGTTCAATGTAATTCAC 413
QY 121 GGTGAAGTTCACAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
   |||||||
Db 414 GGTGAAGTTCACAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 473
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGTACAGTCTCT 240
   |||||||
Db 474 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGTACAGTCTCT 533
QY 241 CTGCTCCCCAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 300
   |||||||
Db 534 CTGCTCCCCAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 593
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCTCGCCCTCAGCCATGCTCCGCAC 360
   |||||||
Db 594 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCTCGCCCTCAGCCATGCTCCGCAC 653
QY 361 CACCATCCT 369
   |||||||
Db 654 CACCATCCT 662

```

RESULT 10

ABT03284
ID ABL03284 standard; cDNA; 1897 BP.

AC ABL03284;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PE 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for
detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PI
XX
XX
PS Claim 2; Page 196; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

SO Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:

Query Match 99.0%; Score 365.4; DB 24; Length 1897;
Best Local Similarity 99.2%; Pred. No. 1.2e-109;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGCACCTTTTGGGATGTTCTTCTTCCTTNCAGGCTTTGCGTCAATTCAGTGTACCA 60
   |||||||
Db 280 GGCACCTTTTGGGATGTTCTTCTTCCTTNCAGGCTTTGCGTCAATTCAGTGTACCA 339
QY 61 GTGTGAAGAATTCAGCTGGAACAAGACTGCTCTCCCGAGTTCAATGTAATTCAC 120
   |||||||
Db 340 GTGTGAAGAATTCAGCTGGAACAAGACTGCTCTCCCGAGTTCAATGTAATTCAC 399
QY 121 GGTGAAGTTCACAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 180
   |||||||
Db 400 GGTGAAGTTCACAGCATGTGTCAAGAAAGATGATGAGCAAAAGTGGCGGATCATGTA 459
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGTACAGTCTCT 240
   |||||||
Db 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGGCGGTACAGTCTCT 519
QY 241 CTGCTCCCCAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 300
   |||||||
Db 520 CTGCTCCCCAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 579
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCTCGCCCTCAGCCATGCTCCGCAC 360
   |||||||
Db 580 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCTCGCCCTCAGCCATGCTCCGCAC 639
QY 361 CACCATCCT 369
   |||||||
Db 640 CACCATCCT 648

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RESULT 11

ABL40352
ID ABL40352 standard; cDNA; 1897 BP.

AC ABL40352;

DT 28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 260..685

FT /tag- a /product- "Ovarian carcinoma protein O1034C/O591S"

PN US2002004491-A1.

PD 10-JAN-2002.

PE 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI XU J, STOLK JA, ALGATE PA, FLING SP;
XX
DR WPI: 2002-171027/22.
XX P-PSDB: ABB09417.
XX
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer
XX
PS Claim 1a; Page 127-128; 131pp; English.
XX
XX The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The current
XX sequence represents the ovarian carcinoma O1034C/O591S consensus
XX nucleotide sequence.
SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:
Query Match 99.0%; Score 365.4; DB 24; Length 1897;
Best Local Similarity 99.2%; Pred. No. 1.2e-109;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
OY 1 GGCACCTTTTGGCGATGTTCTTCTTCAAGGCTTTCGCGCAATCCAGTGTACCA 60
DB 280 GGCACCTTTTGGCGATGTTCTTCTTCAAGGCTTTCGCGCAATCCAGTGTACCA 339
OY 61 GTGTGAAGATTTCCAGCTGAACACGACTGCTCTCCCGCGAGTTGATTTGAC 120
DB 340 GTGTGAAGATTTCCAGCTGAACACGACTGCTCTCCCGCGAGTTGATTTGAC 399
OY 121 GGTGAAGCTTCAAGCATCTGTCAAGAAAGTGAAGAGCAAGTGGCGGATCATGTA 180
DB 400 GGTGAAGCTTCAAGCATCTGTCAAGAAAGTGAAGAGCAAGTGGCGGATCATGTA 459
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGGCGGATCATGCTT 240
DB 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGGCTTGGCGGATCATGCTT 519
OY 241 CTGCTCCCGAGGAAATGCACTGATTTGCACTCAGCTGCTGCAACACCCCTTTTGTAA 300
DB 520 CTGCTCCCGAGGAAATGCACTGATTTGCACTCAGCTGCTGCAACACCCCTTTTGTAA 579
OY 301 CGGGCCAAAGCCCAAGAAAGGGAAGTCTGCTCGGCGCTCAGGCTGCTCGGAC 360
DB 580 CGGGCCAAAGCCCAAGAAAGGGAAGTCTGCTCGGCGCTCAGGCTGCTCGGAC 639
OY 361 CACCATCTT 369
DB 640 CACCATCTT 648
RESULT 12

AAF22400/C
ID AAF22400 standard; cDNA; 1953 BP.
XX
AC AAF22400;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human secreted protein gene 28 SEQ ID NO:38.
XX
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; viruscide;
XX fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
XX rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
XX cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
XX angioneurosis; nervous system disorder; Alzheimer's disease; infection;
XX ocular disorder; corneal infection; wound healing; skin aging;
XX food additive; preservative; ss.
XX
OS Homo sapiens.
XX
FN W0200061629-A1.
XX
XX 19-OCT-2000.
XX
PD 06-APR-2000; 2000WO-US09071.
XX
PE 09-APR-1999; 99US-0128694.
XX
PR 20-JAN-2000; 2000US-0176931.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Ruben SM, Komatsoulis G;
XX WPI: 2000-647420/62.
XX
XX P-PSDB: AAB63161.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; Page 440; 533pp; English.
XX
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
XX to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
XX and polypeptides homologous to them. Human secreted proteins have
XX activities based on the tissues and cells the genes are expressed in.
XX Examples of activities include: immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; viruscide;
XX fungicide; and ophthalmological. The polynucleotides and proteins can be
XX used to prevent, treat or ameliorate a medical condition in e.g. humans,
XX mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
XX also used in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular
XX disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
XX ischaemia, angioneurosis, nervous system disorders e.g. Alzheimer's
XX disease, infections caused by bacteria, viruses and fungi and ocular
XX disorders e.g. corneal infection. The polypeptides can also be used to
XX aid wound healing and epithelial cell proliferation, to prevent skin
XX aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis. The polypeptides can also be used as a food additive or
XX preservative to increase or decrease storage capabilities. AAF22364 to
XX AAF22372 and AAB63133 represent sequences used in the exemplification of
XX the present invention.
SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other:
Query Match 95.5%; Score 352.4; DB 21; Length 1953;
Best Local Similarity 98.6%; Pred. No. 2.4e-105;

Matches 364; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY	1	GGCAACATTTTGGGATATGTTCTTGGCTTTCAGGCTTGGCGCTGCATATCCAGTGTCTACCA	60
Db	1674	GGCAACTTTTTCGGATATGTTCTTGGCTTTCAGGCTTGGCGCTGCATATCCAGTGTCTACCA	1615
OY	61	GGTGAAGAATTCACAGTCAACACACATGCTCTCTCCCGAGTTTCATTGTGAATTCAC	120
Db	1614	GGTGAAGAATTCACAGTCAACACACATGCTCTCTCCCGAGTTTCATTGTGAATTCAC	1555
OY	121	GGTGAACGTTCAAGACATGTCGTAGAAAGAAGTATGGATGGACCAAGTCCGGGATCATGTA	180
Db	1554	GGTGAACGTTCAAGACATGTCGTAGAAAGAAGTATGGATGGACCAAGTCCGGGATCATGTA	1495
OY	181	CCGCAAGTCTCTGCATCATACAGCGGCGCTCTCATCGCCTTGCCGGGTACCAAGTCTCT	240
Db	1494	CCGCAAGTCTCTGCATCATACAGCGGCGCTCTCATCGCCTTGCCGGGTACCAAGTCTCT	1435
OY	241	CTGCTCTCCCAAGGAAACTGAACTCAGTTTGCATCAGCTGCTGCACACCCCTCTTTGTAA	300
Db	1434	CTGCTCTCCCAAGGAAACTGAACTCAGTTTGCATCAGCTGCTGCACACCCCTCTTTGTAA	1375
OY	301	CGGGCCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCTTGGGCCCTTANGCCATGCTCTCGCAC	360
Db	1374	CGGGCCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCTTGGGCCCTTANGCCATGCTCTCGCAC	1316
OY	361	CACCAATCCT 369	
Db	1315	CACCAATCCT 1307	

RESULT 13
AAF64188/C
ID AAF64188 standard; cDNA; 1956 BP.
vv

AC AAF6418B;

DT 06-APR-2001 (first entry)
XY

DE	Human secreted protein gene 13	SEQ ID NO:23.
YY		

KM Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KM antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KM neuroprotective; antibacterial; virucide; fungicide;
KM ophthalmological; vulnerability; autoimmune disease; cardiovascular disorder;
KM hyperproliferative disorders; cerebrovascular disorder; wound healing;
KM nervous system disorder; ocular disorder; skin aging; chemotaxis;
KM food additive; ss.

Homo sapiens.

PN WO200077026-A1

PD 21-DEC-2000

01-JUN-2000; 2000WO-US14973

PR 11-JUN-1999; 99US-0138630.

PA (HUMA-) HUMAN GENOME SCI INC.

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DR P-PSDB; AAB75518.

PT Nucleic acid mole

PT Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
 XX
 PS Claim 1, Page 443-444, 542pp: English.

Human secreted proteins AAB75506- AAB75554 are encoded by polynucleotide sequences AAF64116 - AAF64224. The specification includes amino acid sequences AAB75555 - AAB75605 which represent fragments of the human secreted proteins, and protein sequences with which they share homology. The proteins and polynucleotides, their agonists and antagonists have activities dependent on the tissues and cells in which they are expressed, examples of these activities include; immunosuppressive; antithalritic; antineumatic; antiproliferative; cytostatic; cardiatic; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virulide; fungicide; ophthalmological; and vulnary. The proteins, polynucleotides, agonists and antagonists can be used to treat or detect or diagnose various diseases and disorders including, autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are polynucleotide sequences AAF64157 - AAF64175 and peptide AAB75505 which are used in the isolation, identification and characterisation of the proteins of the invention.

50 Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match	95.5%;	Score 352.4;	DB 22;	Length 1956;
Best Local Similarity	98.6%;	Pred. No. 2.4e-105;		
Matches 364;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1

QY	1	GGCAACTTTTGGCGATTGTTCTTGCTTGNAGGCTTGGCGTGCACAAATCCAGTGGTACCA	60
Db	1674	GGCAACTTTTGGCGATTGTTCTTGCTTCCAGGCTTTGGCTGCACAAATCCAGTGGTACCA	1615
QY	61	GTGTGAAGAAATTCAGCTGAACAACGACGTCTCTCCCGGAGTTTCATTGTGAATTTGAC	120
Db	1614	GTGTGAAGAAATTCAGCTGAACAACGACGTCTCTCCCGGAGTTTCATTGTGAATTTGAC	1555
QY	121	GGTAAAGCTTCAGACACTGTGTGACAAAAGATGATGAGACAAAGTCCCGGATCATGTA	180
Db	1554	GGTAAAGCTTCAGACACTGTGTGACAAAAGATGATGAGACAAAGTCCCGGATCATGTA	1495
QY	181	CCGGAATCTCTGTGCATCATCAGCGGCGTGTCTCATCGGCTCTGGCGGGTTACCACTCTT	240
Db	1494	CCGGAATCTCTGTGCATCATCAGCGGCGTGTCTCATCGGCTCTGGCGGGTTACCACTCTT	1435
QY	241	CTGCTCTCCCAAGGAAACTGTAACCTGATTGGCATCAGCTCTCTCAACACCCCTCTTGTAA	300
Db	1434	CTGCTCTCCCAAGGAAACTGTAACCTGATTGGCATCAGCTCTCTCAACACCCCTCTTGTAA	1375
QY	301	CGGGCCCAAGGCCCAAGAAAAGGGGAAAGTTCTGCTCTCGGCCCTCANGCCATGGCTCCGAC	360
Db	1374	CGGGCCCAAGGCCCAAGAAAAGGGGAAAGTTCTGCTCTCGGCCCTCANGG - CAGGGCTCCGAC	1316
QY	361	CACCATCCT 369	
Db	1315	CACCATCCT 1307	

RESULT 14	
AAF94818	
ID	AAF94818 standard; CDNA; 396 BP
XY	

AC AAF94818,
VV

DT 23-MAY-2001 (first entry)
 YY

Human ovarian cancer associated coding sequence SEQ ID NO: 9

KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

XX Homo sapiens.
 OS
 XX
 XX WO200118046-A2.
 PN
 XX
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-US24827.
 XX
 PR 10-SEP-1999; 99US-0394374.
 XX
 PR 01-MAY-2000; 2000US-0561778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Xu J, Stolk JA;
 XX
 DR WPI; 2001-211395/21.
 XX
 PT Isolated polypeptides associated with ovarian carcinoma, and the
 PT nucleic acids that encode them, useful for the prevention diagnosis and
 PT treatment of ovarian cancers -
 PS
 PS Claim 5; Page 119; 189pp; English.
 XX
 CC The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences.
 CC
 SO Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 93.1%; Score 343.4; DB 22; Length 396;
 Best Local Similarity 96.8%; Pred. No. 1.1e-102;
 Matches 359; Conservative 0; Mismatches 10; Indels 2; Gaps 1;
 OY 1 GGCACTTTTGGCGATGTTCTTCTTCCTTNCAGAGCTTTGCGTGCAGAAATCCAGTGTACCA 60
 DB 11 GGCACTTTTGGCGATGTTCTTCTTCCTTNCAGAGCTTTGCGTGCAGAAATCCAGTGTACCA 70
 OY 61 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCGCCGAGTTCAATTGTGAATTGCAC 120
 DB 71 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCGCCGAGTTCAATTGTGAATTGCAC 130
 OY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 180
 DB 131 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 190
 OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGCAGGATACAGTCTT 240
 DB 191 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGCAGGATACAGTCTT 250
 OY 241 CTGCTCCCGAGGAAAGTGAACCTGATTGCATCAGCTGCTGCAACACCCCTCTTTGTA 300
 DB 251 CTGCTCCCGAGGAAAGTGAACCTGATTGCATCAGCTGCTGCAACACCCCTCTTTGTA 310
 OY 301 CGGGCCAGAGGCCAAGAAAGGGGAA--GTTCGCTCGGCCCTCANGCCATGGCTCCGC 358
 DB 311 CGGGCCAGAGGCCAAGAAAGGGGAAAGTTCTGNCCTCGGCCCTCAGGCGAGGCTCCGC 370
 OY 359 ACCACCATCT 369
 DB 371 ACCACCATCT 381

RESULT 15
 ABT03085
 ID ABT03085 standard; CDNA; 396 BP.
 XX
 XX ABT03085;
 AC
 XX

DT 05-SEP-2002 (first entry)
 XX
 XX Human ovarian carcinoma associated coding sequence spq ID NO: 9.
 DE
 XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KW cyostatic; gene; ss.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO200239885-A2.
 PN
 XX
 PD 23-MAY-2002.
 XX
 PF 13-NOV-2001; 2001WO-US45395.
 XX
 PR 14-NOV-2000; 2000US-0713550.
 PR 03-APR-2001; 2001US-0825294.
 PR 02-OCT-2001; 2001US-0970966.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
 XX
 DR WPI; 2002-500186/53.
 XX
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for
 PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PT
 PS Example 1; Page 116; 197pp; English.
 XX
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 CC
 SO Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 93.1%; Score 343.4; DB 24; Length 396;
 Best Local Similarity 96.8%; Pred. No. 1.1e-102;
 Matches 359; Conservative 0; Mismatches 10; Indels 2; Gaps 1;
 OY 1 GGCACTTTTGGCGATGTTCTTCTTCCTTNCAGAGCTTTGCGTGCAGAAATCCAGTGTACCA 60
 DB 11 GGCACTTTTGGCGATGTTCTTCTTCCTTNCAGAGCTTTGCGTGCAGAAATCCAGTGTACCA 70
 OY 61 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCGCCGAGTTCAATTGTGAATTGCAC 120
 DB 71 GTGTGAAGATTTCCAGCTGAACAACGACTGCTCTCCGCCGAGTTCAATTGTGAATTGCAC 130
 OY 121 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 180
 DB 131 GGTGAAGCTTCAAGCATGTGTCAAGAAAGATGTGAGCAAAAGTCCCGGATCATGTA 190
 OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGCAGGATACAGTCTT 240
 DB 191 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGCAGGATACAGTCTT 250
 OY 241 CTGCTCCCGAGGAAAGTGAACCTGATTGCATCAGCTGCTGCAACACCCCTCTTTGTA 300
 DB 251 CTGCTCCCGAGGAAAGTGAACCTGATTGCATCAGCTGCTGCAACACCCCTCTTTGTA 310
 OY 301 CGGGCCAGAGGCCAAGAAAGGGGAA--GTTCGCTCGGCCCTCANGCCATGGCTCCGC 358
 DB 311 CGGGCCAGAGGCCAAGAAAGGGGAAAGTTCTGNCCTCGGCCCTCAGGCGAGGCTCCGC 370
 OY 359 ACCACCATCT 369
 DB 371 ACCACCATCT 381

Search completed: November 7, 2002, 10:10:07

Fri Nov 8 18:56:48 2002

us-09-970-966-199.std.rng

Page 11

Job time : 78.6545 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 13.8273 Seconds
(without alignments)
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Title: US-09-970-966-199
Perfect score: 369
Sequence: 1 ggcacatttcgcatgtgtt.....tgctccgcacacatcct 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 443362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/pdata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.8	9.2	440365	4 US-09-103-840A-2	Sequence 2, Appli
2	31.8	8.6	759	2 US-08-484-126-6	Sequence 6, Appli
3	30.4	8.2	3373	2 US-08-897-443-2	Sequence 2, Appli
4	30.4	8.2	152331	3 US-09-128-155-16	Sequence 16, Appli
5	30.4	8.2	176373	3 US-09-128-155-17	Sequence 17, Appli
6	30.2	8.2	327	4 US-09-443-184-67	Sequence 67, Appli
7	30	8.1	4154	1 US-08-131-365B-37	Sequence 37, Appli
8	30	8.1	4154	2 US-08-668-123-37	Sequence 37, Appli
9	29.6	8.0	2205	1 US-08-035-392-3	Sequence 3, Appli
10	29.6	8.0	2205	1 US-08-504-511A-3	Sequence 3, Appli
11	29.2	7.9	1534	1 US-08-592-126-97	Sequence 97, Appli
12	28.8	7.8	1107	1 US-08-292-845-5	Sequence 5, Appli
13	28.8	7.8	1107	1 US-08-252-073A-5	Sequence 5, Appli
14	28.8	7.8	1107	5 PCT-US93-12074-5	Sequence 5, Appli
15	28.8	7.8	4403765	4 US-09-103-840A-2	Sequence 2, Appli
16	28.8	7.8	441529	4 US-09-103-840A-2	Sequence 2, Appli
17	28.6	7.8	637	4 US-09-280-116-42	Sequence 42, Appli
18	28.4	7.7	500	4 US-08-998-416-35	Sequence 35, Appli
19	28.2	7.6	2470	1 US-07-745-206A-14	Sequence 14, Appli
20	28.2	7.6	2470	2 US-08-311-363-14	Sequence 14, Appli
21	28.2	7.6	5467	1 US-07-745-206A-12	Sequence 12, Appli
22	28.2	7.6	5467	2 US-08-311-363-12	Sequence 12, Appli
23	28.2	7.6	6519	1 US-08-588-985-1	Sequence 1, Appli
24	28.2	7.6	6519	1 US-08-971-988-1	Sequence 1, Appli
25	28	7.6	570	4 US-09-095-855-202	Sequence 202, App
26	28	7.6	570	4 US-09-205-426-202	Sequence 202, App
27	28	7.6	6085	4 US-09-479-122-8	Sequence 8, Appli

28	27.8	7.5	8060	4	US-08-766-528-1	Sequence 1, Appl	
c	29	27.6	7.5	343	4	US-09-423-233-27	Sequence 27, Appl
c	30	27.6	7.5	344	4	US-09-423-233-26	Sequence 26, Appl
c	31	27.6	7.5	3355	4	US-08-991-944-3	Sequence 3, Appl
c	32	27.6	7.5	3812	4	US-09-784-316-1	Sequence 1, Appl
c	33	27.4	7.4	656	4	US-09-404-879A-313	Sequence 313, Appl
c	34	27.4	7.4	3487	1	US-08-410-540-4	Sequence 4, Appl
c	35	27.4	7.4	7680	5	PCT-US95-09819-6	Sequence 6, Appl
c	36	27.4	7.4	7705	1	US-08-259-569-16	Sequence 16, Appl
c	37	27.4	7.4	7705	2	US-08-826-885-16	Sequence 16, Appl
c	38	27.4	7.4	7705	6	545158-2	Patent No. 545158
c	39	27.4	7.4	7803	2	US-08-551-356-1	Sequence 1, Appl
c	40	27.4	7.4	7803	5	PCT-US93-12687-1	Sequence 1, Appl
c	41	27.2	7.4	818	3	US-09-154-083-25	Sequence 25, Appl
c	42	27.2	7.4	1828	4	US-08-858-207A-52	Sequence 52, Appl
c	43	27.2	7.4	2348	4	US-09-393-554-10	Sequence 10, Appl
c	44	27.2	7.4	3563	4	US-09-041-886-20	Sequence 20, Appl
c	45	27.2	7.4	3596	2	US-08-779-801-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; US-09-103-840A-2

Query Match          9.2% Score 33.8; DB 4; Length 4403765;
Best Local Similarity 53.4%; Pred. No. 7.8;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 203 GCGGCTGCTCTATCCGCTGCGGGTACAGTCTTGTGCTCCGAGGAAGTGAAC 262
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2688777 GCGGCTTGGGGGGGGGCGCAATCGTTGGCGCCCGCCCTCGAACCAGAA 2688778
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 263 TCAGTTGCATCAGCTGCTGCAACACCCCTCTTGTGAACGGGCCAAGCCCAAGGA 322
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2688777 CCAGCTCATACAGCTGCAAGATCGGCGCACACCGAGCCGAGACGCGGATG 2688718
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 323 GGAAGTTCGGCC 335
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2688717 ATCAGTGAACCT 2688705
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RESULT 2
US-08-484-126-6
; Sequence 6, Application US/08484126
; Patent No. 598565
; GENERAL INFORMATION:
; APPLICANT: Anderson, W. French
; APPLICANT: Baltrick, Leon F.
```

```

1  APPLICANT: Mason, James M.
2  TITLE OF INVENTION: Targetable Vector Particles
3  NUMBER OF SEQUENCES: 8
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
6  ADDRESSEE: Cecchi, Stewart & Olstein
7  STREET: 6 Becker Farm Road
8  CITY: Roseland
9  STATE: New Jersey
10 COUNTRY: USA
11 ZIP: 07068
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: 3.5 inch diskette
14 COMPUTER: IBM PS/2
15 OPERATING SYSTEM: MS-DOS
16 SOFTWARE: Word Perfect 5.1
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/484,126
19 FILING DATE: 07-JUN-1995
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/326,347
23 FILING DATE: 20-OCT-1994
24 APPLICATION NUMBER: 08/573,307
25 FILING DATE: 09-NOV-1992
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Lillie, Raymond J.
28 REGISTRATION NUMBER: 31,778
29 REFERENCE/DOCKET NUMBER: 271010-281
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 201-994-1700
32 TELEFAX: 201-994-1744
33 INFORMATION FOR SEQ ID NO: 6:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 759 bases
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: genomic DNA
40 PUBLICATION INFORMATION:
41 AUTHORS: Ray, et al.
42 TITLE:
43 JOURNAL: Biochem. and Biophys. Res. Comm.
44 VOLUME: 178
45 ISSUE: NO. 2
46 PAGES: 507-513
47 DATE: 1991
48 US-08-484-126-6
49
50 Query Match 8.6%; Score 31.8; DB 2; Length 759;
51 Best Local Similarity 50.7%; Pred. No. 0.61;
52 Matches 75; Conservative 0; Mismatches 73; Indels 0; Gaps 0.
53
54 220 CTCCTCCGGGTTGACAGTCTTCTGCTCCCGCAGGAACGTGACATGATTCATCAGCTG 279
55      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
56 3 CTCCTCCGTCGCTCCACGCGCTCTGTGTCACACATGCGCCCTCGGCGCTCGCGCTC 62
57
58 280 CTCGACACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTTCTGCCTCGCG 339
59      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 63 CGACCGTCCTGCTGCTGTCATGCCACGAGCAGCAGCGTGTCGCAACTTTCGACACAGC 122
61
62 340 CCTCAGCCATGCTCCGACACCATC 367
63      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 123 CCTATCACCAATGCCACCCCTGGACGAGC 150
65
66 RESULT 3
67 US-08-897-443-2/C
68 : Sequence 2, Application US/08897443
69 : Patent No. 5981263
70 : GENERAL INFORMATION:
71 : APPLICANT: Hillman, Jennifer L.
72 : APPLICANT: Lal, Preeti

```

```

APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Kaser, Mathew
TITLE OF INVENTION: HUMAN MATRILIN-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0348 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3373 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSN0702
CLONE: 681719
US-08-897-443-2

Query Match      8.2%; Score 30.4; DB 2; Length 3373;
Best Local Similarity 46.4%; Pred. No. 3.6;
Matches 97; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 161 CAAGTGGCGGAGTCATGTACCGCAAGTCGTGCATCATCAGCGGCTGTCTCATCGCC 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 638 CCAATGGCAAGATTAAGATGCGCCGTGCGCGCTTAGCAGCACCCTGGCCACGAG 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 221 TGTGCGGGGTACCACTCCTTCTGCTCCCGCAGGAAACTGAACTCACTGATCAGCTGC 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 578 TCTGAGAGGTCCCATCTGTCAAGATCAATTATGACCCGTGGCACAATTCTCCCTCAGGGGC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 TGCACACCCCTCTTGTATACGGGGCAGAGGCCCAAGAAAGGGAAGTTCTGCTCGGCC 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 518 CGGGCCCCCTTCTGCTTCTGACAGATCGATTTCTCAGAGGCATACCTGATGGCCAGCCGGTCC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 341 CTCANGCCATGGCTCCGACCAACCATCCCT 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 458 ATGTGTCCCGTGACACGATGCCGCATCCT 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-128-155-16/c
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03

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EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 8.2% Score 30.4: DB 3: Length 152331;
Best Local Similarity 49.4% Pred. No. 22;
Matches 79: Conservative 0: Mismatches 81: Indels 0: Gaps 0;

QY 36 TTGGCGTGCAGTCCAGTGTACAGTGTGAAGATTCAGCTGACAGCAGCTGCTCT 95
DB 106016 TTGGGTCGAGTACATTTGGGAGTGGGAGCTGTAAAGCAGACTTGACCTTTCT 105957
QY 96 CCCCCAGTTCATGTGATTCGACGCTGAACGTTCAAGACATGTGTGAGAAAGTGA 155
DB 105956 TCTACCAAGTACCTGTCTATTGAAATTTTGAAGAAAAAACTCAGAGAGAGAGA 105897

QY 156 TGGAGCAAGTCCGGGATCATGTACCGCAGTCTCTGTC 195
DB 105896 AGGAGCAGAGAGAGAGAGATGTCTTAAGTATTTGC 105857

RESULT 5
US-09-128-155-17
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 8.2% Score 30.4: DB 3: Length 176373;
Best Local Similarity 49.4% Pred. No. 23;
Matches 79: Conservative 0: Mismatches 81: Indels 0: Gaps 0;

QY 36 TTGGCGTGCAGTCCAGTGTACAGTGTGAAGATTCAGCTGACAGCAGCTGCTCT 95
DB 77454 TTGGGTCGAGTACATTTGGGAGTGGGAGCTGTAAAGCAGACTTGACCTTTCT 77513
QY 96 CCCCCAGTTCATGTGATTCGACGCTGAACGTTCAAGACATGTGTGAGAAAGTGA 155
DB 77514 TCTACCAAGTACCTGTCTATTGAAATTTTGAAGAAAAAACTCAGAGAGAGAGA 77573
QY 156 TGGAGCAAGTCCGGGATCATGTACCGCAGTCTCTGTC 195

DB 77574 AGGAGCAGAGAGAGAGAGATGTCTTAAGTATTTGC 77613

RESULT 6
US-09-443-184-67
Sequence 67, Application US/09443184A
Patent No. 6372431
GENERAL INFORMATION:
APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweigler, Gary
APPLICANT: Kaiser, Matthew R.
APPLICANT: Panzer, Scott
APPLICANT: Selhammer, Jeffrey J.
APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah
APPLICANT: Azimzal, Yalda
APPLICANT: Lal, Preeti
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 67
LENGTH: 327
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6372431 701649802H1
US-09-443-184-67

Query Match 8.2% Score 30.2: DB 4: Length 327;
Best Local Similarity 50.0% Pred. No. 1.4;
Matches 74: Conservative 0: Mismatches 74: Indels 0: Gaps 0;

QY 150 AACTGATGAGCAAGTCCGGGATCATGTACCGCAGTCTGTGATCATCAGCGGCT 209
DB 36 AACTGATGAGCAAGTCCGGGATCATGTACCGCAGTCTGTGATCATCAGCGGCT 95
QY 210 GTCTCATGCGCTCTGCGGATGACGCTGTGCTGCTCCAGGAGAACTGACTGATT 269
DB 96 GGCATATGCGGCTCTGCGGATGACGCTGTGCTGCTCCAGGAGAACTGACTGATT 155
QY 270 GCATGAGTCTGTCACACACCCCTTTG 297
DB 156 CCCTCCCTGCTGTGAGCTCTTCTTTG 183

RESULT 7
US-08-131-365B-37
Sequence 37, Application US/08131365B
Patent No. 5527690
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO STEROID REGULATORY ELEMENT BINDING
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P O Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131.365B
FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PPAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 4154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 167..3607
US-08-131-365B-37
Query Match 8.1%; Score 30; DB 1; Length 4154;
Best Local Similarity 56.8%; Pred. No. 5.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
DB 1711 CTCAGATACACACGCTGTACCATAGCCCTGGCGCAACGCTGGCGAAGCAG 1770
QY 262 CTCAGTTGATCAGCTGCTGCACACCCCTTTGTAAAGGGCCAGCCCAAGAAAG 321
11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1711 CTCAGATACACACGCTGTACCATAGCCCTGGCGCAACGCTGGCGAAGCAG 1770
QY 322 GGAAGCTTCTGCTGGCGCCCTCANGCCATGCTCC 356
11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1771 AGATGGCCCTGGCTGGCGCCAGTGGCTGTGCTGCC 1805
RESULT 8
US-08-668-123-37
Sequence 37, Application US/08668123
Patent No. 3891631
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
NUMBER OF INVENTIONS: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/131.365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PPAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 4154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 167..3607
US-08-668-123-37
Query Match 8.1%; Score 30; DB 2; Length 4154;
Best Local Similarity 56.8%; Pred. No. 5.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
DB 1711 CTCAGATACACACGCTGTACCATAGCCCTGGCGCAACGCTGGCGAAGCAG 1770
QY 262 CTCAGTTGATCAGCTGCTGCACACCCCTTTGTAAAGGGCCAGCCCAAGAAAG 321
11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1711 CTCAGATACACACGCTGTACCATAGCCCTGGCGCAACGCTGGCGAAGCAG 1770
QY 322 GGAAGCTTCTGCTGGCGCCCTCANGCCATGCTCC 356
11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1771 AGATGGCCCTGGCTGGCGCCAGTGGCTGTGCTGCC 1805
RESULT 9
US-08-035-392-3/C
Sequence 3, Application US/08035392
Patent No. 5484732
GENERAL INFORMATION:
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF INVENTIONS: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2205 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Skn-1a
FEATURE:
NAME/KEY: CDS
LOCATION: 46..1338
US-08-035-392-3

Query Match 8.0%; Score 29.6; DB 1; Length 2205;
Best Local Similarity 64.7%; Pred. No. 5.4;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 245 TCCCCAGGGAAGTGAACAGTTCGATCGCTGCAACACCCCTTTGTAAGGG 304
DB 92 TCCCCAGTATCTGTGTCATGCGGCTCCAGATTCACCATCTCCGACGGG 33
QY 305 CCAAGGCC 312
DB 32 CCAAGGCC 25

RESULT 10

US-08-504-511A-3/C
Sequence 3, Application US/08504511A
Patent No. 5561224

GENERAL INFORMATION:
APPLICANT: Rosenfield, M. G.

APPLICANT: Andersen, B.

TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504, 511A

FILING DATE: 20-JUL-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/002002

TELEPHONE: (619) 678-3070

TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 2205 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:
CLONE: Skn-1a

FEATURE:
NAME/KEY: CDS

LOCATION: 46..1338

US-08-504-511A-3

Query Match 8.0%; Score 29.6; DB 1; Length 2205;
Best Local Similarity 64.7%; Pred. No. 5.4;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 245 TCCCCAGGGAAGTGAACAGTTCGATCGCTGCAACACCCCTTTGTAAGGG 304
DB 92 TCCCCAGTATCTGTGTCATGCGGCTCCAGATTCACCATCTCCGACGGG 33
QY 305 CCAAGGCC 312
DB 32 CCAAGGCC 25

RESULT 11

US-08-592-126-97/C
Sequence 97, Application US/08592126
Patent No. 5821091

GENERAL INFORMATION:
APPLICANT: Gregory Dolganov

TITLE OF INVENTION: Transcripts Encoding Immunomodulatory

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 151

CORRESPONDENCE ADDRESS:
ADDRESS: Denlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600-0111

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:
LENGTH: 1534 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Septin-2.seq

US-08-592-126-97

Query Match 7.9%; Score 29.2; DB 1; Length 1534;
Best Local Similarity 46.3%; Pred. No. 6.1;
Matches 94; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 167 GCCGGATCATGTACCGCAGTCTGTCATCAGGCGGCTGTCATGCCCTGCGC 226
DB 1392 GCGTGGTCTCTCTCCCAAGTCCCGGCGCTTTCCTCACCCTTGCTCTCTG 1333
QY 227 GGGTACCAAGTCTTCTGCTCCCGAGGAACTGATGATGATGATGATGATG 286
DB 1332 TGGACCGCGCTCAGAGTCTCAAACTTCATGAGAGCTCCCTTCTCTGAGCTCC 1273
QY 287 ACCCTCTTTGTAAGGCGCCAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCTCANG 346
DB 1272 AGCTCTGCTCTCTCTCAATTTGTAACAACATGCTCATCTCTCTCTCTGTC 1213
QY 347 CCATGCGTCCGACACCATCT 369
DB 1212 AGTCACTTGAAGACTCTTCT 1190

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1      RESULT 12
2      US-08-292-945-5
3      : Sequence 5, Application US/08292945
4      : Patent No. 5585478
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Lim, Bing
9      : APPLICANT: Lelias, Jean-Michel
10     : APPLICANT: Adira, Chaker
11     : APPLICANT: KO, Jone
12     :
13     : TITLE OF INVENTION: D4 Gene and Methods of Use Thereof
14     : NUMBER OF SEQUENCES: 8
15     : CORRESPONDENCE ADDRESS:
16     :
17     : ADDRESSEE: Kilpatrick & Cody
18     : STREET: 1100 Peachtree Street, Suite 2800
19     :
20     : CITY: Atlanta
21     : STATE: Georgia
22     : COUNTRY: United States
23     : ZIP: 30309-4530
24     :
25     : COMPUTER READABLE FORM:
26     :
27     : MEDIUM TYPE: Floppy disk
28     : COMPUTER: IBM PC compatible
29     : OPERATING SYSTEM: PC-DOS/MS-DOS
30     : SOFTWARE: Patent In Release #1.0, Version #1.25
31     : CURRENT APPLICATION DATA:
32     :
33     : APPLICATION NUMBER: US/08/292,945
34     :
35     : FILING DATE:
36     :
37     : CLASSIFICATION: 435
38     :
39     : PRIOR APPLICATION DATA:
40     :
41     : APPLICATION NUMBER: US 07/990,337
42     : FILING DATE: December 10, 1992
43     :
44     : ATTORNEY/AGENT INFORMATION:
45     :
46     : NAME: Pabst, Patricia L.
47     : REGISTRATION NUMBER: 31,284
48     : REFERENCE/DOCKET NUMBER: MED107
49     : TELECOMMUNICATION INFORMATION:
50     :
51     : TELEPHONE: (404) 815-6508
52     : TELEFAX: (404) 815-6555
53     : INFORMATION FOR SEQ ID NO: 5:
54     :
55     : SEQUENCE CHARACTERISTICS:
56     :
57     : LENGTH: 1107 base pairs
58     : TYPE: nucleic acid
59     : STRANDEDNESS: single
60     : TOPOLOGY: linear
61     : MOLECULE TYPE: CDNA
62     : HYPOTHETICAL: NO
63     : ANTI-SENSE: NO
64     : ORIGINAL SOURCE:
65     :
66     : ORGANISM: Mutiline
67     :
68     : US-08-292-945-5

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Query Match	7.8%;	Score 28.8;	DB 1,	length 1107;
Best Local Similarity	48.8%;	Pred. No. 7.1;		
Matches	78;	Conservative	0;	Mismatches 82; Indels 0; Gaps 0.
QY	68	CAATTCCAGCTGACACACAGACTGCTCTCCGCCGAGTTCATGTGTAATTCACGGGTGAAC	127	
Db	345	GAATTCACAGGGTCGAAATTTAACTTCAAAAGTGAATAAGGATATGTGTCTGGCTCGAAGTAT	404	
QY	128	GTTCAAGACATGTGTGCAGAAAGAACTGATGTAGAGCAAGAGCCGGGATCATGTATACCGCAAG	187	
Db	405	GTTCAACACACATACCGGACCTGGCATGTGAGATGTGATTAAGCCACATTCATGTGTGGCAGC	464	
QY	188	TCCTGTGCATCATCAGCGGCGCTGTCTCATTCGCGCTTCGGCG	227	
Db	465	TATGGGCCCGACGACGAGAGTACGAAATTCCTCACTCCAG	504	

RESULT 13
 US-08-252-073A-5
 ; Sequence 5, Application US/08252073A
 Patent No. 5767073

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1 GENERAL INFORMATION:
2 APPLICANT: Bing Lim, et al.
3 TITLE OF INVENTION: D4 Gene and Methods of Use Thereof
4 NUMBER OF SEQUENCES: 21
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Patrea L. Pabst
7 STREET: 2800 One Atlantic Center,
8 STREET: 1201 West Peachtree Street
9 CITY: Atlanta
10 STATE: Georgia
11 COUNTRY: US
12 ZIP: 30306-3450
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/252,073A
22 FILING DATE: 1-JUN-1994
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/990,337
26 FILING DATE: 10-DEC-1992
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Pabst, Patrea L.
30 REGISTRATION NUMBER: 31,284
31 REFERENCE/DOCKET NUMBER: MED107c1p
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (404)873-8794
34 TELEFAX: (404)873-8795
35
36 INFORMATION FOR SEQ ID NO: 5:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 1107 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: CDNA
43 HYPOTHETICAL: NO
44 ANTI-SENSE: NO
45 ORIGINAL SOURCE:
46 ORGANISM: Murine
47
48 US-08-252-073A-5

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Query Match      7.8%; Score 28.8; DB 1; Length 1107;
Best Local Similarity 48.8%; Pred. No. 7.1;
Matches 78; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY   68 GAATTCGACTGCAGCAACGAACTGCTCCGCCCGAGTTCAATTGTGAATTCAGCGGTGAAC 127
Db    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   345 GAATTAAGGGTGTAATAAATTAATTAAGTGAATGAATGAATATATGTCTGCGCCTGAAGTAT 404

QY   128 GTTCAAGACCATGTGTGCAGAAAGAAGTATGTGACGCAAATGCCGGGATCATGTACCACAAG 187
Db    ||||| ||| | | | | | | | | | | | | | | | | | | | | |
Db   405 GTTCAACACACATATCCGAGCTGGCATGAGAGTAGTGAAGCAACATCATGATGTTGGCAGC 464

QY   188 TCGTGTGCATCATCAGCGGCGCTGTCTCATTCGCCCTCTGGCG 227
Db    | | | | | | | | | | | | | | | | | | | | | |
Db   465 TATGGCCCCGACGACGAGAGTACGAATTCCTCACTCCAG 504

RESULT 14
PCT-US93-12074-5
? Sequence 5, Application PC/TUS9312074
? GENERAL INFORMATION:
? APPLICANT:
? TITLE OF INVENTION: D4 Gene and Methods of Use Thereof
? NUMBER OF SEQUENCES: 8
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
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Search completed: November 7, 2002, 15:58:03
Job time : 3169.83 secs

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APPLICATION NUMBER: PCT/US93/12074
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,337
FILING DATE: 10-DEC-1992
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Murine
PCT-US93-12074-5

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```

Query Match
Best Local Similarity 7.8%; Score 28.8; DB 5; Length 1107;
Matches 78; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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QY 68 GAATTCAGCTGACACAGACTGCTCCCTCCCGAGTTGATGTGATTCAGCGTGAC 127
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DB 345 GAATACAGGGTGAATAATTAATTCAAGTGAATAGATATTGTGCTGCGGAGTAT 404
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 GTTCAAGACATGTGTCAAGAAAGAGTGTGAGCAAGTCCGGATCATACCGCAG 187
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 405 GTTCAACACACATACCGGATGAGATGATTAAGCCACATTCATGTTGGCAGC 464
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 TCCGTGATCATCAGCGGCGCTGTCTCATCCGCTGCGC 227
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 465 TATGGCCCCGACGAGAGTACGATTCCTCACTCCAG 504
    | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 15
US-09-103-840A-2
: Sequence 2, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-2007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 2
: LENGTH: 4403765
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: OTHER INFORMATION: CDC 1551
: OTHER INFORMATION: "n" bases at various positions throughout the sequence
: US-09-103-840A-2

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Query Match
Best Local Similarity 7.8%; Score 28.8; DB 4; Length 4403765;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 299 AACGGGCCAAGCCCAAGAAAGAGTTGCTGCGCCCTCANGCCATGGCTCCGC 358
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2200565 AAGGGCGAAGCGAATCAACAAAGCAGCCCGCGCTCTCAAGTTCTCG 2200624
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 359 ACCAC 363
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2200625 AACAC 2200629
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 13:45:13 ; Search time 16.0364 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacatttgcgagatgt.....tggctcgcacacacatcct 369

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCNUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367	99.5	369	US-09-825-294-199	Sequence 199, App
2	365.4	99.0	1619	US-09-825-294-205	Sequence 205, App
3	365.4	99.0	1619	US-09-825-294-211	Sequence 211, App
4	365.4	99.0	1897	US-09-825-294-214	Sequence 214, App
5	343.4	92.6	396	US-09-825-294-9	Sequence 9, Appl
6	341.8	92.6	1010	US-09-825-294-212	Sequence 212, App
7	196.8	53.3	480	US-09-825-294-212	Sequence 212, App
8	86.4	23.4	430	US-09-867-701-4251	Sequence 4251, App
9	32.6	8.8	407	US-09-960-352-3015	Sequence 3015, App
10	32.6	8.8	412	US-09-960-352-3015	Sequence 3015, App
11	32.6	8.8	423	US-09-960-352-3015	Sequence 3015, App
12	32.6	8.8	458	US-09-960-352-3015	Sequence 3015, App
13	31.6	8.6	544	US-09-834-975-1886	Sequence 1886, App
14	31.6	8.6	775	US-09-770-445-893	Sequence 893, App
15	31.4	8.5	1656	US-10-033-109-13	Sequence 13, Appl
16	30.6	8.3	7386	US-09-764-855-208	Sequence 208, App
17	30.2	8.2	498	US-09-783-590-457	Sequence 457, App
18	30.2	8.2	1063	US-09-764-898-137	Sequence 137, Appl
19	29.4	8.0	4780	US-09-886-241-1	Sequence 1, Appl

20	29.2	7.9	484	10	US-09-764-846-66	Sequence 66, Appl
21	29.2	7.9	713	10	US-09-764-846-136	Sequence 136, App
22	29.2	7.9	1347	10	US-09-822-830A-187	Sequence 187, App
23	29.2	7.9	1518	9	US-09-934-060A-23	Sequence 23, Appl
24	29.2	7.9	1518	9	US-09-934-060A-29	Sequence 29, Appl
25	29.2	7.9	1668	9	US-09-934-060A-29	Sequence 29, Appl
26	29.2	7.9	2159	9	US-09-934-060A-1	Sequence 1, Appl
27	29.2	7.9	2159	9	US-09-934-060A-3	Sequence 3, Appl
28	29.2	7.9	4344	10	US-09-880-107-1754	Sequence 1754, App
29	29.2	7.9	4870	12	US-10-044-090-121	Sequence 121, App
30	29.2	7.9	373	10	US-09-878-574-964	Sequence 964, App
31	28.8	7.8	296	10	US-09-216-393-97	Sequence 97, Appl
32	28.8	7.8	942	10	US-09-974-300-6410	Sequence 6410, App
33	28.8	7.8	3449	9	US-09-905-291A-33	Sequence 33, Appl
34	28.8	7.8	3449	10	US-09-909-320-33	Sequence 33, Appl
35	28.8	7.8	3449	10	US-09-909-088B-33	Sequence 33, Appl
36	28.6	7.8	212	10	US-09-864-761-21354	Sequence 21354, A
37	28.6	7.8	377	10	US-09-880-107-1729	Sequence 1729, App
38	28.6	7.8	466	10	US-09-864-761-4612	Sequence 4612, App
39	28.6	7.8	1995	10	US-09-780-525-1	Sequence 1, Appl
40	28.4	7.7	264	10	US-09-923-876-5109	Sequence 5109, App
41	28.4	7.7	415	10	US-09-960-352-14418	Sequence 14418, A
42	28.4	7.7	628	10	US-09-764-853-72	Sequence 72, Appl
43	28.2	7.6	404	10	US-09-867-701-5083	Sequence 5083, App
44	28.2	7.6	440	10	US-09-783-590-6440	Sequence 6440, App
45	28.2	7.6	470	10	US-09-867-701-5284	Sequence 5284, App

ALIGNMENTS

RESULT 1
US-09-825-294-199 Application US/09825294
Sequence 199, App
Patent No. US2002004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 199
LENGTH: 369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(369)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

Query Match 99.5%; Score 367; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.6e-111;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCACTTTTTCGCGATGCTTTCGCTTNCAGCTTTCGCTCAATTCAGTCTACCA	60
DB	1	GGCACTTTTTCGCGATGCTTTCGCTTNCAGCTTTCGCTCAATTCAGTCTACCA	60
QY	61	GGTGAAGATTCACGCTGACCAACGACGCTCTCCCGAGTTCATTGTGATTCAC	120
DB	61	GGTGAAGATTCACGCTGACCAACGACGCTCTCCCGAGTTCATTGTGATTCAC	120
QY	121	GGTGAAGATTCACGCTGACCAACGACGCTCTCCCGAGTTCATTGTGATTCAC	180
DB	121	GGTGAAGATTCACGCTGACCAACGACGCTCTCCCGAGTTCATTGTGATTCAC	180

```

OY 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
DB 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
OY 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
DB 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

RESULT 2

US-09-825-294-205

Sequence 205 Application US/09825294

Patent No. US2002000491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

THERAPY AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.4845

CURRENT APPLICATION NUMBER: US/09/825,294

CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 205

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

US-09-825-294-205

Query Match 99.0% Score 365.4 DB 10 Length 1619

Best Local Similarity 99.2% Pred. No. 1.1e-110

Matches 366 Conservative 0 Mismatches 3 Indels 0 Gaps 0

```

OY 1 GCGCACTTTTGGGATGTTCTTCTGCTTNCAGGCTTGGCTGCAATCAGTCTACCA 60
DB 1 GCGCACTTTTGGGATGTTCTTCTGCTTNCAGGCTTGGCTGCAATCAGTCTACCA 60
OY 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCCGAGTTGATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCCGAGTTGATTTGTAATTGCAC 120
OY 121 GGTGAACGTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
OY 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
DB 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
OY 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
DB 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

RESULT 3

US-09-825-294-211

Sequence 211 Application US/09825294

Patent No. US2002000491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

THERAPY AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.4845

CURRENT APPLICATION NUMBER: US/09/825,294

CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 211

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

US-09-825-294-211

Query Match 99.0% Score 365.4 DB 10 Length 1619

Best Local Similarity 99.2% Pred. No. 1.1e-110

Matches 366 Conservative 0 Mismatches 3 Indels 0 Gaps 0

```

OY 1 GCGCACTTTTGGGATGTTCTTCTGCTTNCAGGCTTGGCTGCAATCAGTCTACCA 60
DB 1 GCGCACTTTTGGGATGTTCTTCTGCTTNCAGGCTTGGCTGCAATCAGTCTACCA 60
OY 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCCGAGTTGATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGTCAACAGAGCTCTCCCGAGTTGATTTGTAATTGCAC 120
OY 121 GGTGAACGTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
OY 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
DB 181 CCGCAAGTCCTGTCATCATCAGCGGCCCTGCTCAGCCGCTGACAGTCTT 240
OY 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
DB 241 CTGCTCCCCAGGGAAGTCACTGATTGCTGATCAGCTGTCACACCCCTTTGTA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAAGTTCTGCTCGGCCCTCANGCCATGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

RESULT 4

US-09-825-294-214

Sequence 214 Application US/09825294

Patent No. US2002000491A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolk, John A.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

THERAPY AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.4845

CURRENT APPLICATION NUMBER: US/09/825,294

CURRENT FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 215

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 214

LENGTH: 1897

TYPE: DNA


```

; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (1)..(1897)
;
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

```

Query Match	99.0%	Score 365.4	DB 10	Length 1897
Best Local Similarity	99.2%	Pred. No. 1.2e-110		
Matches 366	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

QY	1	GGCAAGCTTTTGGCGAATGTCTCTGCTTNGAGGCTTTGGCGTGGCAATCCAGAGCTACCA	60
Db	280	GGCAACTTTTGGCGAATGTCTCTGCTTCCAGGCTTTGGCGTGGCAATCCAGAGCTACCA	339
QY	61	GTTGTAAGAATTTCCAGCTGAACAACGACACTGCTCCGCCGAGTTCAATTGTGAATTGCAC	120
Db	340	GTTGTAAGAATTTCCAGCTGAACAACGACACTGCTCCGCCGAGTTCAATTGTGAATTGCAC	399
QY	121	GGTGAACCTTCAACACATGTGTCAAGAAAGATATGGAGCAAAAGTCCCGGATCATGTA	180
Db	400	GGTGAACCTTCAACACATGTGTCAAGAAAGATATGGAGCAAAAGTCCCGGATCATGTA	459
QY	181	CCGCAAGTCCGTGTCAATCATCAGGGGCTGTCTATGCGCTTCGGCGGGTACACAGTCTT	240
Db	460	CCGCAAGTCCGTGTCAATCATCAGGGGCTGTCTATGCGCTTCGGCGGGTACACAGTCTT	519
QY	241	CTGTCTCCCCAGGGAACCTGACTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTAA	300
Db	520	CTGTCTCCCCAGGGAACCTGACTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTAA	579
QY	301	CGGGCAAGGCCCAAGAAAAGGGAAGTTCTGGCTCGGGCCCTCANGCCATAGCTCCGCAC	360
Db	580	CGGGCAAGGCCCAAGAAAAGGGAAGTTCTGGCTCGGGCCCTCANGCCATAGCTCCGCAC	639
QY	361	CACCATCTCT 369	
Db	640	CACCATCTCT 648	

```

RESULT 5
US-09-825-294-9
; Sequence 9, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9

```

Query Match	Similarity	93.1%	Score 34.3	4: DB 10:	Length 396:
Best Local	Similarity	96.8%	Pred. No. 9.7e-104:		
Matches	359:	Conservative	0:	Mismatches 10:	Indels 2: Gaps 1
Qy	1	GGCAACTTTTGGCGATGTTCTTGCTTTCAGAGCTTGGCGTCAAAATCAAGTCTACCA	60		
Db	11	GGCAACTTTTGGCGATGTTCTTGCTTTCAGAGCTTGGCGTCAAAATCAAGTCTACCA	70		

Oy	61	GGTGAACAATTCCAGCTGAGCAACAGACTGGCTCCGCCCGGAGTTCATTGTGAATTGCAC	120
Db	71	GGTGAACAATTCCAGCTGAGCAACAGACTGGCTCCGCCCGGAGTTCATTGTGAATTGCAC	130
Oy	121	GGTGAACCTTCAAGCATGTGTGCAGAAAGAAGTATGGACCAAAAGTCCGGGATCATGTA	180
Db	131	GGTGAACCTTCAAGCATGTGTGCAGAAAGAAGTATGGACCAAAAGTCCGGGATCATGTA	190
Oy	181	CCGCAAGTCGTGTGATCATCAGCGGCGCTGTCTTCATCGCCTCTGCGCGGGTACCAAGTCCCT	240
Db	191	CCGCAAGTCGTGTGATCATCAGCGGCGCTGTCTTCATCGCCTCTGCGCGGGTACCAAGTCCCT	250
Oy	241	CTGTCTCCCCAGGAACTGAACCTAGTTTGCATCAGCTGCTGCACAACCCCTCTTTGTAA	300
Db	251	CTGTCTCCCCAGGAACTGAACCTAGTTTGCATCAGCTGCTGCACAACCCCTCTTTGTAA	310
Oy	301	CGGGCCAGGCGCCAAAGAAAGGGGAA--CTTCTCCCTTCGGGCCCTCAGACCCATGGCTCCGC	358
Db	311	CGGGCCAGGCGCCAAAGAAAGGGGAAAGTTCTGNCCTTCGGGCCCTCAGACCGAGGCGTCCGC	370
Oy	359	ACCACCATCTCT	369
Db	371	ACCACCATCTCT	381

```

US-09-825-294-212
RESULT:6
US-09-825-294-212
: Sequence 212, Application US/09825294
: Patent NO. US20020004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS
: TITLE OF INVENTION: THERAPY AND DIAGNOSTIC
: FILE REFERENCE: 210121,484C5
: CURRENT APPLICATION NUMBER: US/09/825, 294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0.0
: SEQ ID NO 212
: LENGTH: 1010
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-825-294-212

```

Query Match	92.6%	Score 341.8	DB 10	Length 1010
Best Local Similarity	98.4%	Pred. No. 5.2e-103		
Matches 365	Conservative	4	Indels 2	Gaps 2
		0	Mismatches	

QY	1	GGCACTTTTTCGGCAATGTCTTGCTTTC-N-AGGCTTTGGGCTCCAAATCAGTGCATCC	59
Db	227	GGCAACTTTTTCGGGATTTGTTCTTCTGCTCCAAAGGCTTTGGGCTCCAAATCAGTGCATCC	266
QY	60	ACTGTGAAGAAATTCACGCTGAACAACGACTGCTCTCTCCCGAATTCATTTGTGAATTGCA	119
Db	287	AGTGTGAAGAAATTCACGCTGAACAACGACTGCTCTCTCCCGAATTCATTTGTGAATTGCA	346
QY	120	CGGTAAAGTTCACACATGTGTGTGCAAGAAAGTATGATGAGCAAAATGCGGGGATCATGT	179
Db	347	CGGTAAAGTTCACACATGTGTGTGCAAGAAAGTATGATGAGCAAAATGCGGGGATCATGT	406
QY	180	ACCGCAAGTCTGTGCATCATCAGCGGGCTGTGCATCGGCTCTGCGGGGTACCAAGTCT	239
Db	407	ACCGCAAGTCTGTGCATCATCAGCGGGCTGTGCATCGGCTCTGCGGGGTACCAAGTCT	466
QY	240	TCTGCTCCCAAGGGGAAATGAAACTGATTTTCATCAGCTGTGTGCAACACCCCTTTTGTGTA	299
Db	467	TCTGCTCCCAAGGGGAAATGAAACTGATTTTCATCAGCTGTGTGCAACACCCCTTTTGTGTA	526
QY	300	A-CGGGCCAAGGCCCAAGAAAGGGGAAGTTCCTCTCGGGCCCTCAAGCCATGGCTTCGC	358

Db 527 ACCGGCCCAAGGCGGGAAGGAGTTCTGCTCGGCCCTCAGGCCAGGGCTCCGA 586
OY 359 ACCAGCATCT 369
Db 587 ACCAGCATCT 597

RESULT 7

US-09-825-294-213
; Sequence 213, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Scolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 213
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-213

Query Match 53.3%; Score 196.8; DB 10; Length 480;
Best Local Similarity 98.5%; Pred. No. 2.3e-55;
Matches 198; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCGAAGTTTGGGGAATGTTCTTGTTCAGGCTTGGCGTCAATTCAGTCTACCA 60
Db 280 GCGAAGTTTGGGGAATGTTCTTGTTCAGGCTTGGCGTCAATTCAGTCTACCA 339
OY 61 GTGTGAAGATTCAGTCAACAGCAGCTCTCCCGAGTTCATTTGAAATTCAC 120
Db 340 GTGTGAAGATTCAGTCAACAGCAGCTCTCCCGAGTTCATTTGAAATTCAC 399
OY 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGAGCAAGATGCGGAGTATGTA 180
Db 400 GGTGAAGTTCAGACATGTGTGAGAAAGATGAGCAAGATGCGGAGTATGTA 459
OY 181 CCGCAAGTCTGTGATCATC 201
Db 460 CCGCAAGTCTGTGATCATC 480

RESULT 8

US-09-867-701-4251
; Sequence 4251, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4251
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4251

Query Match 23.4%; Score 86.4; DB 10; Length 430;

Best Local Similarity 91.2%; Pred. No. 5.6e-19;
Matches 114; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

OY 245 TCCGAGGAAACAGTACTGATTTGATCAGCTGCTGACACACCCCTTTGTAAGGG 304
Db 1 TCCGAGGAAACAGTACTGATTTGATCAGCTGCTGACACACCCCTTTGTAAGGG 60
OY 305 CCAAGGCCCAAGAAAGGGAAGTTGCTCGGCCCTCANGCCATGCTCCGACACC 364
Db 61 CAAAGG---CAAGAAAGGGAAGTTGCTCGGCCCTCAGG-CAGGGCTCCGACACC 116
OY 365 ATCCT 369
Db 117 ATCCT 121

RESULT 9

US-09-960-352-3015
; Sequence 3015, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3015
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB34-071-Q1-E1-D1
US-09-960-352-3015

Query Match 8.8%; Score 32.6; DB 10; Length 407;
Best Local Similarity 51.4%; Pred. No. 0.3;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

OY 24 TCGTTCAGGCTTGGCGTCAATTCAGTCTACCAAGTGTGAAGAATTCAGTACCA 83
Db 227 TCGAGCCAGGCTCAGTCTCAGATCAACCGCTCCATGACAGACTGGCAGCTAGAAA 286
OY 84 ACAGTCTCTCTCCCGGAGTTCATTTGAAATTCAGAGTCAAGTGTGTC 143
Db 287 ACCTCTCAACTCATCATNAGGCAATGTGTGAGCTAGGCAATGATTCCTGTTGACCTTTTG 346
OY 144 AGAAAGAGTATGAGCAAAAGTG 167
Db 347 AGGCCAAGACACTGTGTTGAAGTG 370

RESULT 10

US-09-960-352-13056
; Sequence 13056, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13056
; LENGTH: 412
; TYPE: DNA

```

; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (349),(378)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 56-LIB188-023-Q1-E1-F8
US-09-960-352-13056

```

```

Query Match
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 412;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

```

QY 24 TGCCTTCAGGCTTGGCGTCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACA 83
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 166 TGCAGCCAGGCTCAGTCCCTTAAGATCAACCGCTCCATGCAGAACTGGCACCAGCTAGAAA 225
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 AGCAGCTGCTCCCTCCCGAGTTTATGTGTGAATTCACGCGTGAACGTTCAAGACATGTGTC 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 ACCTCTCCAACTTCATCAATCAAGGCCATGTGTAGCTACGGCATGAATCCTGTGACCTGTTTG 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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```

QY 144 AGAAGAAGTGTATGAGCAAAAGTG 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 AGGCCAAGCAGCTGTTGAAAGTG 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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```

RESULT 11
US-09-960-352-9456
; Sequence 9456, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9456
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 41-LIB188-009-Q1-E1-C10
US-09-960-352-9456

```

```

Query Match
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 423;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

```

QY 24 TGCCTTCAGGCTTGGCGTCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACA 83
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 178 TGCAGCCAGGCTCAGTCCCTTAAGATCAACCGCTCCATGCAGAACTGGCACCAGCTAGAAA 237
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 AGCAGCTGCTCCCTCCCGAGTTTATGTGTGAATTCACGCGTGAACGTTCAAGACATGTGTC 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 238 ACCTCTCCAACTTCATCAATCAAGGCCATGTGTAGCTACGGCATGAATCCTGTGACCTGTTTG 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 144 AGAAGAAGTGTATGAGCAAAAGTG 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 298 AGGCCAAGCAGCTGTTGAAAGTG 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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```

RESULT 12
US-09-960-352-1886
; Sequence 1886, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

```

```

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1886
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 09-LIB188-017-Q1-E1-C9
US-09-960-352-1886

```

```

Query Match
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 458;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

```

QY 24 TGCCTTCAGGCTTGGCGTCGCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACA 83
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 182 TGCAGCCAGGCTCAGTCCCTTAAGATCAACCGCTCCATGCAGAACTGGCACCAGCTAGAAA 241
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 AGCAGCTGCTCCCTCCCGAGTTTATGTGTGAATTCACGCGTGAACGTTCAAGACATGTGTC 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 242 ACCTCTCCAACTTCATCAATCAAGGCCATGTGTAGCTACGGCATGAATCCTGTGACCTGTTTG 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 144 AGAAGAAGTGTATGAGCAAAAGTG 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 AGGCCAAGCAGCTGTTGAAAGTG 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 13
US-09-834-975-262
; Sequence 262, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(544)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-262

```

```

Query Match
Best Local Similarity 8.6%; Score 31.6; DB 10; Length 544;
Matches 85; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

```

```

QY 115 TTGCAAGGTCGAGCTTTCAGACATGTGTAGAAAGAGTATGAGCAAAAGTCCGGGAT 174
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 84 TTGCATGGTNCCTTTTCAACTCATGTGGCCACAGGAGACCTTTTAAATTTATGCCAAAAT 143
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 CATGTACGCGCAAGTCTGTCATCATCAGGCGCTGTCTCATCGCTCGCGGTACCA 234
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 144 TGCATCAATATGTGTTTNNAGATNNAACTGTCATTTTTCGCTATGNSGGCTACTT 203
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 GTCTTCTGCTCCCAAGGAAAGTGAAGTCACTGCTGACGCTGCAACACCCCTCT 294
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 204 TCAGTTTNGTCTNATNATACATTTTNGACTTTAANAGAGCCTTCATTTGCCCTTTNT 263

QY 295 TTGTACCG 303

Db 264 TTTTAAAG 272

RESULT 14

US-09-770-445-893
Sequence 893, Application US/09770445
Patent No. US20020023281A1

GENERAL INFORMATION:

APPLICANT: Gorlach, Jörn

APPLICANT: An, Yong-Qiang

APPLICANT: Hamilton, Carol M.

APPLICANT: Price, Jennifer L.

APPLICANT: Raines, Tracy M.

APPLICANT: Yu, Yang

APPLICANT: Rameaka, Joshua G.

APPLICANT: Page, Amy

APPLICANT: Matthew, Abraham V.

APPLICANT: Ledford, Brooke L.

APPLICANT: Woessner, Jeffrey P.

APPLICANT: Haas, William David

APPLICANT: Garcia, Carlos A.

APPLICANT: Krickler, Maja

APPLICANT: Slader, Ted

APPLICANT: Davis, Keith R.

APPLICANT: Allen, Keith

APPLICANT: Hoffman, Neil

TITLE OF INVENTION: Expressed Sequences of Arabidopsis

FILE REFERENCE: 2023US (PARA-012PRV)

CURRENT APPLICATION NUMBER: US/09/770,445

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: US 60/178,472

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 999

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 893

LENGTH: 775

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-445-893

Query Match 8.6%; Score 31.6; DB 10; Length 775;
Best Local Similarity 56.9%; Pred. No. 0.87;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 89 TGCCTCCCTCCCGGATTCATTTGTAATTCAGCGTGAACGCTCAGACATGTGCAGAA 148

Db 349 TTCTCCTTCGACGATTTCTTGTGCGAAGCCACGCTACATGTAAGAAGCTATTGGAATG 408

QY 149 GAAGTATGAGCAAAAGTCGCGGATCATGTACCGCAAGTCC 190

Db 409 GGAGTGAGAGGAAGGACGCGGAGCTAAGCCACCAACGATAC 450

RESULT 15

US-10-033-109-13
Sequence 13, Application US/10033109
Patent No. US20020142390A1

GENERAL INFORMATION:

APPLICANT: Allen, Stephen M.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION: Nitrogen Transport Metabolism

FILE REFERENCE: BB-1210

CURRENT APPLICATION NUMBER: US/10/033,109

CURRENT FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Microsoft Office 97

SEQ ID NO 13

LENGTH: 1656

TYPE: DNA

ORGANISM: Trifolium aestivum

US-10-033-109-13

Query Match 8.5%; Score 31.4; DB 12; Length 1656;
Best Local Similarity 54.9%; Pred. No. 1.5;
Matches 62; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 206 GCGTGTCTCATGCGCTCGCGGCTACAGCTCTCTGCTCCCGAGGAAGTGAAGTCA 265

Db 645 GCGTGTCTCTTCTCACTGGGCGCTCATCGACTACTCGGCGGTACGTATCCACTCC 704

QY 266 GTTTCATCAGCTGCTGCACACCCCTTTGTAAAGGGCCCAAGCCCAAGAA 318

Db 705 GCGGCGTCCGCGGCTTCAACCGCGGTACTGGTCCGCGCAAGCAAGAA 757

Search completed: November 7, 2002, 17:59:58
Job time: 19.0364 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 : Search time 826.855 Seconds
(without alignments)
11220.326 Million cell updates/sec

Title: US-09-970-966-199
Perfect score: 369
Sequence: 1 ggcacatttcgagatgt.....tggtccgcacaccaccatcct 369

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	367	99.5	369	1	PCT-US01-45395-199		Sequence 199, App
	2	367	99.5	369	25	US-09-656-668-199		Sequence 199, App
	3	367	99.5	369	28	US-09-713-550-199		Sequence 199, App
	4	367	99.5	369	31	US-09-825-294-199		Sequence 199, App
	5	367	99.5	369	36	US-09-970-966-199		Sequence 199, App
	6	367	99.5	369	42	US-10-212-677-199		Sequence 199, App
	7	365.4	99.0	1524	40	US-10-119-480-15		Sequence 15, App
	8	365.4	99.0	1524	42	US-10-216-159A-15		Sequence 15, App
	9	365.4	99.0	1524	42	US-10-216-160-15		Sequence 15, App
	10	365.4	99.0	1524	42	US-10-216-163-15		Sequence 15, App
	11	365.4	99.0	1524	42	US-10-216-163-15		Sequence 15, App
	12	365.4	99.0	1524	42	US-10-216-164-15		Sequence 15, App
	13	365.4	99.0	1524	42	US-10-216-165-15		Sequence 15, App
	14	365.4	99.0	1524	42	US-10-216-166-15		Sequence 15, App
	15	365.4	99.0	1524	42	US-10-216-167-15		Sequence 15, App
	16	365.4	99.0	1524	42	US-10-216-168-15		Sequence 15, App
	17	365.4	99.0	1524	42	US-10-218-612-15		Sequence 15, App
	18	365.4	99.0	1524	42	US-10-218-631-15		Sequence 15, App
	19	365.4	99.0	1524	42	US-10-218-765-15		Sequence 15, App
	20	365.4	99.0	1524	42	US-10-218-784-15		Sequence 15, App
	21	365.4	99.0	1524	42	US-10-218-849-15		Sequence 15, App

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22 365.4 99.0 1524 42 US-10-218-930-15 Sequence 15, Appl
23 365.4 99.0 1524 42 US-10-218-956-15 Sequence 15, Appl
24 365.4 99.0 1524 42 US-10-219-003-15 Sequence 15, Appl
25 365.4 99.0 1524 42 US-10-219-010-15 Sequence 15, Appl
26 365.4 99.0 1524 42 US-10-219-060-15 Sequence 15, Appl
27 365.4 99.0 1524 42 US-10-219-061-15 Sequence 15, Appl
28 365.4 99.0 1524 42 US-10-219-062-15 Sequence 15, Appl
29 365.4 99.0 1524 42 US-10-219-063-15 Sequence 15, Appl
30 365.4 99.0 1524 42 US-10-219-064-15 Sequence 15, Appl
31 365.4 99.0 1524 42 US-10-219-065-15 Sequence 15, Appl
32 365.4 99.0 1524 42 US-10-219-066-15 Sequence 15, Appl
33 365.4 99.0 1524 42 US-10-219-067-15 Sequence 15, Appl
34 365.4 99.0 1524 42 US-10-219-068-15 Sequence 15, Appl
35 365.4 99.0 1524 42 US-10-219-069-15 Sequence 15, Appl
36 365.4 99.0 1524 42 US-10-219-070-15 Sequence 15, Appl
37 365.4 99.0 1524 42 US-10-219-071-15 Sequence 15, Appl
38 365.4 99.0 1524 42 US-10-219-072-15 Sequence 15, Appl
39 365.4 99.0 1524 42 US-10-219-073-15 Sequence 15, Appl
40 365.4 99.0 1524 42 US-10-219-074-15 Sequence 15, Appl
41 365.4 99.0 1524 42 US-10-219-075-15 Sequence 15, Appl
42 365.4 99.0 1524 42 US-10-219-077-15 Sequence 15, Appl
43 365.4 99.0 1524 42 US-10-219-150-15 Sequence 15, Appl
44 365.4 99.0 1524 42 US-10-219-464-15 Sequence 15, Appl
45 365.4 99.0 1524 42 US-10-219-465-15 Sequence 15, Appl
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ALIGNMENTS

```
RESULT 1
PCT-US01-45395-199
: Sequence 199, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolck, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 29, 345
: OTHER INFORMATION: n - A,T,C or G
PCT-US01-45395-199
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Query Match 99.5%; Score 367; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.Be-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACGACGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGCTGACGACGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGATCATGCTT 240
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```
DB 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGATCATGCTT 240
QY 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGATGCTGCAAAACCCCTTTGTAA 300
DB 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGATGCTGCAAAACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCANGCCATGCTCCGAC 360
QY 361 CACCATCCT 369
DB 361 CACCATCCT 369
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```
RESULT 2
US-09-656-668-199
: Sequence 199, Application US/09656668
: GENERAL INFORMATION:
: APPLICANT: Stolck, John A.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
: FILE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: 210121.484C3
: CURRENT APPLICATION NUMBER: US/09/656, 668
: CURRENT FILING DATE: 2000-09-07
: NUMBER OF SEQ ID NOS: 199
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)..(369)
: OTHER INFORMATION: n - A,T,C or G
US-09-656-668-199
```

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Query Match 99.5%; Score 367; DB 25; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.Be-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACGACGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGCTGACGACGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGATCATGCTT 240
DB 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTGCCTGCGGATCATGCTT 240
QY 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGATGCTGCAAAACCCCTTTGTAA 300
DB 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGATGCTGCAAAACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCANGCCATGCTCCGAC 360
QY 361 CACCATCCT 369
DB 361 CACCATCCT 369
```

RESULT 3

```

US-09-713-550-199
: Sequence 199, Application US/09713550
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.484C4
: CURRENT APPLICATION NUMBER: US/09/713,550
: CURRENT FILING DATE: 2000-11-14
: NUMBER OF SEQ ID NOS: 205
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n = A,T,C or G
US-09-713-550-199

```

```

Query Match          99.5%; Score 367; DB 28; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
    1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60

OY 61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120
    61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120
DB 61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120

OY 121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180
    121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180
DB 121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180

OY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240
    181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240
DB 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240

OY 241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300
    241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300
DB 241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300

OY 301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360
    301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360
DB 301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360

OY 361 CACCATCTCT 369
    361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

RESULT 4
US-09-825-294-199
: Sequence 199, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA

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: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

```

Query Match          99.5%; Score 367; DB 31; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
    1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60

OY 61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120
    61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120
DB 61 GTGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 120

OY 121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180
    121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180
DB 121 GGTGAAGATTCACAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 180

OY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240
    181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240
DB 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATTCGCTGCGGATTCAGTCTT 240

OY 241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300
    241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300
DB 241 CTGCTCCCGGATTCAGTCAAGCAAGCACTGCTCCCGGATTCATTTGTAATGAC 300

OY 301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360
    301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360
DB 301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCTTCAGCCATGCTCCGAC 360

OY 361 CACCATCTCT 369
    361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

RESULT 5
US-09-970-966-199
: Sequence 199, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesch, David Alan
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.484C6
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 29, 345
: OTHER INFORMATION: n = A,T,C or G
US-09-970-966-199

```

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Query Match          99.5%; Score 367; DB 36; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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OY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
    1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60
DB 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGCGCTGCAATCCAGTCTACCA 60

```

```

QY 61 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 61 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 120
QY 121 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 180
    |||||||
Db 121 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 240
QY 241 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 300
    |||||||
Db 241 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 300
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 360
    |||||||
Db 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369

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RESULT 6

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US-10-212-677-199
; Sequence 199, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 345
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-199

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Query Match          99.5%; Score 367; DB 42; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCACATTTTGGCGATTTGTTCTTNCAGGCTTTGGCGTGGCAAAATCCATGCTACCA 60
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Db 1 GGCACATTTTGGCGATTTGTTCTTNCAGGCTTTGGCGTGGCAAAATCCATGCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 61 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 120
QY 121 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 180
    |||||||
Db 121 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 240
QY 241 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 300
    |||||||

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Db 241 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 300
    |||||||
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 360
    |||||||
Db 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369

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RESULT 7

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US-10-119-480-15
; Sequence 15, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See file wrapper or Palm
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-15

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Query Match          99.0%; Score 365.4; DB 40; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGCACATTTTGGCGATTTGTTCTTNCAGGCTTTGGCGTGGCAAAATCCATGCTACCA 60
    |||||||
Db 141 GGCACATTTTGGCGATTTGTTCTTNCAGGCTTTGGCGTGGCAAAATCCATGCTACCA 200
QY 61 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 201 GTGTGAAGAAATTCAGCTGAACACAGACTGCTCTCCCGAGATTGATGTAATGGAC 260
QY 121 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 180
    |||||||
Db 261 GGTGAAGCTTAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTGGCCGGGATCATGTA 320
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 240
    |||||||
Db 321 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGTGCGGGGTACAGACTCTT 380
QY 241 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 300
    |||||||
Db 381 CTGCTCCCGAGGAACTGAATCTGATTCATGAGCTGTGCAACACCCCTTTTGTAA 440
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 360
    |||||||
Db 441 CGGGCCCAAGGCCCAAGAAAGGGGAGTTGCTCGGCTCTCAGCCATGCTCCGAC 500
QY 361 CACCATCTCT 369
    |||||||
Db 501 CACCATCTCT 509

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RESULT 8

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US-10-216-159A-15
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QY 301 CGGGCCAAAGGCGGCAAGAAAGGAGTTGCTCGGCGCTCANGCCATGGCTCCGCAC 360
 DB 441 CGGGCCAAAGGCGGCAAGAAAGGAGTTGCTCGGCGCTCANGCCATGGCTCCGCAC 500
 QY 361 CACCATCCT 369
 DB 501 CACCATCCT 509

RESULT 12

US-10-216-164-15
 ; Sequence 15, Application US/10216164

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Geriltsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C5
 ; CURRENT APPLICATION NUMBER: US/10/216,164
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 15
 ; LENGTH: 1524
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-216-164-15

Query Match
 Best Local Similarity 99.0%; Score 365.4; DB 42; Length 1524;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATTGTTGCTTNCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 60
 DB 141 GGCACCTTTTGGCGATTGTTGCTTNCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 200
 QY 61 GGTGTAAGATTCCAGCTGAACAAGCACTGCTCTCCCGAGTTTCATTTGCAATTCAC 120
 DB 201 GGTGTAAGATTCCAGCTGAACAAGCACTGCTCTCCCGAGTTTCATTTGCAATTCAC 260
 QY 121 GGTGAACGTTTCAAGACATGTGTGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
 DB 261 GGTGAACGTTTCAAGACATGTGTGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 320

QY 181 CCGCAATGCTGTGATCATATCAGGCGCTGTCTATCGCTCGGCGGTACCAATTCCT 240
 DB 321 CCGCAATGCTGTGATCATATCAGGCGCTGTCTATCGCTCGGCGGTACCAATTCCT 380
 QY 241 CTGCTCCCGAGGGAAGTAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 381 CTGCTCCCGAGGGAAGTAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 440
 QY 301 CGGGCCAAAGGCGGCAAGAAAGGAGTTGCTCGGCGCTCANGCCATGGCTCCGCAC 360
 DB 441 CGGGCCAAAGGCGGCAAGAAAGGAGTTGCTCGGCGCTCANGCCATGGCTCCGCAC 500
 QY 361 CACCATCCT 369
 DB 501 CACCATCCT 509

RESULT 13

US-10-216-165-15
 ; Sequence 15, Application US/10216165

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Geriltsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 15
 ; LENGTH: 1524
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-216-165-15

Query Match
 Best Local Similarity 99.0%; Score 365.4; DB 42; Length 1524;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATTGTTGCTTNCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 60
 DB 141 GGCACCTTTTGGCGATTGTTGCTTNCAGGCTTTGCGCTGCAAAATCCAGTGTACCA 200

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Query Match	Similarity	99.0%;	Score 365.4;	DB 42;	Length 1524;
Best Local	Similarity	99.2%;	Pred. No. 3.3e-98;		
Matches	366;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0;
OY	1	GGCAACCTTTTTCGGAGATTGTTCTTGCTTTCACAGCTTTGCGCTGCAAAATCCAGTGTACCA	60		
Db	141	GGCACTTTTTCGGATTGTTCTTCTCTTCACAGCTTTGCGCTGCAAAATCCAGTGTACCA	200		
OY	61	GTGTAGAGATTCCAGCTGAACACAGACGTCTCTCCGCCGAGTTCATTGTAAATTGCAC	120		
Db	201	GTGTAGAGATTCCAGCTGAACACAGACGTCTCTCCGCCGAGTTCATTGTGAATTGCAC	260		
OY	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGACAAAGTGCCGGATCATGTA	180		
Db	261	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGACAAAGTGCCGGATCATGTA	320		
OY	181	CCGCAAGTCTCTGCATCATCAGCGGCGCTGTCATCGGCTCGCCGGGTACCAGTCTT	240		
Db	321	CCGCAAGTCTCTGCATCATCAGCGGCGCTGTCATCGGCTCTGCGGGTACCAGTCTT	380		
OY	241	CTGCTCTCCAGGGAAGTCAAGTCAAGTTTGATCAGCTCTGCAACACCCTCTTTGTAA	300		
Db	381	CTGCTCTCCAGGGAAGTCAAGTCAAGTTTGATCAGCTCTGCAACACCCTCTTTGTAA	440		
OY	301	CGGGCCAAAGGCCCAAGAAAAAGGGGAAGTTCTGCTTGCGCCCTTCANCCATGGCTCCGCAC	360		
Db	441	CGGGCCAAAGGCCCAAGAAAAAGGGGAAGTTCTGCTTGCGCCCTTCAGGCCAAGGGCTCCGCAC	500		
OY	361	CACCATCTT 369			
Db	501	CACCATCTT 509			

```

RESULT 15
US-10-216-167-15
Sequence 15, Application US/10216167
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
FILE REFERENCE: P3330P1C4
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728

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; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 15
 ; LENGTH: 1524
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-216-167-15

Query Match 99.0%; Score 365.4; DB 42; Length 1524;
 Best Local Similarity 99.2%; Pred. No. 3.3e-98;
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60
 DB 141 GGCACTTTTGGGATGTTCTTCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 200
 QY 61 GTGTGAAGATTCAGCTGAACAGAGACTGCTCTCCCGAGTTCAATTGATGCAC 120
 DB 201 GTGTGAAGATTCAGCTGAACAGAGACTGCTCTCCCGAGTTCAATTGATGCAC 260
 QY 121 GTGAAGATTCAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180
 DB 261 GTGAAGATTCAGACATGTGTGTCAAGAAAGATGATGAGCAAGTCCGGGATCATGTA 320
 QY 181 CCGCAAGTCTGTGATCATCATCAGGCGCTGTCTCATGCGCTTGGCGGATCAAGTCTT 240
 DB 321 CCGCAAGTCTGTGATCATCATCAGGCGCTGTCTCATGCGCTTGGCGGATCAAGTCTT 380
 QY 241 CTGCTCCCAAGGAACTGAACATGTTGATCATGCTGCTGCAACACCCCTTTGTAA 300
 DB 381 CTGCTCCCAAGGAACTGAACATGTTGATCATGCTGCTGCAACACCCCTTTGTAA 440
 QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAAGTCTGCTCGGCCCTCANGCCATGAGCTCCGAC 360
 DB 441 CGGGCCCAAGGCCCAAGAAAGGGGAAGTCTGCTCGGCCCTCANGCCATGAGCTCCGAC 500
 QY 361 CACCATCT 369
 DB 501 CACCATCT 509

Search completed: November 7, 2002, 17:54:11
 Job time : 850.855 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 10.3091 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacatttgcggatgtg.....tgctccgacacacatcct 369

Scoring table: IDENTITY_NUC

Searched: 193892 seqs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCIT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365.4	99.0	1524	6 US-10-230-437-15	Sequence 15, Appl
2	31.4	8.5	4321	6 US-10-085-198-105	Sequence 105, App
3	31.4	8.5	7097	6 US-10-085-198-107	Sequence 107, App
4	30.8	8.3	1860	6 US-10-266-829-18	Sequence 18, Appl
5	29.4	8.0	1372	6 US-10-281-024-16	Sequence 16, Appl
6	28.8	7.8	3449	6 US-10-131-813A-293	Sequence 293, App
7	28.8	7.8	3449	6 US-10-131-819A-293	Sequence 293, App
8	28.8	7.8	3449	6 US-10-131-823A-293	Sequence 293, App
9	28.8	7.8	3449	6 US-10-131-824A-293	Sequence 293, App
10	28.8	7.8	3449	6 US-10-131-826A-293	Sequence 293, App
11	28.8	7.8	3449	6 US-10-131-829A-293	Sequence 293, App
12	28.8	7.8	3449	6 US-10-125-826A-293	Sequence 293, App
13	28.8	7.8	3449	6 US-10-127-829A-293	Sequence 293, App
14	28.8	7.8	3449	6 US-10-127-831A-293	Sequence 293, App
15	28.8	7.8	3449	6 US-10-127-835A-293	Sequence 293, App
16	28.8	7.8	3449	6 US-10-127-837A-293	Sequence 293, App
17	28.8	7.8	3449	6 US-10-127-842A-293	Sequence 293, App
18	28.8	7.8	3449	6 US-10-127-850A-293	Sequence 293, App
19	28.8	7.8	3449	6 US-10-127-901A-293	Sequence 293, App
20	28.8	7.8	3449	6 US-10-128-689A-293	Sequence 293, App
21	28.8	7.8	3449	6 US-10-131-830A-293	Sequence 293, App
22	28.8	7.8	3449	6 US-10-131-833A-293	Sequence 293, App
23	28.8	7.8	3449	6 US-10-131-837A-293	Sequence 293, App
24	28.8	7.8	3449	6 US-10-125-930A-293	Sequence 293, App
25	28.8	7.8	3449	6 US-10-127-825A-293	Sequence 293, App
26	28.8	7.8	3449	6 US-10-127-838B-293	Sequence 293, App

27	28.8	7.8	3449	6 US-10-127-843A-293	Sequence 293, App
28	28.8	7.8	3449	6 US-10-127-849A-293	Sequence 293, App
29	28.8	7.8	3449	6 US-10-128-684A-293	Sequence 293, App
30	28.8	7.8	3449	6 US-10-128-685A-293	Sequence 293, App
31	28.8	7.8	3449	6 US-10-128-686A-293	Sequence 293, App
32	28.8	7.8	3449	6 US-10-128-690A-293	Sequence 293, App
33	28.8	7.8	3449	6 US-10-128-692A-293	Sequence 293, App
34	28.8	7.8	3449	6 US-10-131-821A-293	Sequence 293, App
35	28.8	7.8	3449	6 US-10-131-836A-293	Sequence 293, App
36	28.8	7.8	3449	6 US-10-137-872A-293	Sequence 293, App
37	28.8	7.8	3449	6 US-10-137-873A-293	Sequence 293, App
38	28.2	7.6	470	6 US-10-240-423-128	Sequence 128, App
39	28	7.6	413	5 US-09-513-999C-2172	Sequence 2172, App
40	28	7.6	6085	5 US-09-484-743-8	Sequence 8, Appl1
41	28	7.6	6085	5 US-09-484-331-8	Sequence 8, Appl1
42	28	7.6	6085	5 US-09-455-659A-8	Sequence 8, Appl1
43	27.6	7.5	385	5 US-09-620-607B-20	Sequence 20, Appl
44	27.6	7.5	450	5 US-09-513-999C-2171	Sequence 2171, App
45	27.4	7.4	6227	6 US-10-240-425-364	Sequence 364, App

ALIGNMENTS

RESULT 1
US-10-230-437-15
; Sequence 15, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P350P1C94
; CURRENT FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-230-437-15
Query Match 99.0%; Score 365.4; DB 6; Length 1524;

Best Local Similarity 99.2%; Pred. No. 6,7e-109;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAACCTTTGGGAGTGTCTTCCTTCAGCTTGGCGCTGCAATCCAGTCTACCA 60
Db 141 GGAACCTTTGGGAGTGTCTTCCTTCAGCTTGGCGCTGCAATCCAGTCTACCA 200
QY 61 GTGTGAAGATTCAGTGAACAAGCAGCTCTCCCGGAGTTCATTTGAATTCAC 120
Db 201 GTGTGAAGATTCAGTGAACAAGCAGCTCTCTCCCGGAGTTCATTTGAATTCAC 260
QY 121 GTGTGAAGATTCAGTGAACAAGCAGTGTGAGAAAGATGAGACCAAGTCCGGATCATGTA 180
Db 261 GTGTGAAGATTCAGTGAACAAGCAGTGTGAGAAAGATGAGACCAAGTCCGGATCATGTA 320
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTCTCTCATCGCTTCGCGGGATACAGTCTT 240
Db 321 CCGCAAGTCTGTGATCATCAGCGGCTCTCTCATCGCTTCGCGGGATACAGTCTT 380
QY 241 CTGCTCCCGGAGAACTGACTCAGTTTGCATCAGCTGCTGCAACCCCTCTTTGTAA 300
Db 381 CTGCTCCCGGAGAACTGACTCAGTTTGCATCAGCTGCTGCAACCCCTCTTTGTAA 440
QY 301 CCGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTGCGGCGCTGAMGCCATGGCTCCGAC 360
Db 441 CCGGCGCAAGGCGCCAGAAAGGGAAGTTCTGCTGCGGCGCTGAMGCCATGGCTCCGAC 500
QY 361 CACCATCTCT 369
Db 501 CACCATCTCT 509
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RESULT 2

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US-10-085-198-105
; Sequence 105, Application US/10085198
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 105
; LENGTH: 4321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-198-105
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Query Match 8.5%; Score 31.4; DB 6; Length 4321;
Best Local Similarity 51.4%; Pred. No. 1.2;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 232 CCACTCTTCTGCTCCCGGAGAACTGACTGATTGATCATGCTGCTGCAACACCC 291

Db 3800 CCACTCTTCTGCTCCCGGAGAACTGACTGATTGATCATGCTGCTGCAACACCC 3859

QY 292 TCTTTGTAAAGGCGGCAAGGCGCCAGAAAGGGAAGTTCTGCTCGGCGCTGANGCCATG 351

Db 3860 TCCCGGCTCTGACTCTGACCAAGGCGCCCTGACGCTCCGACCGGCTCCCTGAGCTC 3919

QY 352 GCTCCGACCAACATCTCT 369

Db 3920 GCGCGCGCTGCGGCGCT 3937

RESULT 3

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US-10-085-198-107
; Sequence 107, Application US/10085198
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 107
; LENGTH: 7097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-198-107
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Query Match 8.5%; Score 31.4; DB 6; Length 7097;
Best Local Similarity 51.4%; Pred. No. 1.6;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 232 CCACTCTTCTGCTCCCGGAGAACTGACTGATTGATCATGCTGCTGCAACACCC 291

Db 3556 CCACTCTTCTGCTCCCGGAGAACTGACTGATTGATCATGCTGCTGCAACACCC 3615

QY 292 TCTTTGTAAAGGCGGCAAGGCGCCAGAAAGGGAAGTTCTGCTCGGCGCTGANGCCATG 351

Db 3616 TCCCGGCTCTGACTCTGACCAAGGCGCCCTGACGCTCCGACCGGCTCCCTGAGCTC 3675

QY 352 GCTCCGACCAACATCTCT 369

Db 3676 GCGCGCGCTGCGGCGCT 3693

RESULT 4

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US-10-266-829-18
; Sequence 18, Application US/10266829
; GENERAL INFORMATION:
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QY	281	TGCAACACCCCTCTTTTGAACGGGCGCAAGGCCCAAGAAAAGGGAACTTGTGCTGGGC	340
Db	667	CGGGCCCCCTCTGCTTCTTGAGAAATGCGATGTTCAAGGCGATACGTGATGGCGACGCCAGTC	608
QY	341	CTCANGGCATGCGCTCCGACACCATGCT	369
Db	607	ATGTGTCGCCCTGAGACAGATGGCCGATCTT	579

RESULT 9
US-10-13

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US-10-131-824A-293/c
Sequence 293, Application US/10131824A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C126
CURRENT APPLICATION NUMBER: US/10/131,824A
CURRENT FILING DATE: 2002-04-24
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining Prio Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 293
LENGTH: 3449
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-824A-293

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Query Match	7.8%	Score 28.8	DB 6	Length 3445
Best Local Similarity	45.9%	Pred. No. 7.5		
Matches	96	Conservative	0	Mismatches 113; Indels 0; Gaps 0;
QY	161	CAAGTGGCGGAGTCACTGACCGCAAGTCTGTGCATCATCAGCGGCTGTGTCATCGCC	220	
Db	787	CCAATGGCAAGATATGATGATGCCCTGTCTCCGTGCTTAGCAGCCACTCGGCGACGGAG	728	
QY	221	TCTGCGGGTACCACTCTTCTGTCTCCCGAGGAACACTGAACCTGATTCACAGCTGC	280	

D _b	727	TCCGAGGCTTC	CCCATCTG	TACATATT	ATGACC	CGGTGGCA	CATTTCTC	CTCTAC	GGGGC	668	
O _y	281	TGCACAAC	CCCCCTT	TTTTGA	CGGCCA	AGGGCCA	AAGA	AAAGGG	AAATTT	TGCTCG	340
D _b	667	CGGGCC	CCCCCT	TGTTCT	TGAA	TATG	CATG	TTCAC	GGSCAT	ACTTG	608
O _y	341	CTCANG	CCCATG	CTCCG	CACAC	CACAT	CTCT				369
D _b	607	ATGGT	GCCCGT	TGAC	ACAG	TGCGG	ATCTCT				579

RESULT 1C

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US-10-131-826A-293/C
Sequence 293, Application US/10131826A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C128
CURRENT FILING DATE: 2002-04-24
CURRENT APPLICATION NUMBER: US/10/131,826A
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 293
LENGTH: 3449
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-293

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Query Match	7.8%	Score 28.8	DB 6	Length 3449
Best Local Similarity	45.9%	Pred. No. 7.5		
Matches	96	Conservative	0	Mismatches 113; Indels 0; Gaps 0
QY	161	CAAAAGTGGCGGATCATATACCGCAAGTCCTCTGTGCATCATACGCGGCGCTGTCTCATCGCC	220	
Db	787	CCAAATGGCAAAATAGATGATGCGCTGTGTCCTGCTTATGACGCGCACCTCGGCGACGAG	728	

Oy	221	TC GCGGGGTACAGATCTCTTGCTCCCGCAGGAACAATGAATCACTAGTTTGCATCAGCTGC	280
Db	727	TCTGAGGTCTCCCATCTGTGTACGATCATTAATGACCCTGGCACATCTCTCCCTACAGGGG	668
Oy	281	TGCAAACACCCTCTTTTGTACAGGGGCCAAGGCCCAAAGAAAAGGGGAATTCTGCTCGGCC	340
Db	667	GCGGGCCCCCTTGCTTCTGCAAAATGCGATGTTTCAGGGCATATCGAATGGCCAGCCAGTC	608
Oy	341	CTCANGCCATGGCTCCGACACCACCATCCT	369
Db	607	ATGCTGCCCTGACACAGATGCGGCATCCT	579

RESULT 11
US-10-131-829A-293/c
; Sequence 293, Application US/10131829A

```

: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gunney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,829A
: CURRENT FILING DATE: 2002-04-27
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 293
: LENGTH: 3449
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-131-829A-293

```

	Query Match	7.8%	Score 28.8;	DB 6;	Length 3449;
	Best Local Similarity	45.9%	Pred. No. 7.5;		
	Matches 96;	Conservative	0;	Mismatches 113;	Indels 0;
0y	161	CAAGTCCGGGATATGTACCGCAAGTCTCTTGATCATCATCAGCGGCTGTCTCATGCC	220		

Dd	787	CCATGCGCAAGATTAGSANTCCCCGTGCCGGTCCCTTAGCAGCACACTGGGCACGAG	728
Qy	221	TCTCGCGGGTACGAGTCCTTGCTGCCACGGAACCTGAACTGATTGGTSCATCAGCTGC	280
Dd	727	TCTGAGSTCTCCCATCTGTGTCAGCATATTATGACCCTGGACATTTCTCCTCAGGGGC	688
Qy	281	TGCAACACCCCTCTTTGTACGGGCCAAGGCCCAAGAAGAAAGGSACTTCTGCTCGGCC	340
Dd	667	CGGGCCCCCTCTGCTTCTGAAATGCGATGTTTCAGGGCATCTGAGTGGCCAGCCCAGTC	608
Qy	341	CTCAGCCGATGGTCCGACCAACCATCTT	369
Dd	607	ATGCTGCCGTGGACAGATGCCGACATCTT	579

RESULT 12
US-10-125-926A-293/C
; Sequence 293, Application US/10125926A

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1 / GENERAL INFORMATION:
2 / APPLICANT: Baker, Kevin P.
3 / APPLICANT: Beresini, Maureen
4 / APPLICANT: DeForge, Laura
5 / APPLICANT: Desnoyers, Luc
6 / APPLICANT: Filvaroff, Ellen
7 / APPLICANT: Gao, Wei-Qiang
8 / APPLICANT: Gerritsen, Mary E.
9 / APPLICANT: Goddard, Audrey
10 / APPLICANT: Godowski, Paul J.
11 / APPLICANT: Guiney, Austin L.
12 / APPLICANT: Sherwood, Steven
13 / APPLICANT: Smith, Victoria
14 / APPLICANT: Stewart, Timothy A.
15 / APPLICANT: Tumanabe, Daniel
16 / APPLICANT: Tumanabe, Colin K
17 / APPLICANT: Wood, William
18 / APPLICANT: Zhang, Zhenli
19 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
20 / TITLE OF INVENTION: ACIDS ENCODING THE SAME
21 / FILE REFERENCE: P3330R1C80
22 / CURRENT APPLICATION NUMBER: US/10/125,926A
23 / CURRENT FILING DATE: 2002-10-15
24 / PRIOR APPLICATION NUMBER: 60/049911
25 / PRIOR FILING DATE: 1997-06-18
26 / PRIOR APPLICATION NUMBER: 60/056974
27 / PRIOR FILING DATE: 1997-08-26
28 / PRIOR APPLICATION NUMBER: 60/059113
29 / PRIOR FILING DATE: 1997-09-17
30 / PRIOR APPLICATION NUMBER: 60/059115
31 / PRIOR FILING DATE: 1997-09-17
32 / PRIOR APPLICATION NUMBER: 60/059117
33 / PRIOR FILING DATE: 1997-09-17
34 / PRIOR APPLICATION NUMBER: 60/059122
35 / PRIOR FILING DATE: 1997-09-17
36 / PRIOR APPLICATION NUMBER: 60/059184
37 / PRIOR FILING DATE: 1997-09-17
38 / PRIOR APPLICATION NUMBER: 60/059263
39 / PRIOR FILING DATE: 1997-09-18
40 / PRIOR APPLICATION NUMBER: 60/059352
41 / PRIOR FILING DATE: 1997-09-19
42 / PRIOR APPLICATION NUMBER: 60/059588
43 / PRIOR FILING DATE: 1997-09-19
44 / Remaining Prior Application data removed - See File Wrapper or PALM.
45 / NUMBER OF SEQ ID NOS: 550
46 / SEQ ID NO 293
47 / LENGTH: 3449
48 / TYPE: DNA
49 / ORGANISM: Homo Sapien
50 / US-10-125-926A-293

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Query Match	7.8;	Score 28.8;	DB 6;	Length 3449;
Best Local Similarity	45.98;	Pred. No. 7.5;		
Matches 96;	Conservative	0;	Mismatches 113;	Indels 0;
				Gaps 0;

QY 161 CAAAGTGGCGGGATCATGTACCGGAAGCGCTGCATCATCAGGGCGCTGCATATCGC 220
 Db 787 CCAATGGCAAGATTAGAGATGCCGTGTCCGTTCCTTAGCAGCACTGGCCACGGAG 728
 QY 221 TCTGCGCGGGTACAGTCCCTTCTGCTCCCAAGGAAACTGAATCACTGATTGCATCAGTGC 280
 Db 727 TCTGAGAGTCTCCCATCTGTGCATCATATTATGACCCGTGGCAATTCTCCCTCAGAGGC 668
 QY 281 TGCAAACACCCTCTTTTGTAAAGGGCCCAAGGCCCAAGAAAAGGGAGATTCTGCTCGGCC 340
 Db 667 CGGGCCCCCTCTGCTTGTGAAATATGCATGTTCAGGGCATATCTGATGCGCACCCAGTC 608
 QY 341 CTCANCCATGGCTCCGACACCAACCATCT 369
 Db 607 ATGTGTGCCCTGGACACATGCCGATCTCT 579

RESULT 13
US-10-127

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1 Sequence 293, Application US/10127829A
2
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Kevin P.
5 APPLICANT: Beresini, Maureen
6 APPLICANT: DeForge, Laura
7 APPLICANT: Desnoyers, Luc
8 APPLICANT: Filvaroff, Ellen
9 APPLICANT: Gao, Wei-Qiang
10 APPLICANT: Gerritsen, Mary E.
11 APPLICANT: Goddard, Audrey
12 APPLICANT: Godowski, Paul J.
13 APPLICANT: Gurney, Austin L.
14 APPLICANT: Sherwood, Steven
15 APPLICANT: Smith, Victoria
16 APPLICANT: Stewart, Timothy A.
17 APPLICANT: Tumas, Daniel
18 APPLICANT: Watanabe, Colin K
19 APPLICANT: Wood, William
20 APPLICANT: Zhang, Zemin
21
22 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
23 FILE REFERENCE: P3330R1C85
24
25 CURRENT APPLICATION NUMBER: US/10/127, 829A
26
27 PRIOR APPLICATION NUMBER: 60/049911
28
29 PRIOR FILING DATE: 1997-06-18
30
31 PRIOR APPLICATION NUMBER: 60/056974
32
33 PRIOR FILING DATE: 1997-08-26
34
35 PRIOR APPLICATION NUMBER: 60/059113
36
37 PRIOR FILING DATE: 1997-09-17
38
39 PRIOR APPLICATION NUMBER: 60/059115
40
41 PRIOR FILING DATE: 1997-09-17
42
43 PRIOR APPLICATION NUMBER: 60/059117
44
45 PRIOR FILING DATE: 1997-09-17
46
47 PRIOR APPLICATION NUMBER: 60/059122
48
49 PRIOR FILING DATE: 1997-09-17
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51 PRIOR APPLICATION NUMBER: 60/059184
52
53 PRIOR FILING DATE: 1997-09-17
54
55 PRIOR APPLICATION NUMBER: 60/059263
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57 PRIOR FILING DATE: 1997-09-18
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59 PRIOR APPLICATION NUMBER: 60/059352
60
61 PRIOR FILING DATE: 1997-09-19
62
63 PRIOR APPLICATION NUMBER: 60/059588
64
65 PRIOR FILING DATE: 1997-09-19
66
67 Remaining Prior Application data removed - See File Wrapper or PALM.
68
69 NUMBER OF SEQ ID NOS: 550
70
71 SEQ ID NO 293
72
73 LENGTH: 3449
74
75 TYPE: DNA
76
77 ORGANISM: Homo Sapien
78
79 US-10-127-829A-293

```

Query Match	7.88;	Score 28.8;	DB 6;	Length 3449;
Best Local Similarity	45.98;	Pred. NO. 7.5;		

[illegible]

RESULT 14

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US-10-127-831A-293/G
; Sequence 293, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
; FILE REFERENCE: P333081C107
; CURRENT APPLICATION NUMBER: US/10/127, 831A
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 293
; LENGTH: 3449
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-127-831A-293

```

US-10-127-831A-293

```

Query Match          7.88; Score 28.8; DB 6; Length 3449;
Best Local Similarity 45.98; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 113;
QY 161 CAAAGTCCGGGATCATGTACCGCAAGTCCGTGTCATCATCAGCGGCTGTCTCATGCC 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 787 CCAATGGCAAGATTTAGATGCGCGTGTCCGCTTAGCAGCACCTCGGCCACGGAG 728
QY 221 TCCTGCCGGGTACAGTCTCTCTGCTCCCGCAGGAACCTGAATCACTTTCATCAGCTGC 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 727 TCCTGAGGTCTCCCATCTGTGACATGATGACCCGTGACACATTTCTCCCTCAGGGGC 668
QY 281 TGCACACCCCTCTTTGTACAGGGCCCAAGGCCCAAGAAAGGGGAAGTTTGCCCTCGGCC 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 667 CGGGCCCCCTCTGCTTCTGAGAAATGCAATGTTCAAGGCACATCTGATGGCCAGCCCAATC 608
QY 341 CTCANGCCATGCTCTCCGACACCATCTCT 369
DB 607 ATGTTGCCCTGTGACAGATGCGCATCTCT 579

```

RESULT 15

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US-10-127-835A-293/c
; Sequence 293, Application US/10127835A

```

GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Fliviaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C102
; CURRENT APPLICATION NUMBER: US/10/127,835A
; PRIOR APPLICATION NUMBER: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
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; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 293
; LENGTH: 3449
; TYPE: DNA
; ORGANISM: Homo Sapien

```

```

US-10-127-835A-293
Query Match          7.88; Score 28.8; DB 6; Length 3449;
Best Local Similarity 45.98; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 113;
QY 161 CAAAGTCCGGGATCATGTACCGCAAGTCCGTGTCATCATCAGCGGCTGTCTCATGCC 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 787 CCAATGGCAAGATTTAGATGCGCGTGTCCGCTTAGCAGCACCTCGGCCACGGAG 728
QY 221 TCCTGCCGGGTACAGTCTCTCTGCTCCCGCAGGAACCTGAATCACTTTCATCAGCTGC 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 727 TCCTGAGGTCTCCCATCTGTGACATGATGACCCGTGACACATTTCTCCCTCAGGGGC 668
QY 281 TGCACACCCCTCTTTGTACAGGGCCCAAGGCCCAAGAAAGGGGAAGTTTGCCCTCGGCC 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 667 CGGGCCCCCTCTGCTTCTGAGAAATGCAATGTTCAAGGCACATCTGATGGCCAGCCCAATC 608
QY 341 CTCANGCCATGCTCTCCGACACCATCTCT 369
DB 607 ATGTTGCCCTGTGACAGATGCGCATCTCT 579

```

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Search completed: November 7, 2002, 17:56:44
Job time : 28.3091 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 1589.8 Seconds

(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agttctcttcgagagagact.....gnaaaaaaaaaaaaaa 625

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1389073

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcg_hum:*
40: em_hcg_mus:*
41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	606	97.0	129676	9	AC079773 Homo sapi
2	555	88.8	826	9	BC011449 Homo sapi
3	555	88.8	1832	9	AK094501 Homo sapi
4	549	87.8	1890	6	AX136281 Sequence
5	393	62.9	1524	6	AX358762 Sequence
6	393	62.9	1524	6	AX362255 Sequence
7	365	58.4	587	6	AX136698 Sequence
8	359	57.4	1362	6	AX139942 Sequence
9	359	57.4	1362	9	AF034633 Homo sapi
10	359	57.4	2528	6	AX139944 Sequence
11	352	56.3	444	6	AX150120 Sequence
12	27	4.3	92874	2	AC112072 Rattus no
13	24	3.8	70395	2	AC099984 Mus muscu
14	23	3.7	94718	9	AC026770 Homo sapi
15	23	3.7	167693	2	AC011639 Homo sapi
16	23	3.7	176967	2	AC022742 Homo sapi
17	23	3.7	180837	2	AC022824 Homo sapi
18	23	3.7	184485	2	AC096679 Homo sapi
19	23	3.7	192464	9	AC090971 Homo sapi
20	23	3.7	200145	2	AC126666 Rattus no
21	22	3.5	256	6	AX393645 Sequence
22	22	3.5	1388	8	AT065052 Arabidops
23	22	3.5	1982	8	NTA294474 Nicotiana
24	22	3.5	2666	8	AF035577 Amblyomma
25	22	3.5	3190	3	AB019231 Arabidops
26	22	3.5	43570	8	AB019231 Arabidops
27	22	3.5	86093	2	AC114102 Rattus no
28	22	3.5	90020	8	AT024418 Rattus no
29	22	3.5	94029	2	AC117309 Rattus no
30	22	3.5	98506	8	AT024418 Rattus no
31	22	3.5	99541	2	AC126575 Rattus no
32	22	3.5	110000	2	AC098517 Rattus no
33	22	3.5	11914	10	AL596180 Mouse DNA
34	22	3.5	11382	2	AC103498 Rattus no
35	22	3.5	115643	2	AC094168 Rattus no
36	22	3.5	126363	2	AC123419 Rattus no
37	22	3.5	138918	9	AL445433 Human DNA
38	22	3.5	158728	2	AC114056 Rattus no
39	22	3.5	160008	2	AC022823 Homo sapi
40	22	3.5	163932	2	AC020693 Homo sapi
41	22	3.5	194402	2	AC096152 Rattus no
42	22	3.5	196863	2	AC107560 Rattus no
43	22	3.5	198843	2	AC102588 Mus muscu
44	22	3.5	206648	2	AC123116 Rattus no
45	22	3.5	209095	2	AC094585 Rattus no

ALIGNMENTS

RESULT 1
AC079773/c 129676 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone Rpl1-258B17 from 2, complete sequence.
AC079773
AC079773.8 GI:15145561
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 129676)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 129676)
 AUTHORS Shah,N., Meyer,R., Boyer,E. and Dignan,G.
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 129676)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 129676)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 129676)
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Aug 9, 2001 this sequence version replaced gi:14488388.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@watson.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenos, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong (http://dpcpac.med.buffalo.edu) and coworkers at the Roswell Park Cancer Institute (http://pbaec3.6)

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES
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 Location/Qualifiers
 1..129676
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 /db_xref="taxon:9606"

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/map="2"
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1388..1412
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1397..3331
/rpt_family="L1"
2346..2370
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11961..11969
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12697..12739
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20170..20305
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25485..25805
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26417..26463
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26466..26655
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27048..27149
/rpt_family="MER2_type"
27246..27403

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QY 61 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGCTGCTGCTG 120
 DB 250 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGCTGCTGCTG 309
 QY 121 CAGCGACAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
 DB 310 CAGCGACAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 369
 QY 181 CGGTACAGCAGCGCGGTGATGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240
 DB 370 CGGTACAGCAGCGCGGTGATGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 429
 QY 241 GAGGATCATGTACGCGCGGAGTAGACCTCGTCCAGTGTGCTGCTGCTGCTGCTG 300
 DB 430 GAGGATCATGTACGCGCGGAGTAGACCTCGTCCAGTGTGCTGCTGCTGCTGCTG 489
 QY 301 CATGATCTCTCCGAATCTGCTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 360
 DB 490 CATGATCTCTCCGAATCTGCTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 549
 QY 361 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 DB 550 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 609
 QY 421 TAAATGAATAAACCAATTAATATTATTAGCCCTCTGCTGCTGCTGCTGCTGCTG 480
 DB 610 TAAATGAATAAACCAATTAATATTATTAGCCCTCTGCTGCTGCTGCTGCTGCTG 669
 QY 481 GGTACCAATTTTTCAGTGTGACCTTGACAGCTCTCTTTTCCACAAGCAAGAGAAATTT 540
 DB 670 GGTACCAATTTTTCAGTGTGACCTTGACAGCTCTCTTTTCCACAAGCAAGAGAAATTT 729
 QY 541 AACACGTTTCAACCCCGGGGGAGTGGCTGTGTTAAGAAGACCATTAATGCTTTAG 600
 DB 730 AACACGTTTCAACCCCGGGGGAGTGGCTGTGTTAAGAAGACCATTAATGCTTTAG 789
 QY 601 ACAGTG 606
 DB 790 ACAGTG 795
 RESULT 3
 AK094501 1832 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens CDNA FLJ137182.f1s, clone BRALZ2001350, weakly similar
 DEFINITION to Homo sapiens Gz-selective GTPase-activating protein (GGS20)
 mRNA.
 ACCESSION AK094501 GI:21753575
 VERSION AK094501.1 GI:21753575
 KEYWORDS oligo capping; f1s (full insert sequence).
 SOURCE Homo sapiens alzheimer cortex CDNA to mRNA, clone_11b:BRALZ2
 clone:BRALZ2001350.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS 1 Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kaneda, K.,
 Waga, S., M., Murakawa, K., Kanehori, K., Takahashi, F., Fujii, A.,
 Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K.,
 and Isogai, T.
 TITLE NED0 human cdna sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1832)
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 COMMENT NED0 human cdna sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.
 FEATURES
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 1. 1832
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 /clone="BRALZ2001350"
 /tissue_type="alzheimer cortex"
 /clone_11b="BRALZ2"
 /note="cloning vector: pME18SFL3"
 215..640
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="BAC04368.1"
 /db_xref="GI:21753576"
 /translation="MNVLGIAATFCGLFLPGLALQICQCEEFQLNNDSSPEFIV
 NCTVVDMDCKEVEVDSAGIMYRKSASMAALIASAGYGFSPKLNISVCSCN
 TPLCNGPRKRGSSASALRPLRTTILFKLALSAHC"
 BASE COUNT 411 a 501 c 513 g 407 t
 ORIGIN
 Query Match 88.8%; Score 555; DB 9; Length 1832;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGTTCTCTTTCAGAGAGAGTGGCGCGGAGCGGAGAGCAAGCGGCGCTGCAAAAGCG 60
 DB 1226 AGTTCTCTTTCAGAGAGAGTGGCGCGGAGCGGAGAGCAAGCGGCGCTGCAAAAGCG 1285
 QY 61 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGCTGCTGCTG 120
 DB 1286 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGCTGCTGCTG 1345
 QY 121 CAGCGACAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
 DB 1346 CAGCGACAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1405
 QY 181 CGGTACAGCAGCGCGGTGATGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240
 DB 1406 CGGTACAGCAGCGCGGTGATGACGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1465
 QY 241 GAGGATCATGTACGCGCGGAGTAGACCTCGTCCAGTGTGCTGCTGCTGCTGCTG 300
 DB 1466 GAGGATCATGTACGCGCGGAGTAGACCTCGTCCAGTGTGCTGCTGCTGCTGCTG 1525
 QY 301 CATGATCTCTCCGAATCTGCTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 360
 DB 1526 CATGATCTCTCCGAATCTGCTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 1585
 QY 361 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 DB 1586 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1645
 QY 421 TAAATGAATAAACCAATTAATATTATTAGCCCTCTGCTGCTGCTGCTGCTGCTG 480
 DB 1646 TAAATGAATAAACCAATTAATATTATTAGCCCTCTGCTGCTGCTGCTGCTGCTG 1705
 QY 481 GGTACCAATTTTTCAGTGTGACCTTGACAGCTCTCTTTTCCACAAGCAAGAGAAATTT 540
 DB 1706 GGTACCAATTTTTCAGTGTGACCTTGACAGCTCTCTTTTCCACAAGCAAGAGAAATTT 1765
 QY 541 AACACTGTTTCAACCCCGGGGGAGTGGCTGTGTTAAGAAGACCATTAATGCTTTAG 600
 DB 1766 AACACTGTTTCAACCCCGGGGGAGTGGCTGTGTTAAGAAGACCATTAATGCTTTAG 1825
 QY 601 ACAGTG 606
 DB 1826 ACAGTG 1831

RESULT 4	AX136281	1890 bp	DNA	Linear	PAT 30-MAY-2001
LOCUS	AX136281	Sequence 203 from Patent EP1067182.			
DEFINITION	AX136281				
ACCESSION	AX136281				
VERSION	AX136281.1	GI:14272687			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 1890)				
AUTHORS	Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.				
TITLE	Secretory protein or membrane protein				
JOURNAL	Patent: EP 1067182-A 203 10-JAN-2001;				
FEATURES	Helix Research Institute (JP)				
source	Location/Qualifiers				
	1..1890				
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	274..771				
CDS	/note="unnamed protein product"				
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	/protein_id="C0C39782.1"				
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	/translation="MWVILIAATPCGLFLBGFALIOGYOCBEFOLNDCSSPEFV				
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	TPICNDRPKKRSGSASALRPLGLRTITLFLFKLASRHTAELEKMPPEPALFPDPSPT				
	PHLPE"				
BASE COUNT	419 a 528 c 533 g 410 t				
ORIGIN					
Query Match	87.8%; Score 549; DB 6; Length 1890;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches	599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Y	7 CCTTGCAGAGCAGCTGGCGCGCGGAGCGGAGAGCAGCAACGCGGCTGCACAAACGGCGCCT 66				
Db	1290 CCTTGCAGAGCAGCTGGCGCGCGGAGCGGAGAGCAGCAACGCGGCTGCACAAACGGCGCCT 1349				
Y	67 GTCGGTGTGAGTGGCGGAGTGTAGCGCGGAGCGGCTTCGTCGTCGTCGTCGTCGTCGTCGTCG 126				
Db	1350 GTCGGTGTGAGTGGCGGAGTGTAGCGCGGAGCGGCTTCGTCGTCGTCGTCGTCGTCGTCGTCG 1409				
Y	127 CAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 186				
Db	1410 CAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1469				
Y	187 CAGAGCGCGCTTGTATGACCCGAGCTGAGGTACAAAAAGCTCTCCGAGAAAGGAGAGAGAT 246				
Db	1470 CAGAGCGCGCTTGTATGACCCGAGCTGAGGTACAAAAAGCTCTCCGAGAAAGGAGAGAGAT 1529				
Y	247 CATGTACGCCCGGAGAGTGTAGACCTGTCACATCGTGTGTGGTTGGCGGAGCATGAT 306				
Db	1530 CATGTACGCCCGGAGAGTGTAGACCTGTCACATCGTGTGTGGTTGGCGGAGCATGAT 1589				
Y	307 CCTCCGAATCTGTGTGGGCAATCCAGCATACGCCAATGTCAACAATCAGCCCTGGGCA 366				
Db	1590 CCTCCGAATCTGTGTGGGCAATCCAGCATACGCCAATGTCAACAATCAGCCCTGGGCA 1649				
Y	367 GACACGAGCAG 426				
Db	1650 GACACGAGCAG 1709				
Y	427 AATAAACCATTAATATATTTAGCCCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 486				
Db	1710 AATAAACCATTAATATATTTAGCCCTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1769				
Y	487 AATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAGCAAGAGAAATTTAACACT 546				

Db	1770	AAITTTTACAGTGGGACTTGACACCTCTTTTGGCCACAGCAAGCAAGAAATTTAACCT	1829
QY	547	GTTCCTCAACCCCGGGGAGATTGGCTGTGTAAAGAAGCACTTAATATGCTTTAGACACTG	606
Db	1830	GTTCCTCAACCCCGGGGAGATTGGCTGTGTAAAGAAGCACTTAATATGCTTTAGACACTG	1889
RESULT 5			
AX358762			
LOCUS	AX358762	1524 bp	DNA
DEFINITION	Sequence 15 from Patent WO0193983.		linear
ACCESSION	AX358762		
VERSION	AX358762.1	GI:18675282	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godwin, P.J., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P., Metanabe, C.K. and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0193983-A 15 13-DEC-2001.		
FEATURES	Genetech Inc. (US)		
SOURCE	Location/Qualifiers		
	1..1524		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	321 a 433 c 435 g 335 t		
ORIGIN			
Query Match	62.9%: Score 393; DB 6; Length 1524;		
Query Similarity	100.0%: Pred. NO. 1.8e-228;		
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AGTTCTCTCTTSCAGAGACTGGCGCGGAGCGAGCAAGCAACGGCGCTGCACAAACCG	60
Db	1132	AGTTCTCTCTTSCAGAGACTGGCGCGGAGCGAGCAAGCAACGGCGCTGCACAAACCG	1191
QY	61	GGCCCTGTCGGTGGTGGAGTGGCATGTACCGCGCAGCGCTTCTGCTGTGGCTGCTG	120
Db	1192	GGCCCTGTCGGTGGTGGAGTGGCATGTACCGCGCAGCGCTTCTGCTGTGGCTGCTG	1251
QY	121	CAGGACAGGCGGAGCAGCAGCACCCTGCAGCAACACCGCGGAAACTCTCGAGAGACAC	180
Db	1252	CAGGACAGGCGGAGCAGCAGCACCCTGCAGCAACACCGCGGAAACTCTCGAGAGACAC	1311
QY	181	CGTGTACAGAGCGGGTGTATGACCGAGCTAGAGTAAAGAAACGCTCTCGAAGGGAG	240
Db	1312	CGTGTACAGAGCGGGTGTATGACCGAGCTAGAGTAAAGAAACGCTCTCGAAGGGAG	1371
QY	241	GAGATCATGTACGCCCGCGAGTAGAGACCTGTCACAGCGTGGGTTGGCGCGAGC	300
Db	1372	GAGATCATGTACGCCCGCGAGTAGAGACCTGTCACAGCGTGGGTTGGCGCGAGC	1431
QY	301	CATGATCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTACACAATACGCC	360
Db	1432	CATGATCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTACACAATACGCC	1491
QY	361	TGGGACAGACAGACAGAGAGGAGAGACAGAGA 393	
Db	1492	TGGGACAGACAGACAGAGAGGAGAGACAGAGA 1524	
RESULT 6			
AX362255			
LOCUS	AX362255	1524 bp	DNA
DEFINITION	Sequence 15 from Patent WO0208288.		linear
ACCESSION	AX362255		
VERSION	AX362255.1	GI:18694585	
KEYWORDS			

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerlitsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..1524
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 321 a 433 c 435 g 335 t
ORIGIN

Query Match 62.9%; Score 393; DB 6; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.8e-228;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGAGAGAGACTGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGCG 60
DB 1132 AGTTCTCTTGAGAGAGACTGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGCG 1191

QY 61 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 1192 GCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251

QY 121 CAGCGAGAGCGGAG 180
DB 1252 CAGCGAGAGCGGAG 1311

QY 181 CCGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTCTCGAGAGAGGAG 240
DB 1312 CCGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTCTCGAGAGAGGAG 1371

QY 241 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 1372 GAGGATCATGTACGCGCGGAG 1431

QY 301 CATGATCTCTCGCAATCTGCTTGGGCTCCAGCATACGGCCAAATGTCAACAATCAGCCC 360
DB 1432 CATGATCTCTCGCAATCTGCTTGGGCTCCAGCATACGGCCAAATGTCAACAATCAGCCC 1491

QY 361 TGGGACAGACAG 393
DB 1492 TGGGACAGACAG 1524

RESULT 7
AX136698/c 587 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 620 from Patent EP1067182.
DEFINITION AX136698
ACCESSION AX136698
VERSION AX136698.1 GI:14273102
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 587)
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 620 10-JAN-2001;
Helix Research Institute (JP)
FEATURES Location/Qualifiers
source 1..587
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BASE COUNT 117 a 162 c 140 g 162 t 6 others
ORIGIN

Query Match 58.4%; Score 365; DB 6; Length 587;
Best Local Similarity 99.8%; Pred. No. 2.3e-211;
Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 191 AGCGGTTGATGACCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 250
DB 417 AGCGGTTGATGACCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 358

QY 251 TAGCGCCGGAAGTAGGACCTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310
DB 357 TAGCGCCGGAAGTAGGACCTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298

QY 311 CGAATCTGTTGGGCAATCCAGCATAGGCGCAATGTACAAACATCAGCCCTGGGCGAGACA 370
DB 297 CGAATCTGTTGGGCAATCCAGCATAGGCGCAATGTACAAACATCAGCCCTGGGCGAGACA 238

QY 371 CGAGCAG 430
DB 237 CGAGCAG 178

QY 431 AAACATTAATAATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
DB 177 AAACATTAATAATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 118

QY 491 TTTTCACTGTTGAGCTTGACAGCTTCTTTGCCAAGCAAGAGAGAGAGAGAGAGAGAGAG 550
DB 117 TTTTCACTGTTGAGCTTGACAGCTTCTTTGCCAAGCAAGAGAGAGAGAGAGAGAGAGAG 58

QY 551 CAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTG 606
DB 57 CAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAGACAGTG 2

RESULT 8
AX139942/c 1362 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 1 from Patent WO0181634.
DEFINITION AX139942
ACCESSION AX139942
VERSION AX139942.1 GI:17901489
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.
TITLE Methods and compositions for the diagnosis and treatment of cardiovascular and tumorigenic disease using 4941
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..1362
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VTSALVALPLFAMGTEYPLVNVPSHRGLTCRRSTRHDEPETSNMSTICNLISRWI
VROSTIFGAFVYLVLVLAFCMNMVQVLAQKSGKSLAGSTRPDLKSSSESTY
AARQRTIFRLIVTLAVCMNPQIRIIMAAKPKHDMTRSYFRAYMILLPSESEFY
LSSVINPLLYTSOOPFRVFOVCCRLSDHANHEKRLRVHAHSTDSARFVORPL
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HEV"

BASE COUNT 263 a 435 c 362 g 302 t
ORIGIN

Query Match 57.4%; Score 359; DB 6; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 1.2e-207;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGACTGCGCCGGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 60
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 DB 1215 AGTTCTCTTGCAGAGAGACTGCGCCGGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 1156

QY 61 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGGCTTCGCGTGGTGGCGTGTG 120
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 DB 1155 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGGCTTCGCGTGGTGGCGTGTG 1096

QY 121 CAGCGACAGCGCGGAG 180
 |||
 DB 1095 CAGCGACAGCGCGGAG 1036

QY 181 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGCGAGAGGGAG 240
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 DB 1035 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGCGAGAGGGAG 976

QY 241 GAGGATCATGTACGCGCGGAGTGGAGCTGTCAGTGGTGGTGGCGGAGC 300
 |||
 DB 975 GAGGATCATGTACGCGCGGAGTGGAGCTGTCAGTGGTGGTGGCGGAGC 916

QY 301 CATGATCTCTCGAATCTGTTGGGCATCCAGATACGCGCAATGTCCAAACATCAGCC 359
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 DB 915 CATGATCTCTCGAATCTGTTGGGCATCCAGATACGCGCAATGTCCAAACATCAGCC 857

RESULT 9
 AF034633/c 1362 bp mRNA linear PRI 13-JUL-1998
 LOCUS Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,
 DEFINITION complete cds.
 ACCESSION AF034633
 VERSION AF034633.1 GI:2654160
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 1362)
 McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,
 Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.
 Cloning and characterization of two human G protein-coupled
 receptor genes (GPR38 and GPR39) related to the growth hormone
 secretagogue and neurotensin receptors
 Genomics 46 (3), 426-434 (1997)

JOURNAL
 MEDLINE
 PUBMED
 98110578
 9441746

REFERENCE
 2 (bases 1 to 1362)
 McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,
 Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.
 Direct Submision
 Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,
 Inc., PO Box 2000, Rahway, NJ 07065, USA

TITLE
 JOURNAL
 Inc., PO Box 2000, Rahway, NJ 07065, USA

FEATURES
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 HEV"

BASE COUNT 263 a 435 c 362 g 302 t
 ORIGIN

Query Match 57.4%; Score 359; DB 9; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 1.2e-207;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGACTGCGCCGGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 60
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 DB 1215 AGTTCTCTTGCAGAGAGACTGCGCCGGGAGCGGAGAGCAACGGCGCTGCACAAAGCG 1156

QY 61 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGGCTTCGCGTGGTGGCGTGTG 120
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 DB 1155 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGGCTTCGCGTGGTGGCGTGTG 1096

QY 121 CAGCGACAGCGCGGAG 180
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 DB 1095 CAGCGACAGCGCGGAG 1036

QY 181 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGCGAGAGGGAG 240
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 DB 1035 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGCGAGAGGGAG 976

QY 241 GAGGATCATGTACGCGCGGAGTGGAGCTGTCAGTGGTGGTGGCGGAGC 300
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 DB 975 GAGGATCATGTACGCGCGGAGTGGAGCTGTCAGTGGTGGTGGCGGAGC 916

QY 301 CATGATCTCTCGAATCTGTTGGGCATCCAGATACGCGCAATGTCCAAACATCAGCC 359
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 DB 915 CATGATCTCTCGAATCTGTTGGGCATCCAGATACGCGCAATGTCCAAACATCAGCC 857

RESULT 10
 AX319944/c 2528 bp DNA linear PAT 14-DEC-2001
 LOCUS Sequence 3 from Patent WO0181634.
 ACCESSION AX319944
 VERSION AX319944.1 GI:17901491
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1
 Galvin,K.A. and Rudolph-Owen,L.A.
 Methods and compositions for the diagnosis and treatment of
 cardiovascular and tumorigenic disease using 4941
 Patent: WO 0181634-A 3 01-NOV-2001;
 Millennium Pharmaceuticals, Inc. (US)

TITLE
 JOURNAL
 Location/Qualifiers

FEATURES
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 1..2528
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 /db_xref="GI:17901492"
 /translation="MASPSLPSSDSCSIIIDSHVPEFEVATWIKITLILVLIIFVWG
 LIGNSATIRVIOVLQKGYLOKEVTDHWSLACSDLVLEIDCMPMEFYSIINPLPTS
 SYTISCKHTLTFEACSVATLHVITLSPERIATCPHPRIRAVSGPCOVKLLIGVW
 VTSALVALPLLFAMGTEYPLVNVPSHRGLTCRRSSRTHRHOPEPTSMKSLCTNLSHMT

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 92874)
Worley, R.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 92874)
Worley, R.C.
Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced g1:20303189.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRJD
Center clone name: CH230-286021
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 32512 bases at least Q40
Consensus quality: 34515 bases at least Q30
Consensus quality: 35930 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1057: contig of 1057 bp in length
1058 1157: gap of unknown length
1158 2410: contig of 1253 bp in length
2411 2510: gap of unknown length
2511 3571: contig of 1061 bp in length
3572 5259: contig of 1588 bp in length
5260 5359: gap of unknown length
5360 6436: contig of 1077 bp in length
6437 6536: gap of unknown length
6537 7705: contig of 1169 bp in length
7706 7805: gap of unknown length
7806 8911: contig of 1106 bp in length
8912 9011: gap of unknown length
9012 10370: contig of 1359 bp in length
10371 10470: gap of unknown length
10471 11914: contig of 1444 bp in length
11915 12014: gap of unknown length
12016 13145: contig of 1131 bp in length
13146 13245: gap of unknown length
13246 14584: contig of 1339 bp in length
14585 14684: gap of unknown length
14686 16004: contig of 1720 bp in length
16005 16504: gap of unknown length
16505 17655: contig of 1151 bp in length
17656 17755: gap of unknown length
17756 19240: contig of 1485 bp in length
19241 19340: gap of unknown length
19341 20647: contig of 1307 bp in length
20648 20747: gap of unknown length
20749 22171: contig of 1424 bp in length
22171

FEATURES
source
1..92874
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-286021"

22172 22271: gap of unknown length
22272 23762: contig of 1491 bp in length
23763 23862: gap of unknown length
23863 25356: contig of 1694 bp in length
25357 25656: gap of unknown length
25657 26711: contig of 1055 bp in length
26712 26811: gap of unknown length
26812 28747: contig of 1936 bp in length
28748 28847: gap of unknown length
28848 30564: contig of 1717 bp in length
30565 30665: gap of unknown length
30666 32046: contig of 1382 bp in length
32047 32146: gap of unknown length
32147 33729: contig of 1583 bp in length
33730 33829: gap of unknown length
33830 35524: contig of 1695 bp in length
35525 35624: gap of unknown length
35625 37292: contig of 1668 bp in length
37293 37392: gap of unknown length
37393 38486: contig of 1094 bp in length
38487 38586: gap of unknown length
38587 40145: contig of 1359 bp in length
40146 40245: gap of unknown length
40246 41925: contig of 1680 bp in length
41926 42025: gap of unknown length
42026 43669: contig of 1644 bp in length
43670 43769: gap of unknown length
43770 45713: contig of 1944 bp in length
45714 45813: gap of unknown length
45814 47315: contig of 1502 bp in length
47316 47415: gap of unknown length
47416 48852: contig of 1437 bp in length
48853 48952: gap of unknown length
48953 50511: contig of 1559 bp in length
50512 50611: gap of unknown length
50612 52672: contig of 2061 bp in length
52673 52772: gap of unknown length
52773 54274: contig of 1502 bp in length
54275 54374: gap of unknown length
54375 56993: contig of 2619 bp in length
56994 57093: gap of unknown length
57094 59515: contig of 2422 bp in length
59516 59615: gap of unknown length
59616 61878: contig of 2263 bp in length
61879 61978: gap of unknown length
61979 64521: contig of 2542 bp in length
64521 67430: gap of unknown length
67431 67530: gap of unknown length
67531 68852: contig of 1322 bp in length
68853 68952: gap of unknown length
68953 70700: contig of 1748 bp in length
70701 70800: gap of unknown length
70801 72350: contig of 1350 bp in length
72351 72450: gap of unknown length
72451 74628: contig of 2178 bp in length
74629 74728: gap of unknown length
74729 76922: contig of 2194 bp in length
76923 77022: gap of unknown length
77023 79345: contig of 2323 bp in length
79346 79445: gap of unknown length
79446 82316: contig of 2871 bp in length
82317 82416: gap of unknown length
82417 84866: contig of 2450 bp in length
84867 84966: gap of unknown length
84967 87959: contig of 2993 bp in length
87960 88060 92874: gap of unknown length
92874: contig of 4815 bp in length.

BASE COUNT 23927 a 19653 c 20425 g 23828 t 5041 others
 ORIGIN

Query Match 4.3%; Score 27; DB 2; Length 92874;
 Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 GAGAGGAGGAGGAGATCATGTACGCC 256
 ||||||||||||||||||||||||||||||||

Db 75643 GAGAGGAGGAGGAGATCATGTACGCC 75669

RESULT 13
 AC099984 70395 bp DNA linear HTG 22-NOV-2001
 LOCUS AC099984 Mus musculus clone RP23-24D9, LOW-PASS SEQUENCE SAMPLING.

DEFINITION AC099984 AC099984.1 GI:17047350

VERSION HTG; HTGS_PHASE0.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WtBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L13721
 Center clone name: 24_D_9

NOTE: This record contains 84 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone

will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 734: contig of 734 bp in length
 735 834: gap of 100 bp
 835 1576: contig of 742 bp in length
 1577 1676: gap of 100 bp
 1677 2451: contig of 775 bp in length
 2452 2551: gap of 100 bp
 2552 3284: contig of 733 bp in length
 3285 3384: gap of 100 bp
 3385 4118: contig of 734 bp in length
 4119 4218: gap of 100 bp
 4219 4957: contig of 739 bp in length
 4958 5057: gap of 100 bp
 5058 5810: contig of 753 bp in length
 5811 5910: gap of 100 bp
 5911 6622: contig of 712 bp in length
 6623 6722: gap of 100 bp
 6723 7458: contig of 736 bp in length
 7459 7558: gap of 100 bp
 7559 8357: contig of 799 bp in length
 8358 8457: gap of 100 bp
 8458 9202: contig of 745 bp in length
 9203 9302: gap of 100 bp
 9303 10054: contig of 752 bp in length
 10055 10154: gap of 100 bp
 10155 10911: contig of 757 bp in length
 10912 11011: gap of 100 bp
 11012 11745: contig of 734 bp in length
 11746 11845: gap of 100 bp
 11846 12584: contig of 739 bp in length
 12585 12684: gap of 100 bp
 12685 13430: contig of 746 bp in length
 13431 13530: gap of 100 bp
 13531 14266: contig of 736 bp in length
 14267 14366: gap of 100 bp
 14367 15105: contig of 739 bp in length
 15106 15205: gap of 100 bp
 15206 15932: contig of 727 bp in length
 15933 16032: gap of 100 bp
 16033 16767: contig of 735 bp in length
 16768 16867: gap of 100 bp
 16868 17607: contig of 740 bp in length
 17608 17707: gap of 100 bp
 17708 18512: contig of 805 bp in length
 18513 18612: gap of 100 bp
 18613 19336: contig of 724 bp in length
 19337 19436: gap of 100 bp
 19437 20162: contig of 726 bp in length
 20163 20262: gap of 100 bp
 20263 21001: contig of 739 bp in length
 21002 21101: gap of 100 bp
 21102 21820: contig of 719 bp in length
 21821 21920: gap of 100 bp
 21921 22647: contig of 727 bp in length
 22648 22747: gap of 100 bp
 22748 23424: contig of 677 bp in length
 23425 23524: gap of 100 bp
 23525 24268: contig of 744 bp in length
 24269 24368: gap of 100 bp
 24369 25107: contig of 739 bp in length
 25108 25207: gap of 100 bp
 25208 25956: contig of 749 bp in length
 25957 26056: gap of 100 bp
 26057 26801: contig of 745 bp in length
 26802 26901: gap of 100 bp
 26902 27633: contig of 732 bp in length
 27634 27733: gap of 100 bp
 27734 28467: contig of 734 bp in length
 28468 28567: gap of 100 bp
 28568 29307: contig of 740 bp in length
 29308 29407: gap of 100 bp


```

* 29408 30149: contig of 742 bp in length
* 30150 30249: gap of 100 bp
* 30250 30990: contig of 741 bp in length
* 30991 31090: gap of 100 bp
* 31091 31820: contig of 730 bp in length
* 31821 31920: gap of 100 bp
* 31921 32656: contig of 736 bp in length
* 32657 32756: gap of 100 bp
* 32757 33499: contig of 743 bp in length
* 33500 33599: gap of 100 bp
* 33600 34356: contig of 757 bp in length
* 34357 34456: gap of 100 bp
* 34457 35196: contig of 740 bp in length
* 35197 35296: gap of 100 bp
* 35297 36000: contig of 704 bp in length
* 36001 36100: gap of 100 bp
* 36101 36891: contig of 791 bp in length
* 36892 36991: gap of 100 bp
* 36992 37721: contig of 730 bp in length
* 37722 37821: gap of 100 bp
* 37822 38559: contig of 738 bp in length
* 38560 38659: gap of 100 bp
* 38660 39409: contig of 750 bp in length
* 39410 39509: gap of 100 bp
* 39510 40227: contig of 718 bp in length
* 40228 40327: gap of 100 bp
* 40328 41093: contig of 766 bp in length
* 41094 41193: gap of 100 bp
* 41194 41952: contig of 759 bp in length
* 41953 42052: gap of 100 bp
* 42053 42793: contig of 741 bp in length
* 42794 42893: gap of 100 bp
* 42894 43623: contig of 730 bp in length
* 43624 43723: gap of 100 bp
* 43724 44474: contig of 751 bp in length
* 44475 44574: gap of 100 bp
* 44575 45323: contig of 749 bp in length
* 45324 45423: gap of 100 bp
* 45424 46156: contig of 733 bp in length
* 46157 46256: gap of 100 bp
* 46257 47052: contig of 766 bp in length
* 47053 47152: gap of 100 bp
* 47153 47886: contig of 734 bp in length
* 47887 47986: gap of 100 bp
* 47987 48723: contig of 737 bp in length
* 48724 48823: gap of 100 bp
* 48824 49570: contig of 747 bp in length
* 49571 49670: gap of 100 bp
* 49671 50408: contig of 738 bp in length
* 50409 50508: gap of 100 bp
* 50509 51207: contig of 699 bp in length
* 51208 51307: gap of 100 bp
* 51308 52094: contig of 787 bp in length
* 52095 52194: gap of 100 bp
* 52195 52922: contig of 728 bp in length
* 52923 53022: gap of 100 bp
* 53023 53755: contig of 733 bp in length
* 53756 53855: gap of 100 bp
* 53856 54570: contig of 715 bp in length
* 54571 54670: gap of 100 bp
* 54671 55385: contig of 715 bp in length
* 55386 55485: gap of 100 bp
* 55486 56162: contig of 677 bp in length
* 56163 56262: gap of 100 bp
* 56263 57001: contig of 739 bp in length
* 57002 57101: gap of 100 bp
* 57102 57848: contig of 747 bp in length
* 57849 57948: gap of 100 bp

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Query Match 3.8%; Score 24; DB 2; Length 70395;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 AGAGACAGAGAAAAAACA 406
 Db 58976 AGAGACAGAGAAAAAACA 58999

RESULT 14

AC026770/c 94718 bp DNA linear PRI 17-NOV-2000
 Homo sapiens chromosome 15 clone CTD-2308G16 map 15q21, complete
 sequence.

ACCESSION

AC026770
 AC026770.6 GI:11192116

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
 Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A.,
 Nesbitt, R., Traicoff, R. and Hood, L.
 Sequencing of human chromosome 15 D15S146-D15S117 region
 Unpublished
 2 (bases 1 to 94718)

TITLE

JOURNAL

AUTHORS

Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
 Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G.,
 James, R., Kaur, A., Madan, A., Owen, M. P., Katcliffe, A., Shaffer, T.
 and Hood, L.
 Direct Submission
 Submitted (24-MAR-2000) Multimegabase Sequencing Center, University
 of Washington, PO BOX 357730, Seattle, WA 98195, USA
 3 (bases 1 to 94718)

REFERENCE

AUTHORS

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
 Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A.,
 Nesbitt, R., Traicoff, R. and Hood, L.
 Direct Submission
 Submitted (17-NOV-2000) Multimegabase Sequencing Center, Institute
 for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
 98105, USA
 On Nov 17, 2000 this sequence version replaced gi:10697426.

TITLE

JOURNAL

Center: Multimegabase Sequencing Center
 Center code: UMWSC
 Web site: http://chroma.mbt.washington.edu/msg_wmw
 Contact: leecrownsystemsbiology.org

COMMENT

JOURNAL

Sequencing vector: pUC18; 108752
 Chemistry: Dye-terminator Big Dye; 90% of reads
 Chemistry: Dye-primer Big Dye; 10% of reads
 Assembly program: Phrap; version 0.990399

FEATURES

SOURCE

Location/Qualifiers
 1..94718
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
 /map="15q21"

FEATURES

SOURCE

clone_11b="Cal Tech human BAC library 11"
 /note="This clone overlaps RP11-313P18, RP11-414J1 and
 RP11-56B16. Data from all of these BACs were combined,
 with an attempt to generate the consensus sequence from
 CTD-2308G16."

FEATURES

SOURCE

1..81828
 /note="Overlap with RP11-414J1, AC020685"
 1..9464
 /note="Overlap with RP11-313P18, AC020892"

FEATURES

SOURCE

66240..72320
 /note="number of Ts unclear"
 72300..72320
 /note="low quality data"
 72960..72980
 /note="low quality data"

FEATURES

SOURCE

misc_feature
 1..9464
 /note="Overlap with RP11-414J1, AC020685"

FEATURES

SOURCE

misc_feature
 1..9464
 /note="Overlap with RP11-414J1, AC020685"

FEATURES

SOURCE

misc_feature
 1..9464
 /note="Overlap with RP11-414J1, AC020685"

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misc_feature      81823. .94718  
/note="overlap with RP11-56B16, AC009679"  
unsure           88020. .88070
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BASE COUNT	28761 a	19737 c	19836 g	26384 t
ORIGIN				

Query Match	3.7%	Score 23;	DB 9;	Length 94718;
Best Local Similarity	100.0%	Pred. No. 0.12;		
Matches 23; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

Qy 382 GAGAGACAGAGAAAAAGAAAAACA 404
|||||
Db 83486 GAGAGACAGAGAAAAAGAAAAACA 83464

RESULT	15
ACOL1639/c	
LOCUS	ACOL1639/c
DEFINITION	ACOL1639 Homo sapiens clone RP11-13h19, WORKING DRAFT SEQUENCE, 8 unordered pieces.
ACCESSION	ACOL1639
VERSION	ACOL1639.9
KEYWORDS	GI:13940716
SOURCE	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Homo sapiens.

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 167693)	Bitren, B., Linton, L., Nussbaum, C. and Lander, E.	Homo sapiens, clone RP11-13H19	unpublished	
2 (bases 1 to 167693)	Bitren, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M.			

JOURNAL

COMMENT

Submitted (08-Oct-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 4, 2001 this sequence version replaced gi:131233327.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

----- Genome Center
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead
Center code: WITBR

Web site: <http://www-seq.wi.mit.edu>

```
----- Project Information -----
contact: sequence_submissions@ncbi.nlm.nih.gov
```

Center project name: L3327
Center clone name: 13_H_19

```
----- Summary Statist
Sequencing vector: M13: M7
```

Sequencing vector: Plasmid
Chemistry: Duet transformator

Chemistry: dye-terminator
Assembly program: Phrap; v

Consensus quality: 164534 bases at least Q40
Consensus quality: 165712 bases at least Q30

Consensus quality: 166331 bases at least Q20
Insert size: 170000: agarose-fn

Insert size: 166993; sum-of-contigs

quality coverage: 1.0 in 420 bases; agarose-1p

```

Quality coverage: 7.9 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
  1 54881: contig of 54881 bp in length
* 54882 54981: gap of 100 bp
* 54982 57393: contig of 2412 bp in length
* 57394 57493: gap of 100 bp
* 57494 64870: contig of 7377 bp in length
* 64871 64970: gap of 100 bp
* 64971 73018: contig of 8048 bp in length
* 73019 73118: gap of 100 bp
* 73119 90139: contig of 17021 bp in length
* 90140 90239: gap of 100 bp
* 90240 120347: contig of 30108 bp in length
* 120348 120447: gap of 100 bp
* 120448 167227: contig of 46780 bp in length
* 167228 167327: gap of 100 bp
* 167328 167593: contig of 366 bp in length.
  Location/Qualifiers
    1..167593

```

[illegible]

Query Match	3.78;	Score 23;	DB 2;	Length 167693;
-------------	-------	-----------	-------	----------------

Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GAGAGACAGAGAAAAAACA 404
 |||||
Db 1669 GAGAGACAGAGAAAAAACA 1647

RESULT	16			
AC022742/c				
LOCUS	AC022742/c	176967 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 15 clone RP11-762A1 map 15,			HTG_09-MAY-2001 WORKING DRAFT
ACCESSION	AC022742			
VERSION	AC022742.4	GI:13123383		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.			
SOURCE	Homo sapiens.			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 176967)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-762A1
Unpublished
2 (bases 1 to 176967)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheters, R., Meldrim, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 25, 2001 this sequence version replaced g1:11990718.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: 762_A-1

Summary Statistics
Sequencing vector: M13; M77815; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 176032 bases at least Q40
Consensus quality: 176449 bases at least Q30
Consensus quality: 176615 bases at least Q20
Insert size: 186000; agarose-efp
Quality coverage: 9.0 in Q20 bases; agarose-efp

NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 14400: contig of 14400 bp in length
* 14401 14500: gap of 100 bp
* 14501 61165: contig of 46665 bp in length
* 61166 61265: gap of 100 bp
* 61266 112521: contig of 51255 bp in length
* 112522 112621: gap of 100 bp
* 112622 176967: contig of 64346 bp in length.

FEATURES
SOURCE

Location/Qualifiers
1. 176967
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
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/clone_11b="RPCT-11 Human Male BAC"

misc-feature

1. 14400

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misc-feature

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61266..112521

misc-feature

/note="assembly-fragment"
112622..176967

misc-feature

/note="assembly-fragment
clone_end:T7
vector_side:right"

BASE COUNT 53791 a 35746 c 36226 g 50904 t 300 others

ORIGIN

Query Match 3 7% Score 23; DB 2; Length 176967;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GAGACAGACAGAAAAGAAAACA 404

Db 166420 GAGACAGACAGAAAAGAAAACA 166398

RESULT 17
AC022824 180837 bp DNA linear HTG 06-AUG-2002
LOCUS

DEFINITION Homo sapiens chromosome 15 clone RP11-81117 map 15, WORKING DRAFT
SEQUENCE, 8 unordered pieces.

ACCESSION AC022824.5 GI:22123655
VERSION AC022824.5

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILLP.
SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 180837)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.

JOURNAL Homo sapiens chromosome 15, clone RP11-81117
REFERENCE 2 (bases 1 to 180837)
AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheters, R., Meldrim, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.

Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 180837)

REFERENCE
AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Lander, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,

LOCUS	AC090971	192464 bp	DNA	linear	PRI 27-NOV-2001
DEFINITION	Homo sapiens chromosome 15 clone RP11-56B16 map 15q21.3, complete sequence.				
ACCESSION	AC090971				
VERSION	AC090971.3	GI:17105278			
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
AUTHORS	1 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dots, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.				
TITLE	Sequencing of human chromosome 15 D15S146-D15S117 region				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dots, M., Dichofoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Tralcoff, R. and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-Mar-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
REFERENCE	3 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dots, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-NOV-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
COMMENT	On Nov 27, 2001 this sequence version replaced gi:13624393. ----- Genome Center Center: Multimegabase Sequencing Center Center code: UMWSC Web site: http://chroma.mbl.washington.edu/msg_wmw Contact: leorowen@systembiology.org ----- Summary Statistics Sequencing vector: pUC18; L08752 Chemistry: Dye-terminator Big Dye; 90% of reads Chemistry: Dye-Primer Big Dye; 10% of reads Assembly program: Phrap; version 0.990399				
FEATURES	Note: Data from overlapping BACs AC026770 [drafting center: UMWSC], AC011639 [drafting center: WBR], AC016824 [drafting center: GTC], and AC090970 [drafting center: UMWSC] was added for finishing.				
source	Location/Qualifiers 1..192464 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="15" /map="15q21.3" /map="15q21.3" /clone="RP11-56B16" /clone.lib="RPCI human BAC library 11" /note="Data from overlapping BACs CTD-2308G16, RP11-13H19, RP11-47K1, and CTD-2650P22 was added and the consensus sequence was determined from RP11-56B16 to the extent possible" 1..167631 /note="Overlap with RP11-13H19 AC011639" 1..12888 /note="Overlap with CTD-2308G16 AC026770" 76219..192464 /note="Overlap with CTD-2650P22 AC090970" 80765..192464 /note="Overlap with RP11-47K1 AC016824"				
BASE COUNT	56858 a 39351 c 40295 g 55960 t				
ORIGIN					

Query Match Similarity 3.7%; Score 23; DB 9; Length 192466;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GAGAGACAGAGAAAAAGAAAAACA 404
|||||
Db 1656 GAGAGACAGAGAAAAAGAAAAACA 1634

RESULT 20
AC126666/C
LOCUS
DEFINITION
ACCESSION
KEYWORDS
KEYWORDS
SOURCE
ORGANISM

AC126666 200145 bp DNA linear HTG 11-JUL-2002
Rattus norvegicus clone CH230-3p12, *** SEQUENCING IN PROGRESS ***
61 unordered pieces.
AC126666 GI:21703541
HTG: HTGS_PHASE1.
Norway rat.
Rattus norvegicus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 200145)
Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrocks,S.L., Amaratinge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Butch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Dayla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Dem,A.L., Ding,X., Dinh,H.H.,
Douthwaite,K.J., Dreper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gablis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,D., Kovar,C.,
Kratovic,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,W., Loulsegel,H.,
Lomado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Mamshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Monabadi,K., Morgan,M., Morris,S.,
Mosier,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokkenko,S., Oguni,M., Okunolu,G.,
Ordunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peterson,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., RojuboKan,I., Rolfe,M., Ruiz,S., Saverly,G.,
Schierer,S., Scott,G., Shen,H., Shooshaki,N., Slison,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,A., Stone,H.,
Sutton,E.A., Sytek,A., Tabors,P., Tamerisa,A., Tameris,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villaalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,
Williams,G., Williamson,A., Wlecyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 200145)
Worley,K.C.
Direct Submission
Submitted (08-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 200145)

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

AUTHORS
TITLE
JOURNAL
COMMENT

Worley, K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GARR
Center clone name: CH230-3p12

----- Summary Statistics
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14114 bases at least Q40
Consensus quality: 15319 bases at least Q30
Consensus quality: 16387 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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2612 2611: contig of 1234 bp in length
2712 2711: gap of unknown length
3824 3823: contig of 1112 bp in length
3924 3923: gap of unknown length
5558 5557: contig of 1634 bp in length
5658 5657: gap of unknown length
6745 6744: contig of 1087 bp in length
6845 6844: gap of unknown length
9032 9031: contig of 2188 bp in length
9132 9131: gap of unknown length
9133 9132: contig of 1034 bp in length
10166 10165: gap of unknown length
10167 10166: gap of unknown length
10267 10266: gap of unknown length
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14983 14982: gap of unknown length
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16143 16142: gap of unknown length
17419 17418: contig of 1276 bp in length
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18766 18765: gap of unknown length
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20344 20343: gap of unknown length
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26064 26063: gap of unknown length
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36633 36732: gap of unknown length
36733 36732: contig of 1974 bp in length
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52797 52896: gap of unknown length
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73161 73260: gap of unknown length
73261 76727: contig of 3467 bp in length
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83251 83350: gap of unknown length
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87387 87486: gap of unknown length
87487 92356: contig of 4770 bp in length
92357 92556: gap of unknown length
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133797 138631: contig of 4835 bp in length
138632 138731: gap of unknown length
138732 144408: contig of 5677 bp in length
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144509 149333: contig of 4825 bp in length
149334 149433: gap of unknown length
149434 153926: contig of 4483 bp in length

Query Match 3.7% Score 23; DB 2; Length 200145;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservatively 0; Mismatches 0; Indels 0; Gaps 0;
07 377 GGAGCGAGACGACGAGAAAGAA 399
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/db_xref="taxon:3702"
/chromosome="5"
/clone="RAF105-01-E17(R21170)"
/notes="ecotype: Columbia"
BASE COUNT      541 a      376 c      450 g      615 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 22; DB 8; Length 1982;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 GCAGGAGGAGACAGAGAGAAA 395
|||||
Db 1697 GCAGGAGGAGAGACAGAGAAA 1718

RESULT 24
LOCUS NTA294474 2666 bp mRNA linear PLN 12-APR-2002
DEFINITION Nicotiana tabacum mRNA for SET-domain-containing protein (set1
gene).
ACCESSION AJ294474
VERSION AJ294474.1 GI:15485583
KEYWORDS SET-domain-containing protein; set1 gene.
SOURCE common tobacco.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1
REFERENCE
AUTHORS Shen, W.H.
TITLE NtSET1, a member of a newly identified subgroup of plant
SET-domain-containing proteins, is chromatin-associated and its
ectopic overexpression inhibits tobacco plant growth
JOURNAL Plant J. 28 (4), 371-383 (2001)
MEDLINE 21605275
PUBMED 11737775
REFERENCE 2 (bases 1 to 2666)
AUTHORS Shen, W.H.
TITLE Direct Submision
JOURNAL Submitted (01-SEP-2000) Shen W.H., Biologie Cellulaire, Institut de
Biologie Molculaire des Plantes, 12 rue du General Zimmer,
Strasbourg 67084, FRANCE
FEATURES
source Location/Qualifiers
1..2666
/organism="Nicotiana tabacum"
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157..2271
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KRGFRKPRRAQAGELPEVEVDVEPLQLITSEFLVLDQVKKADGKELAGRYLL
VFDELRRTQIDESRDGSGRBDPLKASNNMTGKVTNQRIGNAGIEVGDI
FFRMEICLVGLHAPTMAGIDYMSVKLTMEEPYLAIVSGGDDGGGDDVLYTGO
GGVORKDCQVEVDQKLERGNLALEKSVHRANEVYRIVGVDVAYPTGKIYYDLXKIO
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ISAKNGNISIRMHNSCPNVYMWLVVROSNNEDATYHIAFFAIRHIPPQELTFDVG

```

```

BASE COUNT      739 a      477 c      659 g      790 t      1 others
ORIGIN
DKADHRRKKCLCGSLNCRGYFY"

Query Match
Best Local Similarity 100.0%; Score 22; DB 8; Length 2666;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAAAAAAAA 625
|||||
Db 2632 GTGNAAAAAAAAAAAAAAAAAAAA 2653

RESULT 25
LOCUS AF035577 3190 bp mRNA linear INV 05-MAY-2000
DEFINITION Amblyomma americanum retinoid X receptor (RXR1) mRNA, complete cds.
ACCESSION AF035577
VERSION AF035577.1 GI:3098333
KEYWORDS
SOURCE Amblyomma americanum.
ORGANISM Amblyomma americanum
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Amblyomma.
1 (bases 1 to 3190)
Guo, X., Xu, Q., Harmon, M.A., Jin, X., Laudet, V., Mangelsdorf, D.J. and
Palmer, M.J.
Isolation of two functional retinoid X receptor subtypes from the
Ixodid tick, Amblyomma americanum (L.)
Mol. Cell. Endocrinol. 139 (1-2), 45-60 (1998)
9705073
PUBMED 98368771
MEDLINE 98368771
JOURNAL
AUTHORS Palmer, M.J., Guo, X. and Xu, Q.
TITLE Direct Submision
JOURNAL Submitted (24-NOV-1997) Entomology, Oklahoma State University, 127
Noble Research Center, Stillwater, OK 74078, USA
FEATURES
source Location/Qualifiers
1..3190
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/protein_id="AAC15588.1"
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LVQWAKHLPHEEELPLEDRMVLKAGWELLIAAFSHRSVDYDGIYLAATGLVQRRS
AHGAGVGAIIPDRLVLTLELVAKREEMKMDRTLEGLCLAVLYFNEPAKLRFCPSGPGGE
SVSALAEHCROQYDPQGRFAKLRLRLPALRSTIGKLEHLPEFKLIGPTPIDNPLLS
MLEAPSDP"
BASE COUNT      800 a      723 c      785 g      881 t      1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 22; DB 3; Length 3190;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAAAAAAAA 625
|||||
Db 3169 GTGNAAAAAAAAAAAAAAAAAAAA 3190

RESULT 26
LOCUS AB019231/c 4370 bp DNA linear PLN 27-DEC-2000
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone:MG03.

```

ACCESSION AB019231 BA000015
 VERSION AB019231.1 GI:3869070
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (strain:Columbia) DNA, clone_11b:Mitsui P1 clone:MG03.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (sites)
 Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H. and Tabata, S.
 Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones
 DNA Res. 7 (1), 31-63 (2000)
 20181125
 2 (bases 1 to 43570)
 Nakamura, Y.
 Direct Submission
 Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
 Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MG03
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlini.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MMN10 and the 3' clone is F15112.
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Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 426 GAATAAACCATAAATATTTA 447
 Db 33922 GAATAAACCATAAATATTTA 33901

RESULT 27
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 *** 56 unordered pieces.
 ACCESSION AC114102
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 KEYWORDS HTG; HTGS; PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

- Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 86093)
 Murny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
 Albrooks, S.L., Amarantunge, H.C., Are, J.R., Ayale, M., Banks, T.,
 Barbatta, J., Benton, J., Bimage, K., Blankenburg, K., Bonin, D.,
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 Weinstein, G., and Glibbs, R.
 Direct Submission
 2 (bases 1 to 86093)
 Worley, K.C.
 Direct Submission
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 86093)
 Worley, K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:19224429.

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GILW
 Center clone name: CH230-70H23
 ----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap; version: 0.990329
 Consensus quality: 10778 bases at least Q40
 Consensus quality: 11488 bases at least Q30
 Consensus quality: 12089 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 56 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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Query Match 3.5%; Score 22; DB 2; Length 86093;
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 Db 22610 GTGNNAAAAAAAAAAAAA 22631

RESULT 28
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 PROJECT).
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 Arabidopsis thaliana.
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 90020)
 Bevan, M., Robben, J., Grymonprez, B., Volckaert, G., Bancroft, I.,
 Mewes, H.W., Rudd, S., Lemcke, K. and Mayer, K.F.X.
 JOURNAL
 REFERENCE
 2 (bases 1 to 90020)

AUTHORS EU Arabidopsis sequencing project.
TITLE Direct Submission
JOURNAL Submitted (19-Apr-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemche@mips.biochem.mpg.de, may@mips.biochem.mpg.de, project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bsrc.ac.uk
COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

FEATURES Location/Qualifiers
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RESULT 29
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LOCUS Rattus norvegicus clone CH230-49C23, *** SEQUENCING IN PROGRESS
DEFINITION *** 50 unordered pieces.
AC117309
VERSION AC117309.3 GI:21745791
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.
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Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 94029)
Worley,K.C.

Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 94029)
Worley,K.C.

Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20162656.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GTRW
Center clone name: CH230-49C23
Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 46565 bases at least Q40
Consensus quality: 49416 bases at least Q30
Consensus quality: 51546 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 50 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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  Beyer, M., Murphy, G., Ridley, P., Hudson, S., Bancroft, I., Mewes, H.W.,
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JOURNAL
  EU Arabidopsis sequencing project.
  Direct Submission
  Submitted (28-JUN-2001) IBJ/MIPS, National Research Center for
  Environment and Health, Ingolstaedter Landstr. 1, 85758 Neuherberg,
  FRG, E-mail: schoof@sf.de, kmayer@sf.de
  Project Coordinator: Mike
  Beyer, Molecular Genetics Department, Cambridge Laboratory, John
  Innes Centre, Colney Lane, NR4 7UD Norwich, UK, E-mail:
  michael.bevan@bbsrc.ac.uk
COMMENT
  Annotation on performance of analysis and a more detailed
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COSSSSHMTMRVLYELRSALASFIQLVYELDKGEDLVKIPKALPSLLAVINL
FSNLGFSFSLHAYRVEDSSVDSSYPMLVFDRLPEVNEGSSQWTDCELDAIYLCK
HKKPRRMTLTVWRTYTCGAVLSVFSSTILLHSSLSMSSDIENYHDAKEMDFEESD
VEOPLSLIRDELDFERRRKHGVWETEVQITQDSLRMLRNCEQAKTRKVPNASH
QEMLEVYNNRYEKELVHPHNLGELARGLLQVOKLKLDIRLAMELEQILRANET
NFATIALPAFELSVMLTVLRTWLKDSKNOGRGRTARLHRLVVEIERKIMQVOS
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/number=6

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exon			complement(18465)				
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intron			complement(18660)				
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OY	374	CGAGGAGGAGACAGAGAAA	395				
DB	93334	CGAGGAGGAGACAGACAAA	93313				
AC126575		AC126575	99541 bp	DNA	linear	HTG 24-JUL-2002	
LOCUS							
DEFINITION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							

TITLE	Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Mokenko, S., Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojубokan, I., Rolfe, M., Ruiz, S., Savery, G., Scheraga, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Statel, C., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telirod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Glibbs, R.
REFERENCE	Submitted
AUTHORS	Unpublished
TITLE	2 (bases 1 to 99541)
JOURNAL	Worley, K.C.
REFERENCE	Direct Submission
AUTHORS	Submitted (07-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
TITLE	3 (bases 1 to 99541)
JOURNAL	Worley, K.C.
REFERENCE	Direct Submission
AUTHORS	Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
TITLE	Genome Center
JOURNAL	Center: Baylor College of Medicine
REFERENCE	Center code: BCM
AUTHORS	Web site: http://www.hgsc.bcm.tmc.edu/
TITLE	Contact: hgsc-help@bcm.tmc.edu
JOURNAL	Project Information
REFERENCE	Center project name: GZHJ
AUTHORS	Center clone name: CH230-303EL5
TITLE	Summary Statistics
JOURNAL	Sequencing vector: Plasmid;
REFERENCE	Chemistry: Dye-terminator Big Dye; 100% of reads
AUTHORS	Assembly program: Phrap; version 0.99029
TITLE	Consensus quality: 55959 bases at least Q40
JOURNAL	Consensus quality: 60532 bases at least Q30
REFERENCE	Consensus quality: 63142 bases at least Q20
AUTHORS	NOTE: Estimated insert size may differ from sequence length
TITLE	(see http://www.hgsc.bcm.tmc.edu/docs/genbank_difft_data.html).
JOURNAL	NOTE: This is a "working draft" sequence. It currently
REFERENCE	consists of 50 contigs. The true order of the pieces
AUTHORS	is not known and their order in this sequence record is
TITLE	arbitrary. Gaps between the contigs are represented as
JOURNAL	runs of N, but the exact sizes of the gaps are unknown.
REFERENCE	This record will be updated with the finished sequence
AUTHORS	as soon as it is available and the accession number will
TITLE	be preserved.
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REFERENCE	1065: contig of 1064 bp in length
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TITLE	1165
JOURNAL	2166: contig of 1002 bp in length
REFERENCE	2167: gap of unknown length
AUTHORS	2267: contig of 1061 bp in length
TITLE	3328
JOURNAL	3427: gap of unknown length
REFERENCE	3428
AUTHORS	4431: contig of 1004 bp in length
TITLE	4432
JOURNAL	4531: gap of unknown length
REFERENCE	4532
AUTHORS	5539: contig of 1008 bp in length
TITLE	5540
JOURNAL	5639: gap of unknown length
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AUTHORS	7228: contig of 1589 bp in length
TITLE	7229
JOURNAL	7328: gap of unknown length
REFERENCE	8482: contig of 1154 bp in length
AUTHORS	8483
TITLE	8583: gap of unknown length
JOURNAL	9624: contig of 1042 bp in length
REFERENCE	9625
AUTHORS	9724: gap of unknown length
TITLE	9725
JOURNAL	10763: contig of 1038 bp in length
REFERENCE	10763
AUTHORS	10863: gap of unknown length
TITLE	12028: contig of 1166 bp in length
JOURNAL	10863

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* 17509 17608: gap of unknown length
* 17609 18750: contig of 1142 bp in length
* 18751 18850: gap of unknown length
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* 20141 20240: gap of unknown length
* 20241 21555: contig of 1315 bp in length
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Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 516 TTTTCCACACAGCAGAGAGAA 537
Db 6525 TTTTCCACACAGCAGAGAGAA 6546

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RESULT 32
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WPCOMMENT
Sequence split into 4 fragments LOCUS AC098517 Accession AC098517

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AC098517_2        200001    310000
AC098517_3        300001    384467
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DEFINITION Rattus norvegicus clone CH230-6844, *** SEQUENCING IN PROGRESS ***
ACCESSION AC098517
VERSION AC098517.5 GI:21729566
KEYWORDS HTG; HTGS; PHASEL.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 384467)
REFERENCE 1 Muzny D.M., Adams C., Adio-Oduola B., Alt-osman F.R., Allen C.,
AUTHORS Albrooks S.L., Amarantunge H.C., Are J.R., Ayele M., Banks T.,
Barbarta V., Benton J., Bimaye K., Blankenburg K., Bonni D.,
Bouck J., Bowie S., Brieleva M., Brown E., Brown M., Bryant N.P.,
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Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C.,
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Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
DeLaney K.R., Delgado O., Denna A.L., Ding Y., Dinh H.H.,
Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
Earhart C., Edgar D., Edwards C.C., Elhaj C., Escoto M.,
Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frintz P.,
Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R.,
Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K.,
Harris C., Harris K., Hart M., Haylak P., Hawes A., Hernandez J.,
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Maheshwari M., Mapua P., Martin R., Martindale A., Martinez B.,
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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
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Scherer,S., Scott,G., Shen,H., Shooshari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S.,
Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 384467)
Worley,K.C.
Direct Submission
Submitted (24-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 384467)
Worley,K.C.
Direct Submission
Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:18138579.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information
Center project name: GHGA
Center clone name: CH230-68A4
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Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 232783 bases at least Q40
Consensus quality: 246684 bases at least Q30
Consensus quality: 258695 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 171 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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4808 4907: gap of unknown length
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41028 42609: contig of 1582 bp in length
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42710 43867: contig of 1158 bp in length
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Query Match 3.5%; Score 22; DB 2; Length 110000;
 Best Local Similarity 100.0%; Pired. No. 0.48;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 604 GTGNAAAAAAAAAAAAAAAAAAAA 625
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RESULT 33
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 LOCUS Mouse DNA sequence from clone RP23-24338 on chromosome 11, complete
 DEFINITION sequence.
 ACCESSION AL596180 GI:20135751
 VERSION AL596180.7
 KEYWORDS HTG.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 111914)
 TROMANS, A.
 DIRECT SUBMISSION
 Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequests@sanger.ac.uk
 humuery@sanger.ac.uk
 On Apr 10, 2002 this sequence version replaced g1:19068255.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30).
 An attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em., EMBL; SW,
 SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-24338 is
 from the RPI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see http://www.chori.org/dacpac/home.htm
 VECTOR: pBAC3.6.

FEATURES

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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 385 AGACAGAGAGAGAGAGAGAGAGAGACACA 406

Db 97095 AGACAGAGAGAGAGAGAGAGAGAGACACA 97116

RESULT 34
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 DEFINITION *** 75 unordered pieces.
 AC103498
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 AC103498.3 GI:21728661
 HTG: HTGS_PHASE1.
 KEYWORDS Norway rat.
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 114382)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
 Albrooks, S.L., Amarantunga, H.C., Are, J.R., Ayale, M., Banks, T.,
 Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
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 Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
 Homel, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L.E.,
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 Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
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 Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I.,
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 Sutton, A., Syarik, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalongo, D., Vinsion, R., Wang, O.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wlezyk, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 114382)
 Worley, K.C.
 Direct Submission
 Submitted (25-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 114382)
 Worley, K.C.
 Direct Submission
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced g1:17973362.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center Project name: GHTP
Center Clone name: CH230-31P10
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 34683 bases at least Q40
Consensus quality: 37389 bases at least Q30
Consensus quality: 39242 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1055: contig of 1055 bp in length
* 1056 1155: gap of unknown length
* 1156 2293: contig of 1138 bp in length
* 2294 2393: gap of unknown length
* 2394 3428: contig of 1034 bp in length
* 3428 3527: gap of unknown length
* 3528 4697: contig of 1170 bp in length
* 4698 4798: gap of unknown length
* 4798 5881: contig of 1084 bp in length
* 5882 7043: gap of unknown length
* 7044 7143: contig of 1062 bp in length
* 7144 8388: gap of unknown length
* 8389 8488: contig of 1245 bp in length
* 8489 9555: gap of unknown length
* 9556 10774: contig of 1067 bp in length
* 10775 10874: gap of unknown length
* 10875 12131: contig of 1119 bp in length
* 12132 12331: gap of unknown length
* 12332 13467: contig of 1257 bp in length
* 13468 13567: gap of unknown length
* 13568 14710: contig of 1236 bp in length
* 14711 14810: gap of unknown length
* 14811 15845: contig of 1143 bp in length
* 15846 15945: gap of unknown length
* 15946 16981: contig of 1035 bp in length
* 16982 17081: gap of unknown length
* 17082 18114: contig of 1036 bp in length
* 18115 18214: gap of unknown length
* 18215 19548: contig of 1033 bp in length
* 19549 19648: gap of unknown length
* 19649 20553: contig of 1334 bp in length
* 20554 20753: gap of unknown length
* 20754 21925: contig of 1005 bp in length
* 21926 22025: gap of unknown length
* 22026 23103: contig of 1172 bp in length
* 23104 23203: gap of unknown length
* 23204 24208: contig of 1078 bp in length
* 24209 24308: gap of unknown length
* 24309 25459: contig of 1005 bp in length
* 25460 25559: gap of unknown length
* 25560 26562: contig of 1151 bp in length
* 26563 26662: gap of unknown length
* 26663 27802: contig of 1003 bp in length
* 27803 27902: gap of unknown length
* 27903 29043: contig of 1140 bp in length
* 29043: contig of 1141 bp in length

29044 29144 29143: gap of unknown length
* 29144 30740 30739: contig of 1596 bp in length
* 30740 30839: gap of unknown length
* 30839 31919: contig of 1080 bp in length
* 31919 31920: gap of unknown length
* 31920 32020 32019: gap of unknown length
* 32020 33237: contig of 1218 bp in length
* 33237 33338 33337: gap of unknown length
* 33338 34527: contig of 1190 bp in length
* 34527 34627: gap of unknown length
* 34627 35826: contig of 1199 bp in length
* 35826 35927: gap of unknown length
* 35927 37110: contig of 1184 bp in length
* 37110 37210: gap of unknown length
* 37210 37211 37210: gap of unknown length
* 37211 38305: contig of 1096 bp in length
* 38305 38307 38306: gap of unknown length
* 38307 38407: gap of unknown length
* 38407 39787: contig of 1380 bp in length
* 39787 39886: gap of unknown length
* 39886 40893: contig of 1007 bp in length
* 40893 40994: gap of unknown length
* 40994 42175: gap of unknown length
* 42175 42176 42175: contig of 1182 bp in length
* 42176 42275: gap of unknown length
* 42275 43317: contig of 1042 bp in length
* 43317 43417: gap of unknown length
* 43417 44540: contig of 1123 bp in length
* 44540 44541 44540: gap of unknown length
* 44541 44640: gap of unknown length
* 44640 44641 44640: contig of 1655 bp in length
* 44641 46295: gap of unknown length
* 46295 46395: gap of unknown length
* 46395 47604: contig of 1209 bp in length
* 47604 47605 47604: gap of unknown length
* 47605 49329: contig of 1625 bp in length
* 49329 49429: gap of unknown length
* 49429 51093: contig of 1664 bp in length
* 51093 51193: gap of unknown length
* 51193 51994 51993: gap of unknown length
* 51994 52853: contig of 1660 bp in length
* 52853 52953: gap of unknown length
* 52953 53956: contig of 1003 bp in length
* 53956 54057: gap of unknown length
* 54057 55149 55148: contig of 1092 bp in length
* 55149 55248: gap of unknown length
* 55248 56535: contig of 1287 bp in length
* 56535 56635: gap of unknown length
* 56635 58322: contig of 1687 bp in length
* 58322 58423: gap of unknown length
* 58423 58521: gap of unknown length
* 58521 59751: contig of 1229 bp in length
* 59751 60986: gap of unknown length
* 60986 61096: contig of 1245 bp in length
* 61096 62321: gap of unknown length
* 62321 62421: contig of 1225 bp in length
* 62421 63629: gap of unknown length
* 63629 63729: contig of 1208 bp in length
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* 65157 65257: contig of 1428 bp in length
* 65257 65258 65257: gap of unknown length
* 65258 66273: contig of 1016 bp in length
* 66273 66374: gap of unknown length
* 66374 68016: contig of 1643 bp in length
* 68016 68116: gap of unknown length
* 68116 68117 68116: gap of unknown length
* 68117 69190: contig of 1074 bp in length
* 69190 69191 69190: gap of unknown length
* 69191 71362: contig of 2072 bp in length
* 71362 69291 69291: gap of unknown length

Query Match
Best Local Similarity 100.0% Pred. No. 0.49; Length 114382;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3.5%
QY 604 GTGNAAAAAAAAAAAAAA 625
Db 23893 GTGNAAAAAAAAAAAAAA 23914

RESULT 35
AC094168/C
LOCUS AC094168 115643 bp DNA linear HTG 07-JUL-2002

DEFINITION Rattus norvegicus clone CH230-2A19, *** SEQUENCING IN PROGRESS ***
 76 unordered pieces.
 ACCESSION AC094168
 VERSION AC094168.3 GI:21700340
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 115643)
 AUTHORS Wuzny,D.M., Adams,C., Adlo-Oduola,B., All-oman,F.R., Allen,C., Alsbrooks,S.L., Amaralung,H.C., Are,J.R., Ayala,M., Banks,T., Barbala,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinn,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gotrell,J.H., Guevara,W., Gunatane,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havila,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsl,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratoch,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtenarge,O., Lieu,C., Liu,J., Liu,W., Loussegod,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,N., Okunolu,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.U., Qulies,M., Ren,X., Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherag,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Swatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D., Weinstein,G., and Gibbs,R.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 115643)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 115643)
 REFERENCE 3 (bases 1 to 115643)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Jul 6, 2002 this sequence version replaced gi:17940880.

COMMENT ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GACW

Center clone name: CH230-2A19
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 32912 bases at least Q40
 Consensus quality: 35872 bases at least Q30
 Consensus quality: 38277 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a "working draft" sequence. It currently
 * consists of 76 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1042:	contig of 1042 bp in length
1043	1142:	gap of unknown length
1143	2403:	contig of 1261 bp in length
2404	2503:	gap of unknown length
2504	3564:	contig of 1061 bp in length
3565	3664:	gap of unknown length
3665	4714:	contig of 1050 bp in length
4715	4814:	gap of unknown length
4815	6039:	contig of 1225 bp in length
6040	6139:	gap of unknown length
6140	7202:	contig of 1063 bp in length
7203	7302:	gap of unknown length
7303	8504:	contig of 1202 bp in length
8505	8604:	gap of unknown length
8605	9723:	contig of 1119 bp in length
9724	9823:	gap of unknown length
9824	10857:	contig of 1034 bp in length
10858	10957:	gap of unknown length
10958	12147:	contig of 1190 bp in length
12148	12247:	gap of unknown length
12248	13392:	contig of 1045 bp in length
13293	13392:	gap of unknown length
13393	14554:	contig of 1162 bp in length
14555	14654:	gap of unknown length
14655	15795:	contig of 1141 bp in length
15796	15895:	gap of unknown length
15896	16984:	contig of 1089 bp in length
16985	17084:	gap of unknown length
17085	18124:	contig of 1040 bp in length
18125	18224:	gap of unknown length
18225	19344:	contig of 1120 bp in length
18226	19344:	gap of unknown length
19345	19444:	gap of unknown length
19445	20653:	contig of 1209 bp in length
20654	20753:	gap of unknown length
20754	21854:	contig of 1101 bp in length
21855	21954:	gap of unknown length
21956	23134:	contig of 1180 bp in length
23135	23234:	gap of unknown length
23235	24464:	contig of 1230 bp in length
24465	24564:	gap of unknown length
24565	25726:	contig of 1162 bp in length
25727	25826:	gap of unknown length
25827	26904:	contig of 1078 bp in length
26905	27004:	gap of unknown length
27005	28246:	contig of 1242 bp in length
28247	28346:	gap of unknown length
28347	29492:	contig of 1146 bp in length
29493	29592:	gap of unknown length
29593	30720:	contig of 1128 bp in length
30721	30820:	gap of unknown length
30821	31888:	contig of 1068 bp in length
31889	31988:	gap of unknown length
31989	33613:	contig of 1625 bp in length
33614	33713:	gap of unknown length

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*      33714      34755: contig of 1042 bp in length
*      34756      34855: gap of unknown length
*      34856      36263: contig of 1408 bp in length
*      36264      36363: gap of unknown length
*      36364      37976: contig of 1613 bp in length
*      37977      38076: gap of unknown length
*      38077      39087: contig of 1011 bp in length
*      39088      39187: gap of unknown length
*      40414      40514: gap of unknown length
*      40515      41828: contig of 1314 bp in length
*      41829      41928: gap of unknown length
*      41929      43037: contig of 1109 bp in length
*      43038      43137: gap of unknown length
*      43138      44396: contig of 1259 bp in length
*      44397      46018: contig of 1522 bp in length
*      46019      46118: gap of unknown length
*      46119      47247: contig of 1129 bp in length
*      47248      47347: gap of unknown length
*      47348      48380: contig of 1033 bp in length
*      48381      49648: gap of unknown length
*      49649      49748: gap of unknown length
*      49749      51362: contig of 1614 bp in length
*      51363      51462: gap of unknown length
*      51463      52841: contig of 1379 bp in length
*      52842      52941: gap of unknown length
*      52941      54023: contig of 1082 bp in length
*      54024      55123: gap of unknown length
*      55124      55625: contig of 1502 bp in length
*      55626      55725: gap of unknown length
*      55726      56747: gap of unknown length
*      56748      56847: gap of unknown length
*      56848      58321: contig of 1474 bp in length
*      58322      58421: gap of unknown length
*      58422      59874: contig of 1453 bp in length
*      59875      59974: gap of unknown length
*      59975      61027: contig of 1053 bp in length
*      61028      61127: gap of unknown length
*      61128      62295: contig of 1168 bp in length
*      62296      63395: gap of unknown length
*      63396      63706: contig of 1311 bp in length
*      63707      63806: gap of unknown length
*      63807      65223: contig of 1417 bp in length
*      65224      65323: gap of unknown length
*      65324      66551: contig of 1328 bp in length
*      66552      66751: gap of unknown length
*      66752      68012: contig of 1261 bp in length
*      68013      68112: gap of unknown length
*      68113      69345: contig of 1133 bp in length
*      69346      69345: gap of unknown length
*      71454: contig of 2109 bp in length

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Query Match      3.5%: Score 22: DB 2: Length 115643;
Best Local Similarity 100.0%: Pred. No. 0.49;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Oy 604 GTGNNAAAAAAAAAAAAA 625
Db 19119 GTGNNAAAAAAAAAAAAA 19098

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RESULT 36
AC123419      126363 bp      DNA      linear      HTG 23-JUL-2002
LOCUS      Rattus norvegicus clone CH230-248113, *** SEQUENCING IN PROGRESS
DEFINITION
AC123419
AC123419
AC123419.2 GI:21902987
VERSION
KEYWORDS
HTG: HTGS, PHASEL
SOURCE
Rattus norvegicus
ORGANISM
Rattus norvegicus

```

REFERENCE

AUTHORS

- Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
- 1 (bases 1 to 126363)
- Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C., Alsbrooks,S.L., Amarantune,H.C., Are,J.R., Ayele,M., Banks,T., Barbarella,J., Benton,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Kocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Garrel,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hayes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homai,E., Howard,S., Huber,J., Hulik,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Louieged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabac,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okunnu,G., Orgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczek,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G., and Gibbs,R.
- Unpublished
- Direct Submission
- 2 (bases 1 to 126363)
- Worley,K.C.
- Direct Submission
- Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
- 3 (bases 1 to 126363)
- Worley,K.C.
- Direct Submission
- Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
- On Jul 18, 2002 this sequence version replaced gi:21240349.

COMMENT

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXDX
Center clone name: CH230-248113
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 85769 bases at least Q40
Consensus quality: 89524 bases at least Q30

```


Consensus quality: 91611 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 43 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1199: contig of 1199 bp in length
 * 1200 1299: gap of unknown length
 * 1300 3029: contig of 1730 bp in length
 * 3030 3129: gap of unknown length
 * 3130 4251: contig of 1122 bp in length
 * 4252 4351: gap of unknown length
 * 4352 5817: contig of 1466 bp in length
 * 5818 5917: gap of unknown length
 * 5918 6919: contig of 1002 bp in length
 * 6920 7019: gap of unknown length
 * 7020 8031: contig of 1012 bp in length
 * 8032 8131: gap of unknown length
 * 8132 9676: contig of 1545 bp in length
 * 9677 9776: gap of unknown length
 * 9777 11503: contig of 1727 bp in length
 * 11504 11603: gap of unknown length
 * 11604 12879: contig of 1276 bp in length
 * 12880 12979: gap of unknown length
 * 12980 14377: contig of 1398 bp in length
 * 14378 14477: gap of unknown length
 * 14478 15552: contig of 1075 bp in length
 * 15553 15652: gap of unknown length
 * 15653 17398: contig of 1746 bp in length
 * 17399 17498: gap of unknown length
 * 17499 18639: contig of 1141 bp in length
 * 18640 18739: gap of unknown length
 * 18740 19760: contig of 1021 bp in length
 * 19761 19860: gap of unknown length
 * 19861 21195: contig of 1335 bp in length
 * 21196 21295: gap of unknown length
 * 21296 22407: contig of 1112 bp in length
 * 22408 22507: gap of unknown length
 * 22508 23661: contig of 1154 bp in length
 * 23662 23761: gap of unknown length
 * 23762 25364: contig of 1603 bp in length
 * 25365 25464: gap of unknown length
 * 25465 27488: contig of 2024 bp in length
 * 27489 27588: gap of unknown length
 * 27589 30486: contig of 2898 bp in length
 * 30487 30586: gap of unknown length
 * 30587 32686: contig of 2100 bp in length
 * 32687 32786: gap of unknown length
 * 32787 34902: contig of 2116 bp in length
 * 34903 35002: gap of unknown length
 * 35003 36617: contig of 1615 bp in length
 * 36618 36717: gap of unknown length
 * 36719 38714: contig of 1997 bp in length
 * 38715 38814: gap of unknown length
 * 38815 40366: contig of 1552 bp in length
 * 40367 40466: gap of unknown length
 * 40467 43354: contig of 2888 bp in length
 * 43355 43454: gap of unknown length
 * 43455 45904: contig of 2350 bp in length
 * 45905 48611: contig of 2707 bp in length
 * 48612 48711: gap of unknown length
 * 48712 51541: contig of 2830 bp in length
 * 51542 51642: gap of unknown length
 * 51643 54649: contig of 3008 bp in length
 * 54650 56789: gap of unknown length
 * 56790 56789: contig of 2040 bp in length

FEATURES

source

BASE COUNT 34487 a 24052 c 23828 g 37023 t 6973 others

ORIGIN

Query Match 3.5%; Score 22; DB 2; Length 126363;
 Best Local Similarity 100.0%; Pred. No. 0.49;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 ACAGCAGAGAGAAATTAAACA 544

Db 49343 ACAAGCAGAGAGAAATTAAACA 49364

RESULT 37

AL445433

LOCUS

DEFINITION

Human DNA sequence from clone Rpl1-234M17 on chromosome 1, complete

sequence.

ACCESSION

AL445433

VERSION

AL445433.14

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

Barlow, K.

AUTHORS

TITLE

JOURNAL

COMMENT

56790 56889: gap of unknown length
 * 56890 60517: contig of 3628 bp in length
 * 60518 60617: gap of unknown length
 * 60618 64008: contig of 3391 bp in length
 * 64009 64108: gap of unknown length
 * 64109 67932: contig of 3824 bp in length
 * 67933 68032: gap of unknown length
 * 68033 72032: contig of 4000 bp in length
 * 72033 72132: gap of unknown length
 * 72133 75362: contig of 3210 bp in length
 * 75363 75462: gap of unknown length
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 * 80985 81084: gap of unknown length
 * 81085 88023: contig of 6939 bp in length
 * 88024 88123: gap of unknown length
 * 88124 93952: contig of 5829 bp in length
 * 93953 94052: gap of unknown length
 * 94053 101325: contig of 7272 bp in length
 * 101325 101424: gap of unknown length
 * 101425 107850: contig of 6426 bp in length
 * 107851 107950: gap of unknown length
 * 107951 115979: contig of 8029 bp in length
 * 115980 116079: gap of unknown length
 * 116080 126363: contig of 10284 bp in length.
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 /db_xref="taxon:10116"
 /clone="CH230-248113"

AL445433 138918 bp DNA linear PRI 20-APR-2001
 Human DNA sequence from clone Rpl1-234M17 on chromosome 1, complete
 sequence.
 AL445433
 AL445433.14 GI:13751981
 HTG.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 138918)
 Barlow, K.
 Direct Submission
 Submitted (20-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Apr 22, 2001 this sequence version replaced g1:12329466.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following


```

repeat_region /note="MIR repeat: matches 3. .260 of consensus"
34736. .38491
/note="LIPAB repeat: matches 3. .3444 of consensus"
repeat_region /note="LIPAB repeat: matches 3. .3444 of consensus"
34736. .38491
/note="LIPAB repeat: matches 822. .969 of consensus"
repeat_region /note="LIPAB repeat: matches 822. .969 of consensus"
34736. .38491
/note="LIPAB repeat: matches 3512. .5140 of consensus"
repeat_region /note="LIPAB repeat: matches 3512. .5140 of consensus"
34736. .38491
/note="LIPAB repeat: matches 1. .304 of consensus"
repeat_region /note="LIPAB repeat: matches 1. .304 of consensus"
34736. .38491
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repeat_region /note="LIPAB repeat: matches 5942. .6163 of consensus"
34736. .38491
/note="LIPAB repeat: matches 2693. .2710 of consensus"
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34736. .38491
/note="LIPAB repeat: matches 1. .293 of consensus"
repeat_region /note="LIPAB repeat: matches 1. .293 of consensus"
34736. .38491
/note="LIPAB repeat: matches 2673. .2693 of consensus"
repeat_region /note="LIPAB repeat: matches 2673. .2693 of consensus"
34736. .38491
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repeat_region /note="LIPAB repeat: matches 2. .345 of consensus"
34736. .38491
/note="LIPAB repeat: matches 42782. .42805
repeat_region /note="LIPAB repeat: matches 42782. .42805
34736. .38491
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34736. .38491
3.58; Score 22; DB 9; Length 138918;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Y 397 GAAGAACACAGATGAGACAC 418
 Db 36368 GAAGAACACAGATGAGACAC 36389

RESULT 38
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LOCUS
DEFINITION Rattus norvegicus clone CH230-19217, *** SEQUENCING IN PROGRESS
ACCESSION AC114056
VERSION AC114056.3 GI:22218410
KEYWORDS HTG: HTGS: PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 158728)
 Muzny, D., Marle, Metzker, M., Lee, A., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalbech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Bismail, K., Blair, J., Blankenship, K., Blythe, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Fraser, C., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hoggins, M.,
 Hollins, B., Howells, S., Hui, S., Hume, J., Idlebird, D., Jackson, A.,
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyvet, A.,
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowals, C., Kraft, C., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorensheva, L., Louised, H., Lozano, R., Lu, X., Lu, X., Ma, J.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Manungu, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawin, S., McLeod, M., McNeill, T., Meenen, E., Milsosavljevic, A.,
 Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
 Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
 Newton, N., Nguyen, N., Norris, S., Naoxelen, O., Okunou, G.,
 Olariunsaogun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
 Perez, A., Perez, L., Pfankuch, C., Plopper, F., Polinder, A.,
 Popovic, D., Primus, E., Pu, L., Paz, M., Qilroz, J., Rachlin, E.,
 Reeves, K., Regier, M., Reih, R., Reilly, B., Reilly, M., Ren, Y.,
 Reuter, M., Richards, S., Riggs, F., Rives, C., Rodney, T., Rojas, A.,
 Rose, M., Rose, R., Ruiz, S., Sanders, W., Saverly, G., Scherer, S.,
 Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
 Sisson, I., Sitter, C., Sma, J., Sneed, A., Sodergren, E.,
 Song, X., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,
 Stratak, A., Tabor, P., Taylor, C., Taylor, T., Vera, V., Villaseña, D.,
 Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D.,
 Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
 Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleciyk, R.,
 Woodden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, X.,
 Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
 Zhao, S., Zhou, D., von Niederhausern, A., Weiss, R., Smith, D., R.,
 Holt, R., Smith, H., O., Weinstein, G., and Gibbs, R., A.
 Direct Submission
 2 (bases 1 to 158728)
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 158728)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 14, 2002 this sequence version replaced gi:21731615.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GKMZ
 Center clone name: CH230-19217
 ----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap, version 0.990329
 Consensus quality: 92840 bases at least Q40
 Consensus quality: 100722 bases at least Q30
 Consensus quality: 105423 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a "working draft" sequence. It currently
 * consists of 80 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1218: contig of 1218 bp in length
 * 1219 1318: gap of unknown length
 * 1319 2614: contig of 1296 bp in length
 * 2714: gap of unknown length
 * 2715 3714: gap of unknown length
 * 3715 3814: gap of unknown length
 * 3815 5073: contig of 1259 bp in length
 * 5074 5174: gap of unknown length
 * 5174 6512: contig of 1339 bp in length

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* 6513 6612: gap of unknown length
* 6613 7616: contig of 1004 bp in length
* 7617 7616: gap of unknown length
* 7717 8932: contig of 1216 bp in length
* 8933 9032: gap of unknown length
* 9033 10037: contig of 1005 bp in length
* 10038 10137: gap of unknown length
* 10138 11137: contig of 1000 bp in length
* 11138 11287: gap of unknown length
* 11288 12580: contig of 1343 bp in length
* 12581 14096: gap of unknown length
* 14097 14196: gap of 1416 bp in length
* 14197 15253: contig of 1057 bp in length
* 15254 15353: gap of unknown length
* 15354 16871: contig of 1518 bp in length
* 16872 16972: gap of unknown length
* 16972 18101: contig of 1130 bp in length
* 18102 18201: gap of unknown length
* 18202 19384: contig of 1183 bp in length
* 19385 19484: gap of unknown length
* 19485 20717: contig of 1233 bp in length
* 20718 20817: gap of unknown length
* 20818 22030: contig of 1213 bp in length
* 22031 22130: gap of unknown length
* 22131 23543: contig of 1413 bp in length
* 23544 23643: gap of unknown length
* 23644 24802: contig of 1159 bp in length
* 24803 24902: gap of unknown length
* 24903 25902: contig of 1000 bp in length
* 25903 26002: gap of unknown length
* 26003 28216: contig of 2214 bp in length
* 28217 28316: gap of unknown length
* 28317 29850: contig of 1534 bp in length
* 29851 30954: gap of unknown length
* 30955 31094: contig of 1044 bp in length
* 31095 32140: gap of unknown length
* 32141 32240: gap of unknown length
* 32241 33260: contig of 1020 bp in length
* 33261 33360: gap of unknown length
* 33361 34416: contig of 1056 bp in length
* 34417 34516: gap of unknown length
* 34517 36041: contig of 1525 bp in length
* 36042 36141: gap of unknown length
* 36142 37723: contig of 1582 bp in length
* 37724 37823: gap of unknown length
* 37824 38973: contig of 1150 bp in length
* 38974 39073: gap of unknown length
* 39074 40207: gap of 1134 bp in length
* 40208 40307: gap of unknown length
* 40308 42015: contig of 1708 bp in length
* 42016 42115: gap of unknown length
* 42116 44165: contig of 2050 bp in length
* 44166 44265: gap of unknown length
* 44266 45386: contig of 1121 bp in length
* 45387 45486: gap of unknown length
* 45487 47574: contig of 2088 bp in length
* 47575 47674: gap of unknown length
* 47675 48734: contig of 1060 bp in length
* 48735 48834: gap of unknown length
* 48835 50763: contig of 1929 bp in length
* 50764 50863: gap of unknown length
* 50864 52051: contig of 1188 bp in length
* 52052 53549: gap of unknown length
* 53549 53550: contig of 1398 bp in length
* 53550 55005: gap of unknown length
* 55005 55105: contig of 1356 bp in length
* 55106 56212: gap of unknown length
* 56213 56312: gap of unknown length
* 56313 57411: contig of 1099 bp in length
* 57412 57511: gap of unknown length

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```

Query Match      3.5%; Score 22; DB 2; Length 158728;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 604 GTGNNAAAAAAAAAAAAAAAA 625
Db 109216 GTGNNAAAAAAAAAAAAAAAA 109237
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RESULT 39
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LOCUS
DEFINITION
Homo sapiens chromosome 1 clone RP11-76a15 map 1, WORKING DRAFT
SEQUENCE, 38 unordered pieces.
AC022823
VERSION
AC022823.3 GI:7382473
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

```

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REFERENCE
1 (bases 1 to 160008)
AUTHORS
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 160008)
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckwith,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Chepel,Y., Colangelo,M., Collins,S., Collins,M., Cooke,P.,
DeArrelano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,L.,
Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehotzky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGuirk,A., McKernan,K.,
McNeeters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,D., Testaye,S., Theodore,J.,
Tirelli,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

```

```

TITLE
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL
Direct Submission

```

```

REFERENCE
3 (bases 1 to 160008)
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campoliano,A., Castle,A., Chepel,Y., Colangelo,M., Collins,S.,
Collins,M., Cooke,P., DeArrelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
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Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,

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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 397 GAAAAACACGATGAGACAC 418
Db 39279 GAAAAACACGATGAGACAC 39258

RESULT 40
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DEFINITION AC020693
SEQUENCE 8 unordered pieces.
AC020693 GI:7249430
VERSION AC020693.3
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
TITLE 1 (bases 1 to 163932)
JOURNAL Homo sapiens chromosome 6, clone RP11-574H19
AUTHORS Unpublished
2 (bases 1 to 163932)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deatellano, K., Dewar, K., Domingo, M., Doyle, M., Feresstor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Hearford, A., Horton, L.,
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Landers, T., Lehoczy, J., Levine, R., Liu, C., Li, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T., M. Peterson, K.,
Pierre, N., Pisanli, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 163932)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Chapel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Labocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mienna, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,

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TITLE
JOURNAL
COMMENT
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L5272
Center clone name: 574_H19
----- Summary Statistics -----
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159231 bases at least Q40
Consensus quality: 161639 bases at least Q30
Consensus quality: 162468 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 163332; sum-of-ctrls
Quality coverage: 5.4 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-ctrls
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 2756: contig of 2756 bp in length
* 2757 2856: gap of 100 bp
* 2857 7124: contig of 4266 bp in length
* 7125 7224: gap of 100 bp
* 7225 14958: contig of 7734 bp in length
* 14959 15058: gap of 100 bp
* 15059 21054: contig of 5996 bp in length
* 21055 31520: gap of 100 bp
* 31521 31620: contig of 10366 bp in length
* 31621 58637: contig of 27017 bp in length
* 58638 58737: gap of 100 bp
* 58738 110374: contig of 51637 bp in length
* 110375 110474: gap of 100 bp
* 110475 163932: contig of 53458 bp in length.
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Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="6"
/map="6"
/clone="RP11-574H19"
/clone_id="RP11 Human Male BAC"
1. 2756
/note="assembly-fragment
clone_end:77
vector_side:right"
2857..7124
/note="assembly-fragment"
7225..14958
/note="assembly-fragment"
15059..21054

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misc_feature      /note="assembly_fragment"
                  21155..31520
                  /note="assembly_fragment"
misc_feature      31621..58637
                  /note="assembly_fragment"
                  clone_end:SP6
                  vector_side:left"
misc_feature      58738..110374
                  /note="assembly_fragment"
                  110475..163932
                  /note="assembly_fragment"
BASE COUNT      51932 a 30930 c 30043 g 50325 t 702 others
ORIGIN
Query Match      3.5%: Score 22; DB 2; Length 163932;
Best Local Similarity 100.0%; Pident. NO. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 397 GAAACACACACATGAGAACAC 418
Db 124291 GAAACACACACATGAGAACAC 124312

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RESULT 41
AC096152/c
LOCUS
DEFINITION      Rattus norvegicus clone CH230-10H22, *** SEQUENCING IN PROGRESS
***, 77 unordered pieces.
AC096152
VERSION          AC096152.4 GI:21723293
KEYWORDS
SOURCE           Norway rat.
ORGANISM        Rattus norvegicus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 194402)
Munry,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbata,J., Benton,J., Blmage,K., Blankenburg,K., Bonin,D.,
Bouck,J., Bowler,S., Bivela,M., Brown,E., Brown,M., Bryant,N.P.,
Bunyah,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Dayla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeJaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Eathart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,U., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Hawlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulky,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S.,
Karlsom,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,D., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okunolu,G.,
Oregunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Ruiz,S., Savelly,G.,
Rivers,M., Rojas,A., RojudoKan,I., Rolfe,M., Rolfe,S., Savely,G.,
Schier,S., Scott,G., Shen,H., Shoshitari,N., Sisson,T.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,J., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,N., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

```

```

REFERENCE
AUTHORS
JOURNAL

```

```

COMMENT

```

```

Mang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wlezyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 194402)
Worley,K.C.
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 194402)
Worley,K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17943838.
----- genome center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GEN5
Center clone name: CH230-10H22
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 127428 bases at least Q40
Consensus quality: 136154 bases at least Q30
Consensus quality: 142855 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1394: contig of 1394 bp in length
1395
1494: gap of unknown length
1495
2724: contig of 1230 bp in length
2725
4385: gap of unknown length
4386
4485: gap of unknown length
4486
5770: contig of 1285 bp in length
5771
5870: gap of unknown length
5871
7046: contig of 1176 bp in length
7047
7146: gap of unknown length
7147
8157: contig of 1011 bp in length
8158
8257: gap of unknown length
8258
9501: contig of 1244 bp in length
9502
9601: gap of unknown length
9602
10892: contig of 1291 bp in length
10893
10992: gap of unknown length
10993
12125: contig of 1133 bp in length
12126
12225: gap of unknown length
12226
13686: contig of 1461 bp in length
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13786: gap of unknown length
13787
14899: contig of 1113 bp in length
14900
14999: gap of unknown length
15000
16352: contig of 1353 bp in length
16353
16452: gap of unknown length
16453
17981: contig of 1539 bp in length
17982
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19496: gap of unknown length

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19497 20531: contig of 1035 bp in length
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22386 22485: gap of unknown length
22486 24404: contig of 1919 bp in length
24405 24504: gap of unknown length
24505 25961: contig of 1457 bp in length
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27593 29406: gap of unknown length
29407 29506: contig of 1714 bp in length
29507 31006: gap of unknown length
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31107 32452: contig of 1346 bp in length
32453 32552: gap of unknown length
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35948 37058: contig of 1011 bp in length
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40960 41059: gap of unknown length
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59423 59522: gap of unknown length
59523 61124: contig of 1602 bp in length
61125 61224: gap of unknown length
61225 63082: contig of 1858 bp in length
63083 63182: gap of unknown length
63183 63422: contig of 2240 bp in length
63423 65522: gap of unknown length
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68809 70798: contig of 1991 bp in length
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70899 74292: contig of 3394 bp in length
74293 74392: gap of unknown length
74393 76510: contig of 2118 bp in length
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76611 80910: contig of 4300 bp in length
80911 81010: gap of unknown length
81011 83473: contig of 2463 bp in length
83474 83573: gap of unknown length
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85681 85780: gap of unknown length
85781 88048: contig of 2268 bp in length
88049 88148: gap of unknown length
88149 90891: contig of 2743 bp in length
90892 94419: gap of unknown length
94419 94419: contig of 3428 bp in length

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Query Match
Best Local Similarity 100.0%, Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 523 ACAAGCAGAGAGATTATACA 544
DB 126288 ACAAGCAGAGAGATTATACA 126267

RESULT 42
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LOCUS
DEFINITION
Rattus norvegicus clone CH230-101c21, *** SEQUENCING IN PROGRESS
ACCESSION
AC107560.3 GI:21731887
VERSION
AC107560.3
KEYWORDS
HTG; HTGS; PHASEL.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 196863)
REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,
Albrooks,S.L., Amarantunga,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimage,K.C., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowler,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
David,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Dudin,K.J.,
Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoen,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtenarge,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
Lorado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,S., Oguh,M., Okunoye,G.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okunoye,G.,
Oragunye,N., Oyedero,R., Pace,A., Payton,B., Peely,J., Perez,L.,
Peterson,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ruiz,S.,
Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,T.,
Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Swalek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williams,A., Wleczyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
TITLE
JOURNAL
Direct Submission
REFERENCE
2 (bases 1 to 196863)

```


AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Worley, R.C.
Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 196863)
Worley, R.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:18846298.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GLED
Center clone name: CH230-101C21
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 153108 bases at least Q40
Consensus quality: 159647 bases at least Q30
Consensus quality: 166406 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1583: contig of 1583 bp in length
* 1584 1683: gap of unknown length
* 1684 3141: contig of 1458 bp in length
* 3142 3241: gap of unknown length
* 3242 4603: contig of 1362 bp in length
* 4604 4703: gap of unknown length
* 4704 5942: contig of 1239 bp in length
* 5943 6042: gap of unknown length
* 6043 7195: contig of 1154 bp in length
* 7197 7296: gap of unknown length
* 7297 8768: contig of 1472 bp in length
* 8769 8868: gap of unknown length
* 8869 10096: contig of 1228 bp in length
* 10097 10196: gap of unknown length
* 10197 11583: contig of 1387 bp in length
* 11584 11683: gap of unknown length
* 11684 13846: contig of 2163 bp in length
* 13847 13946: gap of unknown length
* 13947 15263: contig of 1317 bp in length
* 15264 15363: gap of unknown length
* 15364 17140: contig of 1777 bp in length
* 17141 17240: gap of unknown length
* 17241 18396: contig of 1156 bp in length
* 18397 18496: gap of unknown length
* 18497 20297: contig of 1801 bp in length
* 20298 20397: gap of unknown length
* 20398 21828: contig of 1431 bp in length
* 21829 21928: gap of unknown length
* 21929 23391: contig of 1463 bp in length
* 23392 23491: gap of unknown length
* 23492 25297: contig of 1806 bp in length
* 25298 25397: gap of unknown length
* 25398 27800: contig of 2403 bp in length
* 27801 27900: gap of unknown length
* 27901 29238: contig of 1338 bp in length

29239 29338: gap of unknown length
* 29339 31283: contig of 1945 bp in length
* 31284 31384: gap of unknown length
* 31384 32976: contig of 1593 bp in length
* 32977 33077: gap of unknown length
* 33077 35169: contig of 2093 bp in length
* 35170 35270: gap of unknown length
* 35270 36663: contig of 1394 bp in length
* 36663 36763: gap of unknown length
* 36764 39319: contig of 2556 bp in length
* 39320 39419: gap of unknown length
* 39420 41952: contig of 2533 bp in length
* 41953 42052: gap of unknown length
* 42053 43696: contig of 1644 bp in length
* 43697 43797: gap of unknown length
* 43797 45388: contig of 1592 bp in length
* 45389 45488: gap of unknown length
* 45489 47654: contig of 2166 bp in length
* 47655 47754: gap of unknown length
* 47755 50476: contig of 2722 bp in length
* 50477 50576: gap of unknown length
* 50577 53202: contig of 2625 bp in length
* 53202 53301: gap of unknown length
* 53302 55187: contig of 1886 bp in length
* 55188 55287: gap of unknown length
* 55288 57206: contig of 1919 bp in length
* 57207 57306: gap of unknown length
* 57307 60628: contig of 3322 bp in length
* 60629 60728: gap of unknown length
* 60729 63444: contig of 2716 bp in length
* 63445 65087: gap of unknown length
* 65088 66187: contig of 2543 bp in length
* 66188 68851: gap of unknown length
* 68852 72845: gap of unknown length
* 72846 72945: contig of 3894 bp in length
* 72946 76703: gap of unknown length
* 76704 76803: contig of 3758 bp in length
* 76804 79385: gap of unknown length
* 79386 79485: contig of 2582 bp in length
* 79486 82229: gap of unknown length
* 82230 82329: gap of unknown length
* 82330 84637: contig of 2308 bp in length
* 84638 84737: gap of unknown length
* 84738 87916: contig of 3179 bp in length
* 87917 88016: gap of unknown length
* 88017 91219: contig of 3203 bp in length
* 91220 91319: gap of unknown length
* 91320 93423: contig of 2104 bp in length
* 93424 93524: gap of unknown length
* 93524 97656: contig of 4133 bp in length
* 97657 97756: gap of unknown length
* 97757 101892: contig of 4136 bp in length
* 101893 101992: gap of unknown length
* 101993 104884: contig of 2892 bp in length
* 104885 104984: gap of unknown length
* 104985 108857: contig of 3873 bp in length
* 108858 108957: gap of unknown length
* 108958 111653: contig of 2696 bp in length
* 111654 111753: gap of unknown length
* 111754 116274: contig of 4421 bp in length
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* 126280 126379: gap of unknown length
* 126380 131332: contig of 4953 bp in length
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* 131433 136580: contig of 5148 bp in length
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Query Match 3.5%; Score 22; DB 2; Length 196863;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

604 GTCNAAAAAAAAAAAAAA 625
 830 GTCNAAAAAAAAAAAAAA 851

RESULT 43
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 DEFINITION Mus musculus clone RP23-334D14, WORKING DRAFT SEQUENCE, 25
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 VERSION AC102588.2 GI:22381577
 KEYWORDS HTG: HTGS.PHASE1; HTGS.DRAFT; HTGS.FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP23-334D14
 Unpublished
 2 (bases 1 to 198843)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
 Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Glinde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,J.,
 Menus,L., Minova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C.,
 Nobu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunhkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnappack,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 198843)
 Birren,B., Nusbaum,C., Lander,E., Allen,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouckgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
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 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrum,J., Menus,L., Minova,T., Mlenka,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunhkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
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 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Aug 21, 2002 this sequence version replaced g1:17061674.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L19066
 Center clone name: 334_D_14

----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap; version 0.960731

Consensus quality: 191519 bases at least Q40
 Consensus quality: 194846 bases at least Q30
 Consensus quality: 195925 bases at least Q20
 Insert size: 198000; agarose-fp
 Insert size: 196443; sum-of-coverage

Quality coverage: 5.8 in Q20 bases; agarose-fp
 Quality coverage: 5.8 in Q20 bases; sum-of-coverage

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 25 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 142 141: contig of 620 bp in length
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 862 1803: contig of 942 bp in length
 1804 1903: gap of 100 bp
 1904 3084: contig of 1181 bp in length
 3085 3184: gap of 100 bp
 3185 4660: contig of 1476 bp in length
 4661 4760: gap of 100 bp
 4761 6442: contig of 1682 bp in length
 6443 6542: gap of 100 bp
 6543 8314: contig of 1772 bp in length
 8315 8414: gap of 100 bp
 8415 10954: contig of 2540 bp in length
 10955 11054: gap of 100 bp
 11055 14504: contig of 3450 bp in length
 14505 14604: gap of 100 bp
 14605 19881: contig of 5277 bp in length
 19882 19981: gap of 100 bp
 19982 24662: contig of 4661 bp in length
 24663 24762: gap of 100 bp
 24763 30542: contig of 5780 bp in length
 30543 30642: gap of 100 bp
 30643 36951: contig of 6309 bp in length
 36952 37051: gap of 100 bp
 37052 44774: contig of 7773 bp in length
 44775 44874: gap of 100 bp
 44875 53156: contig of 8282 bp in length
 53157 53256: gap of 100 bp
 53257 63272: contig of 10016 bp in length
 63273 63372: gap of 100 bp
 63373 73192: contig of 9820 bp in length
 73193 73292: gap of 100 bp
 73293 86006: contig of 12714 bp in length
 86007 86106: gap of 100 bp
 86107 99113: contig of 13007 bp in length
 99114 99213: gap of 100 bp
 99214 135834: contig of 36621 bp in length
 135835 135934: gap of 100 bp
 135935 151141: contig of 15207 bp in length

* 151142 151241: gap of 100 bp
 * 151242 162188: contig of 10947 bp in length
 * 162189 162288: gap of 100 bp
 * 162289 176380: contig of 14092 bp in length
 * 176381 176480: gap of 100 bp
 * 176481 187921: contig of 11441 bp in length
 * 187922 188021: gap of 100 bp
 * 188022 198843: contig of 10822 bp in length.

FEATURES

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 162289. 176380
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 176481. 187921
 /note="assembly-fragment"
 188022. 198843

Query Match 3.5% Score 22; DB 2; Length 198843;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 AGAAGACAGTAATGAATATAAA 433
 DB 122888 AGAAGACAGTAATGAATATAAA 122867

RESULT 44
 AC123116
 LOCUS
 DEFINITION
 Rattus norvegicus clone CH230-68C1, *** SEQUENCING IN PROGRESS ***
 94 unordered pieces.
 AC123116
 AC123116.2 GI:21671831
 HTG; HTGS-PHASE1.
 SOURCE
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 206648)
 Muzny,D.,Marle, Metzker,M.,Lee, Abramson,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Gaveira,M.,
 Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guvarata,W.,
 Gunaratne,P., Haaland,W., Hamli,C., Hamilton,C., Hamilton,K.,
 Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
 Hollins,B., Howells,S., Hulik,S., Hume,J., Idelbrt,D., Jolivet,A.,
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jovanic,A.,
 Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
 Liu,J., Liu,Y., Liu,Y., London,P., Longacre,S., Lopez,J.,
 Lorenshewa,L., Loulsegel,H., Lozado,R.J., Lu,X., Ma,J.,
 Maheshwari,M., Mahindratne,M., Mahmud,M., Malloy,K., Mangum,A.,
 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
 McWhiney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,
 Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
 Morris,S., Mundasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
 Newton,N., Nguyen,N., Norris,S., Nwokilemeh,O., Okunolu,G.,
 Olarinmusaogun,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
 Perez,A., Perez,L., Plankoch,C., Plopper,F., Polindexter,A.,
 Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rachlin,E.,
 Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
 Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
 Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Saverly,G., Scherer,S.,
 Scott,G., Shatsman,S., Shen,H., Shetty,J., Shwartsbeyn,A.,
 Sisson,I., Sitter,C.D., Smajic,D., Steele,A., Sodergren,E.,
 Song,X.-Z., Sorelle,R., Sosa,J., Steindl,M., Strong,R., Sutton,A.,
 Syatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
 Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villaseana,D.,
 Waldron,L., Walker,B., Wang,J., Wang,J., Wang,S., Warren,J.,
 Warren,R., Wei,X., White,F., Williams,G., Willis,R., Wleczyk,R.,
 Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
 Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,Y., Zhou,Z., Zhou,X.,
 Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
 Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS Rat Genome Sequencing Consortium.
 TITLE Direct Submission
 JOURNAL Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Jul 2, 2002 this sequence version replaced gi:21239864.

----- Genome Center

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLUV
 Center clone name: CH230-68C1
 Summary Statistics

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329
 Consensus quality: 135401 bases at least Q40
 Consensus quality: 143073 bases at least Q30
 Consensus quality: 149355 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 94 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1365: contig of 1365 bp in length
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 2489 2588: gap of unknown length
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 6498 6597: gap of unknown length
 6598 7656: contig of 1059 bp in length
 7657 7757: gap of unknown length
 7757 9109: contig of 1353 bp in length
 9110 9209: gap of unknown length
 9210 10592: contig of 1383 bp in length
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 26903 28019: contig of 1117 bp in length

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 28120 29399: contig of 1280 bp in length
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 45426 45525: gap of unknown length
 45526 46902: contig of 1377 bp in length
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 59161 59260: gap of unknown length
 59261 60648: contig of 1388 bp in length
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Query Match 3.5% Score 22: DB 2: Length 206648;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNAAAAAAAAAAAAAA 625
 ||||||||||||||||
 DB 27826 GTGNAAAAAAAAAAAAAA 27847

RESULT 45
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 LOCUS Rattus norvegicus clone CH230-4B10, *** SEQUENCING IN PROGRESS ***
 DEFINITION 50 unordered pieces.

ACCESSION AC094585
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 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 209095)

REFERENCE

1 (bases 1 to 209095)

Mazny,D.M., Adams,C., Adio-Oduola,B., Ali-Usman,F.R., Allen,C.,
 Alsbrook,S.L., Amaralung,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barberia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
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 Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.,
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 Scherer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
 Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,R., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,O.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wlecczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zortilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Unpublished
 2 (bases 1 to 209095)
 Direct Submission
 Worley,K.C.
 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 209095)
 Direct Submission
 Worley,K.C.
 Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 9, 2002 this sequence version replaced gi:17941347.

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Project Information
 Center project name: GAYO
 Center clone name: CH230-4B10
 Summary Statistics

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap, version 0.990329
 Consensus quality: 167289 bases at least Q40
 Consensus quality: 173510 bases at least Q30
 Consensus quality: 178689 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 50 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1	1112:	contig of 1112 bp in length
*	1113	1212: gap of unknown length
*	1213	2236: contig of 1024 bp in length
*	2237	2336: gap of unknown length
*	2337	3580: contig of 1244 bp in length
*	3581	3680: gap of unknown length
*	3681	4766: contig of 1086 bp in length
*	4767	4866: gap of unknown length
*	4867	6218: contig of 1352 bp in length
*	6219	6318: gap of unknown length
*	6319	7371: contig of 1053 bp in length
*	7372	7471: gap of unknown length
*	7472	8840: contig of 1369 bp in length
*	8841	8940: gap of unknown length
*	8941	10775: contig of 1835 bp in length
*	10776	10875: gap of unknown length
*	10876	11921: contig of 1046 bp in length
*	11922	12021: gap of unknown length
*	12022	13777: contig of 1756 bp in length
*	13778	13877: gap of unknown length
*	13878	15074: contig of 1197 bp in length
*	15075	15174: gap of unknown length
*	15175	17379: contig of 2205 bp in length
*	17380	17479: gap of unknown length
*	17480	19141: contig of 1662 bp in length
*	19142	19241: gap of unknown length
*	19242	22076: contig of 2835 bp in length
*	22077	22176: gap of unknown length
*	22177	24873: contig of 2697 bp in length
*	24874	24973: gap of unknown length
*	24974	26892: contig of 1919 bp in length
*	26893	26992: gap of unknown length
*	26993	29416: contig of 2424 bp in length
*	29417	29516: gap of unknown length
*	29517	31342: contig of 1826 bp in length
*	31343	31442: gap of unknown length
*	31443	34482: contig of 3040 bp in length
*	34483	34582: gap of unknown length
*	34583	37422: contig of 2840 bp in length
*	37423	37522: gap of unknown length
*	37523	39813: contig of 2291 bp in length
*	39814	39913: gap of unknown length
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*	42854	42953: gap of unknown length
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*	45286	45385: gap of unknown length
*	45386	47238: contig of 1833 bp in length
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*	47339	49742: contig of 2404 bp in length
*	49743	49842: gap of unknown length
*	49843	53151: contig of 3309 bp in length
*	53152	53251: gap of unknown length
*	53252	57575: contig of 4334 bp in length
*	57576	57676: gap of unknown length
*	57676	61427: contig of 3752 bp in length
*	61428	61527: gap of unknown length

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* 61528 65268: contig of 3741 bp in length
* 65269 65368: gap of unknown length
* 65369 65358: contig of 3990 bp in length
* 65359 65458: gap of unknown length
* 65459 73738: contig of 4280 bp in length
* 73739 73838: gap of unknown length
* 73839 76862: contig of 3144 bp in length
* 76863 77082: gap of unknown length
* 77083 82330: contig of 5248 bp in length
* 82331 82430: gap of unknown length
* 82431 86139: contig of 3709 bp in length
* 86140 86239: gap of unknown length
* 86240 90925: contig of 4686 bp in length
* 90926 91025: gap of unknown length
* 91026 96815: contig of 5790 bp in length
* 96816 96915: gap of unknown length
* 96916 103229: contig of 6314 bp in length
* 103230 103329: gap of unknown length
* 103330 108061: contig of 4732 bp in length
* 108062 108161: gap of unknown length
* 108162 115067: contig of 6906 bp in length
* 115068 115167: gap of unknown length
* 115168 122612: contig of 7445 bp in length
* 122613 122712: gap of unknown length
* 122713 131195: contig of 8483 bp in length
* 131196 131295: gap of unknown length
* 131296 138832: contig of 7537 bp in length
* 138833 138932: gap of unknown length
* 138933 146861: contig of 7929 bp in length
* 146862 146961: gap of unknown length
* 146962 156062: contig of 9101 bp in length
* 156063 156162: gap of unknown length
* 156163 165064: contig of 8902 bp in length
* 165065 165164: gap of unknown length
* 165165 170909: contig of 5745 bp in length
* 170910 171009: gap of unknown length
* 171010 180780: contig of 9771 bp in length
* 180781 180880: gap of unknown length
* 180881 191473: contig of 10593 bp in length
* 191474 191573: gap of unknown length
* 191574 200296: contig of 8723 bp in length
* 200297 200396: gap of unknown length
* 200397 209095: contig of 8699 bp in length.
* Location/Qualifiers
  1..209095
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                   /db_xref="taxon:10116"
                   /clone="CH230-4B10"
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BASE COUNT 57040 a 44873 c 45519 g 56094 t 5569 others
ORIGIN

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Query Match      3.5%: Score 22; DB 2; Length 209095;
Beet Local Similarity 100.0%: Pred.No. 0.52;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 604 GTGNAAAAAAAAAAAAAAAAAAAAA 625
   |||
DB 354 GTGNAAAAAAAAAAAAAAAAAAAAA 375
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Search completed: November 7, 2002, 22:21:03
Job time : 3364.8 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 ; Search time 494.345 Seconds
(without alignments)
12088.985 Million cell updates/sec

Title: US-09-970-966-199
Perfect score: 369
Sequence: 1 ggcacatttgcgagatgt.....tggctccgcacacacatcct 369

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_est1:*
10: gb_est2:*
11: gb_hci:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: gb_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365.4	99.0	704	13	BI919074 603180881
2	363.8	98.6	987	14	BO668420 AGENCOURT
3	360.6	97.7	747	13	BI917149 603181571
4	354.4	96.0	670	12	BG753617 602732803
5	354.4	96.0	707	13	BI913989 603180565
6	353.4	95.8	920	9	AL538562 AL538562

7	352.8	95.6	698	13	BI554034 603235426
8	343.4	93.1	690	12	BI669845 603293440
9	341.8	92.6	1010	12	BF345141 602018318
10	336.4	91.2	593	10	BE386060 601276753
11	331	89.7	704	13	BI823714 602731780
12	328.6	89.1	705	12	BE753353 602731780
13	321.6	87.2	850	12	BE736301 601307087
14	321.4	87.1	340	14	HO6756 Y183B07.r1
15	314.4	85.2	654	12	BE746601 601580186
16	306.8	83.1	576	14	BO942438 AGENCOURT
17	305.6	82.8	948	14	BO882838 AGENCOURT
18	304.2	82.4	795	9	AU080197
19	292	79.1	571	14	BM709964 UI-E-CQ1-
20	285.4	77.3	573	10	BE395206 601309558
21	282	76.4	788	9	AU080744
22	281.4	76.3	664	10	BB552617 BB652617
23	279.4	75.7	1490	11	AK012406 MUS muscu
24	274.4	74.4	570	13	BI831919
25	266.6	72.2	383	9	AI614768
26	266.6	72.2	754	9	AU067460
27	256.4	69.5	352	9	AA349894
28	255.8	68.0	890	10	AM954549 EST56849
29	250.8	68.0	878	12	BF125425
30	241	65.3	878	12	BF125664
31	229.4	62.2	775	9	AU035640
32	227.8	61.7	673	10	BB644064
33	227.8	61.7	806	12	BG704350
34	222.2	60.2	784	9	AU050830
35	215.8	58.5	311	10	AM417548
36	212.2	57.5	688	13	BI544761
37	203.6	55.2	395	14	R20352
38	203.6	55.2	429	14	H17189
39	198.2	53.7	522	9	AI767459
40	198.2	53.7	541	14	BM974798
41	198.2	53.7	651	14	AV717094
42	198.2	53.7	652	14	BM980701
43	198.2	53.7	738	14	BM981455
44	197.8	53.6	1272	14	BQ224442
45	196.8	53.3	480	10	BE336607

ALIGNMENTS

RESULT 1
LOCUS BI919074 704 bp mRNA linear EST 16-OCT-2001
DEFINITION 603180881F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5', mRNA sequence.
ACCESSION BI919074
VERSION BI919074.1 GI:16200128
KEYWORDS EST.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNL1618 row: a column: 21
High quality sequence start: 4
High quality sequence stop: 702.
Location/Qualifiers

FEATURES

source

1. 704

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5244956"

/clone.lib="NIH_MGC_121"

/lab_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORE6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 132 a 237 c 204 g 131 t

ORIGIN

Query Match 99.08; Score 365.4; DB 13; Length 704;

Best Local Similarity 99.28; Pred. No. 8.1e-103;

Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGCACACTTTTGGCGATGTTCTTGCTTCAGGCTTTCGCTCAATCCAGTCTACCA 60

318 GGCACACTTTTGGCGATGTTCTTGCTTCAGGCTTTCGCTCAATCCAGTCTACCA 377

61 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCGAGTTCATTGTGAATGAC 120

378 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCGAGTTCATTGTGAATGAC 437

121 GGTGAAGTTCAAGACATGCTGCAGAAAGAGTATGAGCAAGTGGCGGATCATGTA 180

438 GTGAAGTTCAAGACATGCTGCAGAAAGAGTATGAGCAAGTGGCGGATCATGTA 497

181 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 240

498 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 557

241 CTGCTCCCGAGGAAATGAACTGATGTTGCATCAGCTGTGCAACACCCCTTTGTAA 300

558 CTGCTCCCGAGGAAATGAACTGATGTTGCATCAGCTGTGCAACACCCCTTTGTAA 617

301 CCGGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCGCTCCCTCAGGCAATGCTCCGAC 360

618 CCGGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCGCTCCCTCAGGCAATGCTCCGAC 677

361 CACCATCT 369

678 CACCATCT 686

RESULT 2

B0668420 987 bp mRNA linear EST 15-JUL-2002

LOCUS B0668420

DEFINITION AGENCORT_8301981 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275121

ACCESSION B0668420

VERSION B0668420.1 GI:21778667

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Euthera; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

FEATURES

source

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LNCM2457 row: m column: 10

High quality sequence stop: 583.

Location/Qualifiers

1. 987

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6275121"

/clone.lib="NIH_MGC_102"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 196 a 314 c 285 g 191 t

ORIGIN

Query Match 98.68; Score 363.8; DB 14; Length 987;

Best Local Similarity 98.98; Pred. No. 3.2e-102;

Matches 365; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GGCACACTTTTGGCGATGTTCTTGCTTCAGGCTTTCGCTCAATCCAGTCTACCA 60

272 GGCACACTTTTGGCGATGTTCTTGCTTCAGGCTTTCGCTCAATCCAGTCTACCA 331

61 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCGAGTTCATTGTGAATGAC 120

332 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCGAGTTCATTGTGAATGAC 391

121 GGTGAAGTTCAAGACATGCTGCAGAAAGAGTATGAGCAAGTGGCGGATCATGTA 180

392 GTGAAGTTCAAGACATGCTGCAGAAAGAGTATGAGCAAGTGGCGGATCATGTA 451

181 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 240

452 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 511

241 CTGCTCCCGAGGAAATGAACTGATGTTGCATCAGCTGTGCAACACCCCTTTGTAA 300

512 CTGCTCCCGAGGAAATGAACTGATGTTGCATCAGCTGTGCAACACCCCTTTGTAA 571

301 CCGGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCGCTCCCTCAGGCAATGCTCCGAC 360

572 CCGGCAAGGCGCCCAAGAAAGGGAAGTTGCTGCGCTCCCTCAGGCAATGCTCCGAC 631

361 CACCATCT 369

632 CACCATCT 640

RESULT 3

B1917149 747 bp mRNA linear EST 16-OCT-2001

LOCUS B1917149

DEFINITION 603181571F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245648 5',

ACCESSION B1917149

VERSION B1917149.1 GI:16181111

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Euthera; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1619 row: n column: 17
 High quality sequence stop: 737.

FEATURES
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 1. 747
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 /db_xref="taxon:9606"
 /clone="IMAGE:5245648"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t
 ORIGIN

Query Match 97.7%; Score 360.6; DB 13; Length 747;
 Best Local Similarity 98.4%; Pred. No. 2.7e-101;
 Matches 363; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTCAATCCAGTGTACCA 60
 DB 325 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTCAATCCAGTGTACCA 384
 QY 61 GGTGAAGAATTCAGCTGAACAACGACCTCTCTCCCGAGTTCATTGGAATTGCAC 120
 DB 385 GGTGAAGAATTCAGCTGAACAACGACCTCTCTCCCGAGTTCATTGGAATTGCAC 444
 QY 121 GGTGAAGTTCAGACATGTGTGAGAAGAAGTATGAGCAAGTGCAGGATCATGTA 180
 DB 445 GGTGAAGTTCAGACATGTGTGAGAAGAAGTATGAGCAAGTGCAGGATCATGTA 504
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 240
 DB 505 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 564
 QY 241 CTGCTCCCAAGGAACTGAACATCAGTTTGCATCAGCTGCGCAACCCCTCTTTGTA 300
 DB 565 CTGCTCCCAAGGAACTGAACATCAGTTTGCATCAGCTGCGCAACCCCTCTTTGTA 624
 QY 301 CCGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTCANGCCATGGCTCCGAC 360
 DB 625 CCGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTCANGCCATGGCTCCGAC 684
 QY 361 CACCATCTT 369
 DB 685 CACCATCTT 693

RESULT 4
 BG753617 670 bp mRNA 1linear EST 15-MAY-2001
 LOCUS 602732803f1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4876392 5',
 DEFINITION mRNA sequence.
 ACCESSION BG753617
 VERSION BG753617.1 GI:14064270
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://imgc.mcl.nih.gov/
 TITLE 1 (bases 1 to 670)
 JOURNAL Mammalia: Eutheria: Primates; Catarrhini; Hominiidae; Homo.
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cdna Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1759 row: e column: 01
 High quality sequence stop: 585.

FEATURES
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 1. 670
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4876392"
 /clone_lib="NIH_MGC_43"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. I"

BASE COUNT 144 a 198 c 165 g 163 t
 ORIGIN

Query Match 96.0%; Score 354.4; DB 12; Length 670;
 Best Local Similarity 98.9%; Pred. No. 2.1e-99;
 Matches 366; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTCAATCCAGTGTACCA 60
 DB 32 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTCAATCCAGTGTACCA 91
 QY 61 GGTGAAGAATTCAGCTGAACAACGACCTCTCTCCCGAGTTCATTGGAATTGCAC 120
 DB 92 GGTGAAGAATTCAGCTGAACAACGACCTCTCTCCCGAGTTCATTGGAATTGCAC 151
 QY 121 GGTGAAGTTCAGACATGTGTGAGAAGAAGTATGAGCAAGTGCAGGATCATGTA 180
 DB 152 GGTGAAGTTCAGACATGTGTGAGAAGAAGTATGAGCAAGTGCAGGATCATGTA 211
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 240
 DB 212 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 271
 QY 241 CTGCTCCCAAGG-AAAAGCACTCAGTTTGCATCAGCTGCGCAACCCCTCTTTGTA 299
 DB 272 CTGCTCCCAAGGCAACTGAACATCAGTTTGCATCAGCTGCGCAACCCCTCTTTGTA 331
 QY 300 ACGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTCANGCCATGGCTCCGCA 359
 DB 332 ACGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTCANGCCATGGCTCCGCA 391
 QY 360 CACCATCTT 369
 DB 392 CACCATCTT 401

RESULT 5
 B1913989

LOCUS B1913989 707 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603180565F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244569 5',
 mRNA sequence.
 ACCESSION B1913989
 VERSION B1913989.1 GI:16178286
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 707)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM11617 row: a column: 18
 High quality sequence stop: 698.

FEATURES
 source
 1..707
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5244569"
 /clone_1lb="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1: NotI;
 site: 2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb. Insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t
 ORIGIN

Query Match 96.0%; Score 354.4; DB 13; Length 707;
 Best Local Similarity 98.9%; Pred. No. 2.2e-99;
 Matches 366; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 60
 |||||||
 DB 286 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 345
 |||||||
 OY 61 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 120
 |||||||
 DB 346 GTGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 405
 |||||||
 OY 121 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 180
 |||||||
 DB 406 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 465
 |||||||
 OY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACAGTCTT 240
 |||||||
 DB 466 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACAGTCTT 525
 |||||||
 OY 241 CTGCTCTCCAGGAAAGTAAGTCACTGATGATGATGATGATGATGATGATGAT 300
 |||||||
 DB 526 CTGCTCTCCAGGAAAGTAAGTCACTGATGATGATGATGATGATGATGATGAT 585
 |||||||
 OY 301 CGGGCCAAAGCCCAAGAAAGGGAAGTCTGCTGCGGCTTCAGCCATCGGCTCGGCA 359
 |||||||
 DB 586 CGGGCCAAAGCCCAAGAAAGGGAAGTCTGCTGCGGCTTCAGCCATCGGCTCGGCA 645
 |||||||

OY 360 CCACCATCTCT 369
 |||||||
 DB 646 CCACCATCTCT 655

RESULT 6
 LOCUS AL538562
 DEFINITION AL538562 LTI_FL013_PBrn1 Homo sapiens cDNA clone CSODF024Y004 5
 prime, mRNA sequence.
 ACCESSION AL538562
 VERSION AL538562.1 GI:12866967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 920)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..920
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODF024Y004"
 /clone_1lb="LTI_FL013_PBrn1"
 /dev_stage="pooled tissue from post conception fetuses (20
 week, 24 week and 26 week)"
 /lab_host="DH10B"
 /note="Organ: Fetal brain; Vector: PCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 PCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 172 a 285 c 257 g 199 t
 ORIGIN

Query Match 95.8%; Score 353.4; DB 9; Length 920;
 Best Local Similarity 98.9%; Pred. No. 5.4e-99;
 Matches 365; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 60
 |||||||
 DB 279 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 338
 |||||||
 OY 61 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 120
 |||||||
 DB 339 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 398
 |||||||
 OY 121 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 180
 |||||||
 DB 399 GGTGAGAAATTCAGCTGACAGCAAGCTGCTCCCGGATTCATTGTGAATGCAC 458
 |||||||
 OY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACAGTCTT 240
 |||||||
 DB 459 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACAGTCTT 518
 |||||||
 OY 241 CTGCTCTCCAGGAAAGTAAGTCACTGATGATGATGATGATGATGATGATGAT 300
 |||||||
 DB 519 CTGCTCTCCAGGAAAGTAAGTCACTGATGATGATGATGATGATGATGATGAT 578
 |||||||
 OY 301 CGGGCCAAAGCCCAAGAAAGGGAAGTCTGCTGCGGCTTCAGCCATCGGCTCGGCA 360
 |||||||

Db 579 CGGGCCAGGCCCAAGAAAGGGAGTTCTGCTCGGCCCTCAGG-CAGGGCTCCGAGC 637
QY 361 CACCATCT 369
|||||
Db 638 CACCATCT 646

RESULT 7
BI554034 698 bp mRNA linear EST 05-SEP-2001
LOCUS 603235426F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:5309527
DEFINITION 5', mRNA sequence.
ACCESSION BI554034
VERSION BI554034.1 GI:15441348
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11784 row: d column: 08
High quality sequence stop: 687.
Location/Qualifiers

FEATURES
source
1..698
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5309527"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NCI;
Site:2: Salt; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 131 a 231 c 204 g 132 t
ORIGIN

Query Match 95.6%; Score 352.8; DB 13; Length 698;
Best Local Similarity 98.6%; Pred. No. 6.9e-99;
Matches 365; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GGCACCTTTTGGCGATGTTCTTGTTCAGGCTTTGGCTGCAATTCAGTGTACCA 60
|||||
Db 278 GGCACCTTTTGGCGATGTTCTTGTTCAGGCTTTGGCTGCAATTCAGTGTACCA 337

QY 61 GTGTGAAGATTCACGCTGACAGACAGTGTCTCCCGAGTTCATTTGATTTGCAC 120
|||||
Db 338 GTGTGAAGATTCACGCTGACAGACAGTGTCTCCCGAGTTCATTTGATTTGCAC 397

QY 121 GTGTGAAGTTCAGACATGTGTACAGAA-GAAGTGTAGAGCAAGTCCGGGATCATGT 179
|||||
Db 398 GTGTGAAGTTCAGACATGTGTACAGAAAGTGTAGAGCAAGTCCGGGATCATGT 457

QY 180 ACCGCAAGTCTGTGATATCATAGCGGCTGTCTCATCGCTTCCGGGGTACAGTCTT 239
|||||
Db 458 ACCGCAAGTCTGTGATATCATAGCGGCTGTCTCATCGCTTCCGGGGTACAGTCTT 517

QY 240 TTGTGCTCCCGAGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 299
|||||
Db 518 TTGTGCTCCCGAGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 577

QY 300 ACGGGCCAGGCCCAAGAAAGGGAGTTCTGCTCGGCCCTCAGGCTCCGCA 359
|||||
Db 578 ACGGGCCAGGCCCAAGAAAGGGAGTTCTGCTCGGCCCTCAGGCTCCGCA 637

QY 360 CCACCATCT 369
|||||
Db 638 CCACCATCT 647

RESULT 8
BI669845 690 bp mRNA linear EST 12-SEP-2001
LOCUS 603293440F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312889 5',
DEFINITION mRNA sequence.
ACCESSION BI669845
VERSION BI669845.1 GI:15584078
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 690)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Mikhail Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshnyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11792 row: p column: 10
High quality sequence stop: 690.
Location/Qualifiers

FEATURES
source
1..690
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5312889"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgaag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 127 a 231 c 202 g 130 t
ORIGIN

Query Match 93.1%; Score 343.4; DB 13; Length 690;
Best Local Similarity 98.9%; Pred. No. 5.9e-96;
Matches 366; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 GGCACCTTTTGGCGATGTTCTTGTTCAGGCTTTGGCTGCAATTCAGTGTACCA 60
|||||
Db 303 GGCACCTTTTGGCGATGTTCTTGTTCAGGCTTTGGCTGCAATTCAGTGTACCA 361

QY 61 -GTGTGAAGATTCACGCTGACAGACAGTGTCTCCCGAGTTCATTTGATTTGCA 119
|||||
Db 362 GTGTGAAGATTCACGCTGACAGACAGTGTCTCCCGAGTTCATTTGATTTGCA 421

QY 120 CGGTGAAGTTCAGACATGTGTACAGAAAGTGTAGAGCAAGTCCGGGATCATGT 179
|||||
Db 422 CGGTGAAGTTCAGACATGTGTACAGAAAGTGTAGAGCAAGTCCGGGATCATGT 481

QY 180 ACCGCAAGTCTGTGCATCATGACGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 239
 DB 482 ACCGCAAGTCTGTGCATCATGACGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 541
 QY 240 TCTGCTCCCGAGGAAGTGAAGTCTGTCATGAGTCTGTCGCAACACCCCTTTTGA 299
 DB 542 TCTGCTCCCGAGGAAGTGAAGTCTGTCATGAGTCTGTCGCAACACCCCTTTTGA 601
 QY 300 ACGGGCCAAAGGCGCCAAAGGAAGTCTGTCGCGGCTCTGCAAGCATGCTCCGCA 359
 DB 602 ACGGGCCAAAGGCGCCAAAGGAAGTCTGTCGCGGCTCTGCAAGCATGCTCCGCA 661
 QY 360 CCACCATCTCT 369
 DB 662 CCACCATCTCT 671

RESULT 9
 BE345141 1010 bp mRNA linear EST 22-NOV-2000
 LOCUS 602018318F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153684

DEFINITION 5', mRNA sequence.
 BE345141
 VERSION BE345141.1 GI:11292606
 KEYWORDS EST.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1010)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LTM9422 row: d column: 05
 High quality sequence stop: 649.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4153684"
 /clone_lib="NCI_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1; NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.3 kb. Constructed by life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 266 a 344 c 254 g 146 t
 ORIGIN

Query Match 92.6%; Score 341.8; DB 12; Length 1010;
 Best Local Similarity 98.4%; Pred. No. 2.4e-95;
 Matches 365; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GGCACATTTTGGGATTTGTTCTTNC-AGGCTTGGCGTGCATAATCAGTGTACC 59
 DB 227 GGCACATTTTGGGATTTGTTCTTNC-AGGCTTGGCGTGCATAATCAGTGTACC 286
 QY 60 AGTGTAGAGATTTCCAGTGAACAGAGTCTCTCCCGAGTTCATTGTAATTGCA 119
 DB 287 AGTGTAGAGATTTCCAGTGAACAGAGTCTCTCCCGAGTTCATTGTAATTGCA 346

QY 120 CGGTGAACGTTCAAGCATGTGTCAAGAAAGATGTAGAGCAAGTCCGGGATCATGT 179
 DB 347 CGGTGAACGTTCAAGCATGTGTCAAGAAAGATGTAGAGCAAGTCCGGGATCATGT 406
 QY 180 ACCGCAAGTCTGTGCATCATGACGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 239
 DB 407 ACCGCAAGTCTGTGCATCATGACGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 466
 QY 240 TCTGCTCCCGAGGAAGTGAAGTCTGTCATGAGTCTGTCGCAACACCCCTTTTGA 299
 DB 467 TCTGCTCCCGAGGAAGTGAAGTCTGTCATGAGTCTGTCGCAACACCCCTTTTGA 526
 QY 300 A-CGGGCCAAGGCGCCAAAGGAAGTCTGTCGCGGCTCTGCAAGCATGCTCCGCA 358
 DB 527 A-CGGGCCAAGGCGCCAAAGGAAGTCTGTCGCGGCTCTGCAAGCATGCTCCGCA 586
 QY 359 ACCACCATCTCT 369
 DB 587 ACCACCATCTCT 597

RESULT 10
 BE386060 593 bp mRNA linear EST 21-JUL-2000
 LOCUS 601276753F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617749 5',
 mRNA sequence.

DEFINITION BE386060
 BE386060.1 GI:9331425
 VERSION BE386060
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 593)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC/DCFD/DTF
 Tissue Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
 Plate: LTM285 row: 1 column: 14
 High quality sequence stop: 593.

FEATURES
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 1..593
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3617749"
 /clone_lib="NIH_MGC_20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site: 1; XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 139 a 166 c 183 g 105 t
 ORIGIN

Query Match 91.2%; Score 336.4; DB 10; Length 593;
 Best Local Similarity 99.4%; Pred. No. 8.2e-94;
 Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 AGGCTTGGCGTGCATAATCAGTGTGAGAAATTCAGCTGAACAGACTG 90
 DB 246 AGGCTTGGCGTGCATAATCAGTGTGAGAAATTCAGCTGAACAGACTG 305

QY 91 CTTCTCCCGAGTTCATTTGTAATTCGACGGTGAACATCATGTGTGCAAGAA 150
 |||||
 Db 306 CTCTCTCCCGAGTTCATTTGTAATTCGACGGTGAACATCATGTGTGCAAGAA 365
 |||||
 QY 151 AGTATGAGCAAGATCCCGGATCATGTACCGAAGCTCTGTCATCATGAGCGCTG 210
 |||||
 Db 366 AGTATGAGCAAGATCCCGGATCATGTACCGAAGCTCTGTCATCATGAGCGCTG 425
 |||||
 QY 211 TCTCATGCGCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAGTGAAGTTCG 270
 |||||
 Db 426 TCTCATGCGCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAGTGAAGTTCG 485
 |||||
 QY 271 CATCAGCTGTGCAACACCCCTCTTTTGAACGGCCCAAGGCGCAAGAGGGAGTTC 330
 |||||
 Db 486 CATCAGCTGTGCAACACCCCTCTTTTGAACGGCCCAAGGCGCAAGAGGGAGTTC 545
 |||||
 QY 331 TGCCTGCGCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAGTGAAGTTC 369
 |||||
 Db 546 TGCCTGCGCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAGTGAAGTTC 584
 |||||

RESULT 11
 LOCUS B1823714 704 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603040833f1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181585 5',
 mRNA sequence.
 B1823714
 VERSION B1823714.1 GI:15935264
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 704)
 AUTHORS NIH-MGC http://mgi.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L18M1453 row: a column: 10
 High quality sequence stop: 692.

FEATURES

source
 1..704
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5181585"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 inserted size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH-MGC Library."
 BASE COUNT 135 a 227 c 205 g 137 t

Query Match 89.7%; Score 331; DB 13; Length 704;
 Best Local Similarity 97.5%; Pred. No. 4, 4e-92;
 Matches 356; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 1 GGCACCTTTTGGGAGTATGTTCTTGTTCATGAGCTTTGGCTGCAAAATCCAGTGTACCA 60
 |||||
 Db 280 GGCACCTTTTGGGAGTATGTTCTTGTTCATGAGCTTTGGCTGCAAAATCCAGTGTACCA 339
 |||||
 QY 61 GTGTGAAGATTTCCAGCTGAACACGATGCTCTCCCGAGTTCATTTGTAATTCGAC 120
 |||||
 Db 340 GTGTGAAGATTTCCAGCTGAACACGATGCTCTCCCGAGTTCATTTGTAATTCGAC 399
 |||||
 QY 121 GGTGAAGTTCAGACATGTCGAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA 180
 |||||
 Db 400 GGTGAAGTTCAGACATGTCGAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA 459
 |||||
 QY 181 CCGCAAGTCTGTCATCATACGCGGCTGTCATGCTGCTGCGGGTACCAAGTCTT 240
 |||||
 Db 460 CCGCAAGTCTGTCATCATACGCGGCTGTCATGCTGCTGCGGGTACCAAGTCTT 519
 |||||
 QY 241 CTGCTCCCGAGGAAGTCACTGATGTTGTCATGAGTGTGCAACACCCCTC-TTTGTA 299
 |||||
 Db 520 CTGCTCCCGAGGAAGTCACTGATGTTGTCATGAGTGTGCAACACCCCTCATTGTA 579
 |||||
 QY 300 ACGGCGCAA-GGCGCAAGAAAGGGAAGTTCGCTCGGCGCTTCATGCGCATGCTCCGC 358
 |||||
 Db 580 ACGGCGCAATGGCCCAAGAAAGGGAAGTTCGCTCGGCGCTTCATGCGCATGCTCCGC 639
 |||||
 QY 359 ACCAC 363
 |||||
 Db 640 ACCAC 644

RESULT 12
 LOCUS B6753353 705 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602731780f1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875499 5',
 mRNA sequence.
 B6753353
 VERSION B6753353.1 GI:14064006
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 705)
 AUTHORS NIH-MGC http://mgi.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L18M1756 row: o column: 20
 High quality sequence stop: 481.

FEATURES

source
 1..705
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4875499"
 /clone_lib="NIH_MGC_43"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library. 1"
 BASE COUNT 156 a 214 c 172 g 163 t

ORIGIN

Query Match 89.1%; Score 328.6; DB 12; Length 705;
 Best Local Similarity 96.5%; Pred. No. 2.5e-91;
 Matches 356; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

1 GGCACCTTTTGGGATTTGCTTCTTGCATGAGCTTTGGGCTGCAATATCAGTGTACCA 60
 32 GGCACCTTTTGGGATTTGCTTCTTGCATGAGCTTTGGGCTGCAATATCAGTGTACCA 91
 61 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 120
 92 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 150
 121 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 180
 151 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 210
 181 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 240
 211 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 269
 241 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 300
 270 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 329
 301 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 360
 330 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 389
 361 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 398
 390 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 398

RESULT 13
 BE736301 850 bp mRNA linear EST 15-SEP-2000
 LOCUS BE736301 601307087F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641660 5',
 DEFINITION mRNA sequence.

ACCESSION BE736301 GI:10150293
 VERSION BE736301
 KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 850)
 NIH-MGC http://mgi.nci.nih.gov/.

REFERENCE
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov

TISSUE Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.lnl.gov
 Plate: L1CM347 row: m column: 21
 High quality sequence stop: 662.

FEATURES

location/Qualifiers

1..850

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3641660"

/clone_1="NIH_MGC_39"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the

BASE COUNT

162 a 276 c 265 g 147 t

ORIGIN

Query Match 87.2%; Score 321.6; DB 12; Length 850;
 Best Local Similarity 95.1%; Pred. No. 4.3e-89;
 Matches 352; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

1 GGCACCTTTTGGGATTTGCTTCTTGCATGAGCTTTGGGCTGCAATATCAGTGTACCA 60
 253 GGCACCTTTTGGGATTTGCTTCTTGCATGAGCTTTGGGCTGCAATATCAGTGTACCA 312
 61 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 372
 92 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 432
 121 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 492
 151 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 551
 181 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 599
 211 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 651
 241 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 699
 270 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 751
 301 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 799
 330 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 851
 361 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 899
 390 GGTGAAGATTCACAGTGTGTCAGAAAGAGTGTGAGCAAAAGTGTGAGTGTGATGAC 951

RESULT 14

LOCUS H06756 340 bp mRNA linear EST 21-JUN-1995
 DEFINITION IMAGE:4619 5', mRNA sequence.

ACCESSION

H06756

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 340)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rink, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P., and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

SOURCE

Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Insert Size: 1737

FEATURES

High quality sequence stops: 312

SOURCE

Image Consortium, LNLN

NOTE

This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1737 Std Error: 0.00
 Seq primer: M13RP1

ORIGIN

Following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies).

FEATURES High quality sequence stop: 312.

Location/Qualifiers
1. 340

/organism="Homo sapiens"
/db_xref="GDB:417160"
/db_xref="taxon:9606"
/clone="IMAGE:44619"
/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lactimid BA; Site:1: Not 1; Site:2: Hind III; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5];
ACTGGAAGAATTCGCGCGCGAGGAATTTTATTTTATTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lactimid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT
ORIGIN

77 a 95 c 89 g 79 t

Query Match 87.1%; Score 321.4; DB 14; Length 340;
Best Local Similarity 98.8%; Pred. No. 2.7e-89;
Matches 333; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 11 TCGGATGTTCTTCTGCTTNCAGGCTTGCAGCAATCCAGTGTACAGTGAAGAA 70
DB 1 TCGGATGTTCTTCTGCTTNCAGGCTTGCAGCAATCCAGTGTGAAGAA 60
QY 71 TTCACCTGAACACAGACTCTCTCCCGAGTTTCATTTGAATTGACAGGTGACGTT 130
DB 61 TTCACCTGAACACAGACTCTCTCCCGAGTTTCATTTGAATTGACAGGTGACGTT 120
QY 131 CAAGATATGTGCAAGAAAGATGATGAGCAAGTGCAGGATCATGTACCCAGTCC 190
DB 121 CAAGATATGTGCAAGAAAGATGATGAGCAAGTGCAGGATCATGTACCCAGTCC 180
QY 191 TGTGATCATACAGGCGCTTCTCATGCTTCCGCGGTACAGTCTTGTGCCCCCA 250
DB 181 TGTGATCATACAGGCGCTTCTCATGCTTCCGCGGTACAGTCTTGTGCCCCCA 240
QY 251 GGGAACTGAACTCAAGTTTCATGCTGCAACACCCCTTTTGTACGGGCAAGG 310
DB 241 GGGAACTGAACTCAAGTTTCATGCTGCAACACCCCTTTTGTACGGGCAAGG 300
QY 311 CCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAAGC 347
DB 301 -CCAGAAAAGGGAAGTTCTGCTCGGCCCTCAAGC 336

RESULT 15
BE746601 654 bp mRNA linear EST 15-SEP-2000
LOCUS 601580186F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:392886 5',
DEFINITION mRNA sequence.
ACCESSION BE746601
VERSION BE746601.1 GI:10160593
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 654)
TITLE NIH-MGC http://mgi.ncl.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
plate: LNC9760 row: 1 column: 21
High quality sequence stop: 651.
Location/Qualifiers

FEATURES
source

1. 654

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:392886"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pORF7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(c). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 121 a 219 c 187 g 126 t 1 others

Query Match 85.2%; Score 314.4; DB 12; Length 654;
Best Local Similarity 98.8%; Pred. No. 6.4e-87;
Matches 337; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 GGCACATTTTGGGATGTTCTTNCAGGCTTGCCTGCAAA-TCCAGTGTACC 59
DB 255 GGCACATTTTGGGATGTTCTTNCAGGCTTGCCTGCAAA-TCCAGTGTACC 314
QY 60 AGTGAAGAATTCAGAGCAAGCAAGAGCTCCCGGAGTTATGTGAAATGCA 119
DB 315 AGTGAAGAATTCAGAGCAAGCAAGAGCTCCCGGAGTTATGTGAAATGCA 374
QY 120 CGGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGATCATGT 179
DB 375 CGGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCGGATCATGT 434
QY 180 ACCGCAAGTCTGTGATCATACAGGCGCTGTCTATCGCCTTGCAGGATCATGTCT 239
DB 435 ACCGCAAGTCTGTGATCATACAGGCGCTGTCTATCGCCTTGCAGGATCATGTCT 494
QY 240 TCTGCTCCCGAGGAAGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 299
DB 495 TCTGCTCCCGA-GGAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 553
QY 300 ACGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCC 340
DB 554 ACGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCC 594

Search completed: November 7, 2002, 15:02:30
Job time: 501.345 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 133.06 Seconds
(without alignments)
11437.514 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agttctctcttcagagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 802347

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N.Geneseq_101002.*

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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	625	ABT03280	Human ovarian carc
2	625	100.0	625	ABL40348	Ovarian carcinoma
3	625	100.0	625	ABL87898	Human ovarian carc
4	606	97.0	1897	ABT03284	Human ovarian carc
5	606	97.0	1897	ABL40352	Ovarian carcinoma
6	555	88.8	1608	ABO54231	Human ovarian anti
7	555	88.8	1953	AAE22400	Human secreted pro
8	549	87.8	1856	AAE64188	Human secreted pro
9	549	87.8	1850	AAE93845	Human CDNA encodin

10	486	77.8	1619	24	ABT03277	Human ovarian carc
11	486	77.8	1619	24	ABT03281	Human ovarian carc
12	486	77.8	1619	24	ABL40345	Ovarian carcinoma
13	486	77.8	1619	24	ABL40349	Ovarian carcinoma
14	393	62.9	1524	24	ABK33543	CDNA encoding huma
15	365	58.4	587	22	AAE94186	Primer specific fo
16	359	57.4	1362	24	ABT03279	Human ovarian carc
17	359	57.4	1362	24	ABL40347	Ovarian carcinoma
18	359	57.4	2528	22	AAH18690	Human G protein co
19	352	56.3	444	22	AAH50766	Human tumor assoc
20	314	50.2	373	24	ABL78538	Human ovarian carc
21	307	49.1	349	24	ABL79431	Human ovarian carc
22	263	42.1	409	24	ABL81262	Human ovarian carc
23	166	26.6	201	24	ABL85916	Human ovarian carc
24	154	24.6	390	24	ABL78554	Human ovarian carc
25	120	19.2	558	24	ABL79397	Human ovarian carc
26	92	14.7	381	24	ABL84848	Human ovarian carc
27	26	4.2	50	22	AAE33985	Human SNP oligonuc
28	26	4.2	50	22	AAE33986	Human SNP oligonuc
29	25	4.0	51	22	AAE27277	Human SNP oligonuc
30	23	3.7	263	22	ABAI8284	Human nervous syst
31	23	3.7	377	22	ABAI10167	Human breast cance
32	23	3.7	1539	23	ABV23163	Human prostate exp
33	23	3.7	1539	23	ABV29003	Human prostate exp
34	22	3.5	256	24	ABK53839	Human head and nec
35	22	3.5	377	23	ABV08332	Human prostate exp
36	22	3.5	442	22	AAH7949	Human polynucleoti
37	22	3.5	1329	24	ABL90482	Human polynucleoti
38	22	3.5	1388	24	ABK65378	Human polynucleoti
39	22	3.5	1823	22	AAH34281	Arabidopsis CDNA e
40	22	3.5	2049	24	ABL90818	Human colon cancer
41	21	3.4	259	22	AAH69474	Human polynucleoti
42	21	3.4	288	22	AAE09957	Human cervical can
43	21	3.4	288	23	ABV05091	Human breast cance
44	21	3.4	294	23	ABV05770	Human prostate can
45	21	3.4	359	22	AAH68974	Human prostate exp

ALIGNMENTS

RESULT 1
ABT03280
ID ABT03280 standard; CDNA; 625 BP.
XX
AC ABT03280;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.
XX
KW Human; Ovarian cancer; ovarian carcinoma; gene therapy; Immunotherapy;
KW Cytostatic; gene; ss.
XX
XX Homo sapiens.
OS
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;
XX WPI; 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
PS Claim 2; Page 194; 197pp; English.

expressed sequence tag; EST; ss
Homo sapiens.
US2002004491-A1.
KW expressed sequence tag; EST; ss
XX
OS
XX
PN

CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.

50 Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match	100.0%	Score 625;	DB 24;	Length 625;
100.0%	Score 625;	DB 24;	Length 625;	

```
Matches 625; Conservative 0; Mismatches 0;
```

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	Db	QY
1 AGTCTCTCTTGCACAGAGACTGGGCCCGGAGACGCGCAAMAGCAACGGCGCTGTCACAAAGCG 60	1 AGTCTCTCTTGCACAGAGACTGGGCCCGGAGACGCGCAAMAGCAACGGCGCTGTCACAAAGCG 60	61 GGGCGCTTCGCTGGTGGAGAGCGCATACGCGCGACGGCGCTTCCTGTCGTGGCGTGGCTG 120
61 GGGCGCTTCGCTGGTGGAGAGCGCATACGCGCGACGGCGCTTCCTGTCGTGGCGTGGCTG 120	61 GGGCGCTTCGCTGGTGGAGAGCGCATACGCGCGACGGCGCTTCCTGTCGTGGCGTGGCTG 120	

PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
DR WPI: 2002-171027/22.

121 CAGCGACAGGGCGGCGACACAGCACCCTGCACGAACACCCCGGAAACTGCTGGAGGACAC 180

Claim 1a; Page 125; 131pp; English.

Db 181 CGTACACGACGCGGTTGATGACCGAGCTGAGGTAAGAAAAAGCTTCCGAGAAAGGGAG 240
 |||||
 241 GAGGATCATGTAGCCCGCGGAAGTGGACACTGTCACAGTCGCGTGGGTTGGCCGAGC 300
 |||||
 Db 241 GAGGATCATGTAGCCCGCGGAAGTGGACACTGTCACAGTCGCGTGGGTTGGCCGAGC 300
 |||||

CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for

301 CAGGATCCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACCAATCAGCCC
 301 CAGGATCCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACCAATCAGCCC
 301 CAGGATCCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACCAATCAGCCC

CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and

Db 361 TGGGCGACACGACGAGGAGGAGACAGAGAAAAAAGAAAAACACAGCATGAGAACACAG 420

Oy 421 TAAATGAATAAACCATTAATAATTATTAAGCCCTCTGTCTGTGCTTACATGCGCCAGGAAT 480

CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the ovarian carcinoma O1034C EST clone nucleotide

Db 421 TAATGAATAAACCATAAATATTTAGCCCTCTGTCTGTGCTTACTGGCCAGCAAT 480

Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCCACAAGCAAGAGAGATTT 540

```

XX      Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;
SQ
Query Match      100.0%   Score 625:   DB 24:   Length 625:

```

541 AACACTGTTTCAAAACCGGGGAGTTGGCTGTCTTAAAGAAAGACCATTTAAATGCTTTAG 600

	Matches	625;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	AGTTCTCCTTGACAGAGACTGGCGCCGGGACGCGACAGAGACCAACGGGCGTTCACAAAGCG	60							

Qy	601	ACAGTGNAAAAAAAAAAAAAAAA	625
Db	601	ACAGTGNAAAAAAAAAAAAAAAA	625

61 GGCGCTGCGGTGGTGGAGTGGCATGTACGGCGAGGGCGTCTCTGCGTGGTTGGCGGCTG 120

```

RESULT 2
ABL40348
ID      ABL40348 standard; cDNA; 625 BP.

```

0y 121 CAGCGACAGCGCGCAGCACAGCACCCTGCACGAACACCCCGGAACCTGCTCGAGAGACAC 180
|||||
121 CAGCGACAGCGCGCAGCACAGCACCCTGCACGAACACCCCGGAACCTGCTCGAGAGACAC 180

XX ADDITIONAL,
XX
XX
DT 28-JUN-2002 (first entry)
XX

101 CGGTACAGGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGCTCCGAGMAAGGGAG 240
181 CGGTACAGGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGCTCCGAGMAAGGGAG 240

AA Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer

Db 241 GAGGATCATGTACGCCCGSAGTAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCCCGACG 300

QY 301 CATGATCCCTCCGAATCTGTGGTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCCC 360
 |||||||
 Db 301 CATGATCTCCGAATCTGTGGTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCCC 360
 CC
 QY 361 TGGCGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACACAG 420
 |||||||
 Db 361 TGGCGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACACAG 420
 CC
 QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACGCGCAGGAAT 480
 |||||||
 Db 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACGCGCAGGAAT 480
 CC
 QY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCAGAGAAATTT 540
 |||||||
 Db 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCAGAGAAATTT 540
 CC
 QY 541 AACACTGTTTCAACCCGGGGAGTTGCTGTGTTAAGAAAGACCATTAATGCTTTAG 600
 |||||||
 Db 541 AACACTGTTTCAACCCGGGGAGTTGCTGTGTTAAGAAAGACCATTAATGCTTTAG 600
 CC
 QY 601 ACAGTGNAAAAAAGAAAAA 625
 |||||||
 Db 601 ACAGTGNAAAAAAGAAAAA 625

RESULT 3

ABL87898 standard; DNA; 625 BP.

XX ID ABL87898 standard; DNA; 625 BP.
 XX AC ABL87898;
 XX DT 17-MAY-2002 (first entry)
 XX DE Human ovarian cancer related DNA clone SEQ ID NO:10876.
 XX KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.
 XX OS Homo sapiens.
 XX PN WO200192581-A2.
 XX PD 06-DEC-2001.
 XX PF 29-MAY-2001; 2001WO-US17756.
 XX PR 26-MAY-2000; 2000US-207484P.
 XX (CORI-) CORIXA CORP.
 XX PA Algate PA, Harlocker SL, Jones R;
 XX PI WPI: 2002-122075/16.
 XX DR
 XX PT Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 XX
 XX Claim 1: SEQ ID 10876; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a CDNA sequence
 CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (SI) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour CDNA library using well known
 CC techniques.

XX Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 100.0%; Score 625; DB 24; Length 625;

Best Local Similarity 100.0%; Pred. No. 5.2e-239;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTGCAGAGAGACTGGCCGCGGAGCCGAAAGCAACGGGCGCTGCACAAAGG 60
 |||||||
 Db 1 AGTTCCTCTTGCAGAGAGACTGGCCGCGGAGCCGAAAGCAACGGGCGCTGCACAAAGG 60
 CC
 QY 61 GCGCGTGTGCGGTGAGAGTGGCATGTACGGCGAGGCGCTCTGCTGGTGGCGCTG 120
 |||||||
 Db 61 GCGCGTGTGCGGTGAGAGTGGCATGTACGGCGAGGCGCTCTGCTGGTGGCGCTG 120
 CC
 QY 121 CAGCGACAGCGCGGCGACAGACAGCCTGCACGAACCCCGCAAACTGCTGCGAGAGAC 180
 |||||||
 Db 121 CAGCGACAGCGCGGCGACAGACAGCCTGCACGAACCCCGCAAACTGCTGCGAGAGAC 180
 CC
 QY 181 CGTGTACAGAGAGCGGTTGATATCCGAGCTGAGGTGAAAAACGTCTCCGAGAAAGGAG 240
 |||||||
 Db 181 CGTGTACAGAGAGCGGTTGATATCCGAGCTGAGGTGAAAAACGTCTCCGAGAAAGGAG 240
 CC
 QY 241 GAGGATCATGTACGCCCGGAAAGTAGAGACTCTCCAGTCTGCTGGTGGTTGGCCGAC 300
 |||||||
 Db 241 GAGGATCATGTACGCCCGGAAAGTAGAGACTCTCCAGTCTGCTGGTGGTTGGCCGAC 300
 CC
 QY 301 CATGATCCTCCGAATCTGTGGTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCCC 360
 |||||||
 Db 301 CATGATCCTCCGAATCTGTGGTGGCATCCAGCATACGGCCAAATGTCAACAATCAGCCC 360
 CC
 QY 361 TGGCGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACACAG 420
 |||||||
 Db 361 TGGCGACAGACGAGCAGAGGAGAGAGACAGAGAAAAAGAAAAACACAGCATGAGACACAG 420
 CC
 QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACGCGCAGGAAT 480
 |||||||
 Db 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACGCGCAGGAAT 480
 CC
 QY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCAGAGAAATTT 540
 |||||||
 Db 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCAGAGAAATTT 540
 CC
 QY 541 AACACTGTTTCAACCCGGGGAGTTGCTGTGTTAAGAAAGACCATTAATGCTTTAG 600
 |||||||
 Db 541 AACACTGTTTCAACCCGGGGAGTTGCTGTGTTAAGAAAGACCATTAATGCTTTAG 600
 CC
 QY 601 ACAGTGNAAAAAAGAAAAA 625
 |||||||
 Db 601 ACAGTGNAAAAAAGAAAAA 625

RESULT 4

ABT03284 standard; CDNA; 1897 BP.

XX ID ABT03284 standard; CDNA; 1897 BP.
 XX AC ABT03284;
 XX DT 05-SEP-2002 (first entry)
 XX DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
 XX KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KW cytostatic; gene; ss.

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XX OS Homo sapiens.
XX XX
XX PN WO200239885-A2.
XX PD 23-MAY-2002.
XX PF 13-NOV-2001; 2001WO-US45395.
XX PR 14-NOV-2000; 2000US-0713550.
XX PR 03-APR-2001; 2001US-0825294.
XX PR 02-OCT-2001; 2001US-0970966.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX PF WPI; 2002-500186/53.
XX DR
XX XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX PT detecting the presence of ovarian cancer in a patient, and in
XX PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX PT
XX PS Claim 2; Page 196; 197pp; English.
XX CC The present invention provides human ovarian cancer associated proteins
XX CC and coding sequences. The sequences can be used in the diagnosis and
XX CC treatment of ovarian cancers. The present sequence is a coding sequence
XX CC of the invention.
XX SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

Query Match          97.0%; Score 606; DB 24; Length 1897;
Best Local Similarity 100.0%; Pred. No. 1.6e-231;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTTCAGAGAGACTGGCCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAACCG 60
DB 1271 AGTTCTCTTTCAGAGAGACTGGCCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAACCG 1330
QY 61 GCGGCTGTGGTGGTGGAGTCCGATGACCGCGAGCGGCTTCTGCTGGTGGCGTCTG 120
DB 1331 GCGGCTGTGGTGGTGGAGTCCGATGACCGCGAGCGGCTTCTGCTGGTGGCGTCTG 1390
QY 121 CAGGACAGCGCGGAGCAGACACCTGCACGACCAACCGCGCAAACTCTCTCGAGGACAC 180
DB 1391 CAGGACAGCGCGGAGCAGACACCTGCACGACCAACCGCGCGAACTCTCTCGAGGACAC 1450
QY 181 CGTTACAGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTTCTCGAGAAAGGAG 240
DB 1451 CGTTACAGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTTCTCGAGAAAGGAG 1510
QY 241 GAGGATCATGTAGCGCCGGAGAGTGGACCTGTCAGCTGCTGGTGGTGGCGGACG 300
DB 1511 GAGGATCATGTAGCGCCGGAGAGTGGACCTGTCAGCTGCTGGTGGTGGCGGACG 1570
QY 301 CATGATCTCTCGAATCTGTGGTGGCATTCAGCATACGCGCAATGTCAACAATCAGGCC 360
DB 1571 CATGATCTCTCGAATCTGTGGTGGCATTCAGCATACGCGCAATGTCAACAATCAGGCC 1630
QY 361 TGGGACAGACGAGCAGAGGAGGAGACAGAGAAAAAGAAAAACAGAGCATGAGAACAG 420
DB 1631 TGGGACAGACGAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACAGAGCATGAGAACAG 1690
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGGAAT 480
DB 1691 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGGAAT 1750
QY 481 GGTACCAATTTTTCAGTGTGGACTGACAGCTTCTTTGGCCACAACAGAGGAATTT 540
DB 1751 GGTACCAATTTTTCAGTGTGGACTGACAGCTTCTTTGGCCACAACAGAGGAATTT 1810

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QY 541 AACACTGTTTCAACCCGGGAGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTAG 600
DB 1811 AACACTGTTTCAACCCGGGAGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTAG 1870
QY 601 ACAGTG 606
DB 1871 ACAGTG 1876

RESULT 5
ABL40352
ID ABL40352 standard; cDNA; 1897 BP.
XX AC
XX ABL40352;
XX DT 28-JUN-2002 (first entry)
XX DE Ovarian carcinoma O1034C/0591S consensus nucleotide sequence.
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX KW ss.
XX OS Homo sapiens.
XX FH
XX FT Key Location/Qualifiers
XX FT CDS 260..685
XX FT /*tag= a
XX FT /product= "Ovarian carcinoma protein O1034C/0591S"
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX PS WPI; 2002-171027/22.
XX DR P-PSDB; ABB09417.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX PT prevention and/or treatment of cancer, especially ovarian cancer.
XX PS Claim 1a; Page 127-128; 131pp; English.

The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the ovarian carcinoma O1034C/0591S consensus
CC nucleotide sequence.

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XX SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:
Query Match          97.0%; Score 606; DB 24; Length 1897;
Best Local Similarity 100.0%; Pred. No. 1.6e-231;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTTCTCTTGGACAGAGACTGGCCGCGGAGCGGACAGCAACGGCGCTGCACAAACG 60
    |||||||
DB 1271 AGTTCTCTTGGACAGAGACTGGCCGCGGAGCGGACAGCAACGGCGCTGCACAAACG 1330
    |||||||
OY 61 GCGCGTGTGGTGGAGTGGCCATGTAGCCGAGCGCTCTCTGTGTGGTGGTGTG 120
    |||||||
DB 1331 GCGCGTGTGGTGGAGTGGCCATGTAGCCGAGCGCTCTCTGTGTGGTGGTGTG 1390
    |||||||
OY 121 CAGCGACAGCGCGGACAGCAGCAGCTGCAGCAACACCCGCGGAACCTGCTGAGAGAC 180
    |||||||
DB 1391 CAGCGACAGCGCGGACAGCAGCAGCTGCAGCAACACCCGCGGAACCTGCTGAGAGAC 1450
    |||||||
OY 181 CGGTACAGAGCGGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 240
    |||||||
DB 1451 CGGTACAGAGCGGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 1510
    |||||||
OY 241 GAGGATCATGTACGCCGCGGAGTAGGACCTGCTGCTGCTGGTGGTGGCGGACG 300
    |||||||
DB 1511 GAGGATCATGTACGCCGCGGAGTAGGACCTGCTGCTGCTGGTGGTGGCGGACG 1570
    |||||||
OY 301 CATGATCTCTCGAATCTGTTGGGCATCAGCATACGCCAATGTCAACAAATCAGGCC 360
    |||||||
DB 1571 CATGATCTCTCGAATCTGTTGGGCATCAGCATACGCCAATGTCAACAAATCAGGCC 1630
    |||||||
OY 361 TGGCGACAGCAGCAGAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
    |||||||
DB 1631 TGGCGACAGCAGCAGAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 1690
    |||||||
OY 421 TAAATATTAACCACTAAATATTTAGCCCTGTTCTGTCTGTGGCCAGGAAT 480
    |||||||
DB 1691 TAAATATTAACCACTAAATATTTAGCCCTGTTCTGTCTGTGGCCAGGAAT 1750
    |||||||
OY 481 GGTACCAATTTTCACTGTTGACCTGACAGCTTTTGGCACAAGCAAGAGAAATT 540
    |||||||
DB 1751 GGTACCAATTTTCACTGTTGACCTGACAGCTTTTGGCACAAGCAAGAGAAATT 1810
    |||||||
OY 541 AACACGTGTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 600
    |||||||
DB 1811 AACACGTGTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 1870
    |||||||
OY 601 ACAGTG 606
    |||||||
DB 1871 ACAGTG 1876
    |||||||

RESULT 6
AB054231
ID AB054231 standard; cDNA; 1608 BP.
XX
XX AB054231:
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;
XX gene; ss.

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XX OS Homo sapiens.
XX
XX PN WO200200677-A1.
XX
XX PD 03-JAN-2002.
XX
XX PF 07-JUN-2001; 2001WO-US18569.
XX
XX PR 07-JUN-2000; 2000US-209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX BIASE CE, ROSEN CA;
XX
XX WPI: 2002-147878/19.
XX P-PSDB: ABP41154.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases -
XX
XX PS Claim 1; SEQ ID NO 111; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
XX CC encompasses polypeptides 90% identical and polynucleotides 95% identical
XX CC to the sequences of the invention. The invention additionally relates to
XX CC recombinant vectors and host cells comprising human ovarian antigen
XX CC polynucleotides, antibodies against human ovarian antigens, and the use
XX CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX CC treating, prognosing or preventing various ovary and/or breast-related
XX CC disorders. Such conditions include ovarian cancer and breast cancer, and
XX CC metastatic tumours of ovarian or breast origin, reproductive system
XX CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX CC vaginitis), immune disorders (e.g., congenital and acquired
XX CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX CC respiratory disorders, neurological disorders, gastrointestinal disorders
XX CC and urinary system disorders. Ovarian antigen polypeptides and
XX CC polynucleotides may also be used in screening for compounds which
XX CC modulate ovarian antigen expression or activity. The polynucleotides may
XX CC further be used for gene therapy, chromosome mapping, in the
XX CC identification of individuals and in forensic analysis, and the
XX CC polypeptides may be used as food additives or to prepare antibodies
XX CC useful in disease diagnosis, drug targeting and phenotyping. The present
XX CC sequence represents cDNA encoding a human ovarian antigen of the
XX CC invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences.
XX
XX SQ Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other:
Query Match          88.8%; Score 555; DB 24; Length 1608;
Best Local Similarity 99.8%; Pred. No. 3e-211; 1; Indels 0; Gaps 0;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACTTCTCTTGGACAGAGACTGGCCGCGGAGCGGACAGCAACGGCGCTGCACAAACG 60
    |||||||
DB 925 AGTTCTCTTGGACAGAGACTGGCCGCGGAGCGGACAGCAACGGCGCTGCACAAACG 984
    |||||||
OY 61 GCGCGTGTGGTGGAGTGGCCATGTAGCCGAGCGCTCTCTGTGTGGTGGTGTG 120
    |||||||
DB 985 GCGCGTGTGGTGGAGTGGCCATGTAGCCGAGCGCTCTCTGTGTGGTGGTGTG 1044
    |||||||
OY 121 CAGCGACAGCGCGGACAGCAGCAGCTGCAGCAACACCCGCGGAACCTGCTGAGAGAC 180
    |||||||
DB 1045 CAGCGACAGCGCGGACAGCAGCAGCTGCAGCAACACCCGCGGAACCTGCTGAGAGAC 1104
    |||||||

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QY 181 CGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCCGAGAAAGGAG 240
|||||
Db 1105 CGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCCGAGAAAGGAG 1164
QY 241 GAGGATCATGTAGACCGCGGAAGTAGACCTGCTCCAGTCTGCTTGGGTTGGCCGACG 300
|||||
Db 1165 GAGGATCATGTAGACCGCGGAAGTAGACCTGCTCCAGTCTGCTTGGGTTGGCCGACG 1224
QY 301 CATGATCCTCCGAATCTGCTTGGGATCATGATACGCGCAATGTGCACAAATATAGCCC 360
|||||
Db 1225 CATGATCCTCCGAATCTGCTTGGGATCATGATACGCGCAATGTGCACAAATATAGCCC 1284
QY 361 TGGCGACAGACAGAGAGAGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 420
|||||
Db 1285 TGGCGACAGACAGAGAGAGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 1344
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
|||||
Db 1345 TAAATRAATTAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 1404
QY 481 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 540
|||||
Db 1405 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 1464
QY 541 AACACTGTTTCAAAACCCGCGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
|||||
Db 1465 AACACTGTTTCAAAACCCGCGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 1524
QY 601 ACACTG 606
|||||
Db 1525 ACACTG 1530

RESULT 7

AAF22400/c
ID AAF22400 standard; cDNA; 1953 BP.

XX AAF22400;

DT 26-MAR-2001 (first entry)

XX Human secreted protein gene 28 SEQ ID NO:38.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KM antineumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KM cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KM fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KM rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KM cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KM angiodysplasia; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing; skin aging;
KM food additive; preservative; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO200061629-A1.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09071.

PR 09-APR-1999; 99US-0128694.

PR 20-JAN-2000; 2000US-0176931.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Komatsoulis G;

DR WPI: 2000-647420/62.

DR P-PSDB; AAB63161.

PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; Page 440; 533pp; English.

XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
CC and polypeptides homologous to them. Human secreted proteins have
CC activities based on the tissues and cells the genes are expressed in.
CC Examples of activities include: immunosuppressive; antiarthritic;
CC antineumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The polynucleotides and proteins can be
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
CC also used in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular
CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
CC ischaemia, angiodysplasia, nervous system disorders e.g. Alzheimer's
CC disease, infections caused by bacteria, viruses and fungi and ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. AAF22364 to
CC AAF22372 and AAB63133 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 88.8%; Score 555; DB 21; Length 1953;

Best Local Similarity 99.8%; Pred. No. 2.9e-211;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 AGTTCTCCTTCAGAGAGACTGCGCGGAGCGAAGAGCAACGGCCCTGCACAAACG 60
|||||
Db 684 AGTTCTCCTTCAGAGAGACTGCGCGGAGCGAAGAGCAACGGCCCTGCACAAACG 625
QY 61 GCGCGTGTGCGTGTGAGTGGCGCATGTACGGCGGCGCTTCTGCTGTTGGCGCTG 120
|||||
Db 624 GCGCGTGTGCGTGTGAGTGGCGCATGTACGGCGGCGCTTCTGCTGTTGGCGCTG 565
QY 121 CAGCGACAGGGGCGACACACACCTGACAGAACCCGCGCAATCTCTGAGAGACAC 180
|||||
Db 564 CAGCGACAGGGGCGACACACACCTGACAGAACCCGCGCAATCTCTGAGAGACAC 505
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAAAGAAACGCTCCGAGAAAGGAG 240
|||||
Db 504 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAAAGAAACGCTCCGAGAAAGGAG 445
QY 241 GAGGATCATGTAGACCGCGGAAGTAGACCTGCTCCAGTCTGCTTGGTGGCCGACG 300
|||||
Db 444 GAGGATCATGTAGACCGCGGAAGTAGACCTGCTCCAGTCTGCTTGGTGGCCGACG 385
QY 301 CATGATCCTCCGAATCTGCTTGGGATCATGATACGCGCAATGTGCACAAATATAGCCC 360
|||||
Db 384 CATGATCCTCCGAATCTGCTTGGGATCATGATACGCGCAATGTGCACAAATATAGCCC 325
QY 361 TGGCGACAGACAGAGAGAGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 420
|||||
Db 324 TGGCGACAGACAGAGAGAGAGAGACAGAAAAAGAAAAACACAGCATGAGAACACAG 265
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
|||||
Db 264 TAAATRAATTAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 205
QY 481 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 540
|||||
Db 204 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 145


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|||||
Db 1052 GGGGCTGTCGGTGGTGGATGCGCATGTACGCGAGGCGCTTCTGCTGCTGGCTGCTG 1111
OY 121 CACGACAGGCGGCGAGCAGCACC-TGCAGAACACCCGCGAAGACGTCGCGAGACA 179
Db 1112 CACGACAGGCGGCGAGCAGCACCCTTGCAGAACACCCGCGAAGACGTCGCGAGACA 1171
OY 180 CCGTGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAGAAAGCTCCGAGAGGGA 239
Db 1172 CCCTGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAGAAAGCTCCGAGAGGGA 1231
OY 240 GAGAGATCATGTACGCGCGAAGTAGAAGCTGTCAGTCTGCTGGGTTGGCCGAG 299
Db 1232 GAGAGATCATGTACGCGCGAAGTAGAAGCTGTCAGTCTGCTGGGTTGGCCGAG 1291
OY 300 CCATGATCCTCCGAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCCTCCGAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 1351
OY 360 CTGGGACAGACAGCAGAGAGAGAGACAGAGAAAGAAAGAACACACATGAGAACACA 419
Db 1352 CTGGGACAGACAGCAGAGAGAGAGAGACAGAGAAAGAAAGAACACACATGAGAACACA 1411
OY 420 GTAAATGAATAAACCATTAATTTTAGCCCTCTGCTGCTTACTGCGCAGAAA 479
Db 1412 GTAAATGAATAAACCATTAATTTTAGCCCTCTGCTGCTTACTGCGCAGAAA 1471
OY 480 TGGTACCAATTTTTCAGTGTGACTGTGACAGCTTTTCCACACAGCAGAGAGATT 539
Db 1472 TGGTACCAATTTTTCAGTGTGACTGTGACAGCTTTTCCACACAGCAGAGAGATT 1531
OY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTA 1591
OY 600 GACAGTG 606
Db 1592 GACAGTG 1598

RESULT 11
ABT03281
ID ABT03281 standard; cDNA; 1619 BP.
XX
AC ABT03281;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX
OS cytoskeletal; gene; ss.
XX
PN Homo sapiens.
XX
MO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001MO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
PR 03-APR-2001; 2001US-0825294.
XX
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in

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PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
PS Claim 2; page 195; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 77.8%; Score 486; DB 24; Length 1619;
Best Local Similarity 99.8%; Pred. No. 7.8e-184;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AGTTTCCTTTCAGAGAGACTGCGCCGCGGAGCGGAGAGAACGCGGCTGCACAAACG 60
Db 992 AGTTTCCTTTCAGAGAGACTGCGCCGCGGAGCGGAGAGAACGCGGCTGCACAAACG 1051
OY 61 GCGGCTGCGGTGGTGGAGTGGCCATGTACCGCAGCGCTTCTGCTGCTGGCTGCTG 120
Db 1052 GCGGCTGCGGTGGTGGAGTGGCCATGTACCGCAGCGCTTCTGCTGCTGGCTGCTG 1111
OY 121 CAGCGACAGGCGGCGAGCAGCAGC-TCGACGAAACACCGCGCAACTGCTGCGAGGACA 179
Db 1112 CAGCGACAGGCGGCGAGCAGCAGCCTTTCGACGAAACACCGCGCAACTGCTGCGAGGACA 1171
OY 180 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAAAGAAAGCTCCGAGAGGGA 239
Db 1172 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAAAGAAAGCTCCGAGAGGGA 1231
OY 240 GAGAGATCATGTACGCGCGGAAATAGAGACTCGTCCAGTGTGCTTGGCCGAG 299
Db 1232 GAGAGATCATGTACGCGCGGAAATAGAGACTCGTCCAGTGTGCTTGGCCGAG 1291
OY 300 CCATGATCCTCCGAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCCTCCGAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 1351
OY 360 CTGGGACAGACAGCAGAGAGAGAGACAGAGAAAGAAAGAACACACATGAGAACACA 419
Db 1352 CTGGGACAGACAGCAGAGAGAGAGAGACAGAGAAAGAAAGAACACACATGAGAACACA 1411
OY 420 GTAAATGAATAAACCATTAATTTTAGCCCTCTGCTGCTTACTGCGCAGAAA 479
Db 1412 GTAAATGAATAAACCATTAATTTTAGCCCTCTGCTGCTTACTGCGCAGAAA 1471
OY 480 TGGTACCAATTTTTCAGTGTGACTGTGACAGCTTCTTTCGCAAGAGAGAGATT 539
Db 1472 TGGTACCAATTTTTCAGTGTGACTGTGACAGCTTCTTTCGCAAGAGAGAGATT 1531
OY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTA 1591
OY 600 GACAGTG 606
Db 1592 GACAGTG 1598

RESULT 12
ABL40345
ID ABL40345 standard; cDNA; 1619 BP.
XX
AC ABL40345;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX ss.

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XX OS Homo sapiens.
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGN/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX PS prevention and/or treatment of cancer, especially ovarian cancer -
XX PS Claim 1a; Page 119-120; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or
XX CC gene therapy. Polypeptides and polynucleotides of the invention are
XX CC useful for detecting a cancer in a patient, for stimulating and/or
XX CC expanding T-cells specific for a tumour protein, and for inhibiting the
XX CC development of a cancer in a patient. They are also useful for
XX CC stimulating an immune response in a patient, and for treating a cancer in
XX CC a patient and for determining the presence of a cancer in a patient.
XX CC The isolated polynucleotides of the invention are useful for their
XX CC ability to selectively form duplex molecules with complementary stretches
XX CC of the entire desired gene or gene fragments, and for designing and
XX CC preparing ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX CC invention are also useful in recombinant DNA molecules to direct
XX CC expression of a polypeptide in appropriate host cells. The current
XX CC sequence represents the extended cDNA sequence of ovarian carcinoma
XX CC isolate 57887 given in record ABL48956.
XX SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
XX
XX Query Match 77.8%; Score 486; DB 24; Length 1619;
XX Best Local Similarity 99.8%; Pred. No. 7.8e-184;
XX Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 AGTTCTCTTGCAGAGACTGGCCGGGAGCGGAGCAAGACAGCGCGCTGCACAAACG 60
XX DB 992 AGTTCTCTTGCAGAGACTGGCCGGGAGCGGAGCAAGACAGCGCGCTGCACAAACG 1051
XX
XX QY 61 GCGCGTTCGGTGGTGGATGACCGGATGACCGGAGCGCGCTTCTGCTGGTGGCGTGC 120
XX DB 1052 GCGCGTTCGGTGGTGGATGACCGGATGACCGGAGCGCGCTTCTGCTGGTGGCGTGC 1111
XX
XX QY 121 CAGCAGACGGCGGAGCAGCAGCACC-TGCACGAAACACCGCGGAAACTGCTCGAGAGACA 179
XX DB 1112 CAGCAGACGGCGGAGCAGCAGCACCCTTGCAGCAACACCGCGGAAACTGCTCGAGAGACA 1171
XX
XX QY 180 CCGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAAAGTCTTCGAGAAAGGGA 239
XX DB 1172 CCGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAAAGTCTTCGAGAAAGGGA 1231
XX
XX QY 240 GAGAGATCATGTAGCCCGGAAAGTAGAGACCTGCTCAGTCGGTGGTGGTGGCGGAG 299
XX DB 1232 GAGAGATCATGTAGCCCGGAAAGTAGAGACCTGCTCAGTCGGTGGTGGTGGCGGAG 1291

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QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCATGTGCACAATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCATGTGCACAATCAGCC 1351
QY 360 CTGGGCGAGACAGCAGCAGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACA 419
DB 1352 CTGGGCGAGACAGCAGCAGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACA 1411
QY 420 GTAATGAAATAAAAACCATAAATATTTTAGCCCTCTGTTCTGTGCTTACCTGGCCAGAAA 479
DB 1412 GTAATGAAATAAAAACCATAAATATTTTAGCCCTCTGTTCTGTGCTTACCTGGCCAGAAA 1471
QY 480 TGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGAGAGAAAT 539
DB 1472 TGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAAGAGAGAAAT 1531
QY 540 TAACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAGAAAGCAATTAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAGAAAGCAATTAATGCTTTA 1591
QY 600 GACAGTG 606
DB 1592 GACAGTG 1598

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RESULT 13
ABL40349
ID ABL40349 standard; cDNA; 1619 BP.
XX AC ABL40349;
XX DT 28-JUN-2002 (first entry)
XX DE Ovarian carcinoma O5915 nucleotide sequence.
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGN/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX PS prevention and/or treatment of cancer, especially ovarian cancer -
XX PS Claim 1a; Page 125-126; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or
XX CC gene therapy. Polypeptides and polynucleotides of the invention are
XX CC useful for detecting a cancer in a patient, for stimulating and/or
XX CC expanding T-cells specific for a tumour protein, and for inhibiting the
XX CC development of a cancer in a patient. They are also useful for
XX CC stimulating an immune response in a patient, and for treating a cancer in

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PR	02-OCT-2001; 2001US-0970966.
PA	(CORI-) CORIXA CORP.
PI	Xu J, Stolk JA, Algate PA, Fling SP, Moles DA;
XX	WPI: 2002-500186/53.
DR	
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
PT	detecting the presence of ovarian cancer in a patient, and in
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PS	
XX	Claim 2; Page 193; 197pp; English.
CC	The present invention provides human ovarian cancer associated proteins
CC	and coding sequences. The sequences can be used in the diagnosis and
CC	treatment of ovarian cancers. The present sequence is a coding sequence
CC	of the invention.
XX	
SQ	Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other:
Query Match	57.4%; Score 359; DB 24; Length 1362;
Best Local Similarity	100.0%; Pred. No. 2.3e-133;
Matches 359; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AGTTCCTCCTGGAGAGGACTGGCGCGGAGCGCAAGAAGCAACGGGCCCTGCACAAGCG 60
Db	1215 AGTTCTCCTGTGAAGGACTGGCGCGGAGCGCAAGAAGCAAGGCGCTGCACAAGCG 1156
OY	61 GGCGCTGTGCGTGATGAGTGCGCATGTACGGCGCAGCGCCTTCTCGTGGTTGGCGTGTG 120
Db	1155 GGCGCTGTGCGTGATGAGTGCGCATGTACGGCGCAGCGCCTTCTCGTGGTTGGCGTGTG 1096
OY	121 CAGCACAGCGCGCGCAGCACAGCACCCTGCACGAAACCCCGCAACTGCTGGAGAGCAC 180
Db	1095 CAGCACAGCGCGCGCAGCACAGCACCCTGCACGAAACCCCGCAACTGCTGGAGAGCAC 1036
OY	181 CGTGTACAGGAGCGGGTTGATGATGACCGAGAGCTGAGTGAATAAACGTCTCGAAGAGGGAG 240
Db	1035 CGTGTACAGGAGCGGGTTGATGATGATGACCGAGAGCTGAGTGAATAAACGTCTCGAAGAGGGAG 976
OY	241 GAGGATCATGTATGAGCGCCCGGAAGTAGGACTCGTCCAAGTGTCTTGGGTTTGGCGGACG 300
Db	975 GAGGATCATGTATGAGCGCCCGGAAGTAGGACTCGTCCAAGTGTCTTGGGTTTGGCGGACG 916
OY	301 CATGATCCTCCGAATCTGTTGGGATCCAGATCCAGGATCCGGCAATGTACAAACATCAGCC 359
Db	915 CATGATCCTCCGAATCTGTTGGGATCCAGATCCAGGATCCGGCAATGTACAAACATCAGCC 857
RESULT 17	
ABLA0347/c	
ID	ABLA0347 standard; cDNA: 1362 BP.
XX	
AC	ABLA0347;
XX	
DT	28-JUN-2002 (first entry)
XX	
DE	Ovarian carcinoma GPR39 cDNA.
XX	
KM	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX	ss.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1362
FT	/tag= a
XX	/product= "Ovarian carcinoma protein GPR39"
XX	
XX	US2002004491-A1.

10-JAN-2002.

03-APR-2001: 2001US-0825294.

10-SEP-1999: 990S-0394374.

01-MAY-2000: 2000US-0561778.

15-AUG-2000: 2000US-0640173.

07-SEP-2000: 2000US-0656668.

14-NOV-2000: 2000US-0713550.

(XUJ/) XU J.

(STOL/) STOLK J A.

(ALGA/) ALGATE P A.

(FLIN/) FLING S P.

XU J, Stolk JA, Algate PA, Fling SP;
WPI; 2002-171027/22.
P-PDSB; ABB09416.

Ovarian tumour polypeptide and polynucleotide useful in diagnosis, -
prevention and/or treatment of cancer, especially ovarian cancer

Claim 1a: Page 123-124; 131pp; English.

	CC	The invention relates to ovarian tumour polynucleotides and polypeptides
	CC	that may be utilised in cancer therapy, for example in a vaccine or
	CC	gene therapy. Polypeptides and polynucleotides of the invention are
	CC	useful for detecting a cancer in a patient, for stimulating and/or
	CC	expanding T-cells specific for a tumour protein, and for inhibiting the
	CC	development of a cancer in a patient. They are also useful for
	CC	stimulating an immune response in a patient, and for treating a cancer in
	CC	a patient and for determining the presence of a cancer in a patient.
	CC	The isolated polynucleotides of the invention are useful for their
	CC	ability to selectively form duplex molecules with complementary stretches
	CC	of the entire desired gene or gene fragments, and for designing and
	CC	preparing ribozyme molecules for inhibiting expression of tumour
	CC	polypeptides in tumour cells. Polypeptides and polynucleotides of the
	CC	invention are also useful in recombinant DNA molecules to direct
	CC	expression of a polypeptide in appropriate host cells. The current
	CC	sequence represents the ovarian carcinoma GPR39 cDNA.
SQ	XX	
	Sequence	1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other:
	Query Match	57.4%; Score 359; DB 24; Length 1362;
	Best Local Similarity	100.0%; Pred. No. 2,3e-133;
	Matches 359; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	AGTTTCCTTGGAGAGSACTGCGCGGCAGACCAGAAAGACAACGGCGCTGCACANAAGC 60
DB	1215	ACTTCTCCTTGACAGAGSACTGGCGCGGCAGACGAAGACNACAGCGCCTGCACANAAGC 1156
QY	61	GCGCGCTGTGCGTGTGGAGTAGTGCATGTACGGCGCAGCGCCTTCTGTGGTGGCGTCTG 120
DB	1155	GGCGCTGTGCGTGTGGAGTAGTGCATGTACGGCGCAGCGCCTTCTGTGGTGGCGTCTG 1096
QY	121	CAGCGACAGAGCGCGCAGACAGCACCTGCAAGAACACCCGCCAATCTGTGGAGAGAC 180
DB	1095	CAGCGACAGAGCGCGCAGACAGCACCTGCAAGAACACCCGCCAATCTGTGGAGAGAC 1036
QY	181	CGTGTACAGAGAGCGGGGTGTATACCGAGCTGAGGTAGAATAAACGTCCTCCGAGAAGG 240
DB	1035	CGTGTACAGAGAGCGGGGTGTATACCGAGCTGAGGTAGAATAAACGTCCTCCGAGAAGG 976
QY	241	GAGGATTCATGTACGCCCGGAAGTAGACCTCTCCAGTCGTGCTTGGGTTGGCCGAC 300
DB	975	GAGGATTCATGTACGCCCGGAAGTAGACCTCTCCAGTCGTGCTTGGGTTGGCCGAC 916
QY	301	CATGATCTCTCGAATCTGTGGTGGCATCCAGACATACGGCCAATGTACAAATCAGCC 359
DB	915	CATGATCTCTCGAATCTGTGGGATCCAGACATACGGCCAATGTACAAATCAGCC 857

Db 431 CCGAGCTGAGTAGAAAACTCTCCGAGAGGAGAGATCATGTACGCCCGAGAGT 372
 Qy 264 AGGACCTGTCACAGTGTGCTGGTTGGCCGACCATGATCCCTCCGATCTGGTTGG 323
 Db 371 AGGACCTGTCACAGTGTGCTGGTTGGCCGACCATGATCCCTCCGATCTGGTTGG 312
 Qy 324 GCATCCACATACGGCCCATATGTACACAAATCAGCCCTGGGACAGACAGACAGAGGGA 383
 Db 311 GCATCCACATACGGCCCATATGTACACAAATCAGCCCTGGGACAGACAGACAGAGGGA 252
 Qy 384 GAGACAGAGAAAAAGAAAAACAGCATGAGACAGATGAATGAATGAATGAATGAATGA 443
 Db 251 GAGACAGAGAAAAAGAAAAACAGCATGAGACAGATGAATGAATGAATGAATGAATGA 192
 Qy 444 TTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
 Db 191 TTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
 Qy 504 CTGACAGCTTCTTTTGGCACAAGCAGAGAGATTTAACTGTTTCAAAACCCGGGGGA 563
 Db 131 CTGACAGCTTCTTTTGGCACAAGCAGAGAGATTTAACTGTTTCAAAACCCGGGGGA 72
 Qy 564 GTTGGCTGTGTTAAAGAAAGAACCATTAATGCTTTAGACAGTG 606
 Db 71 GTTGGCTGTGTTAAAGAAAGAACCATTAATGCTTTAGACAGTG 29

RESULT 20
 ABL78538/c
 ID ABL78538 standard; cDNA: 373 BP.
 AC ABL78538;
 XX
 DT 17-MAY-2002 (first entry)
 DE Human ovarian cancer related cDNA clone SEQ ID NO:1516.
 XX
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 OS Homo sapiens.
 XX
 PN W0200192581-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US17756.
 XX
 PR 26-MAY-2000; 2000US-207484P.
 XX
 PA (CORI-) CORIXA CORP.
 PI Algate PA, Harlocker SL, Jones R;
 XX
 DR WPI: 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide
 XX
 PS Claim 1: SEQ ID 1516; 489bp; English.
 XX
 CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polynucleotide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (1) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (S1) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to

CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (II) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.

SQ Sequence 373 BP; 83 A; 96 C; 80 G; 114 T; 0 other;

Query Match 50.2%; Score 314; DB 24; Length 373;

Best Local Similarity 100.0%; Pred. No. 2e-115;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 293 GCCGACCATGATCTCCGATCTGTTGGCATCCAGCATACGCCCATGTCAACACA 352
 Db 315 GCCGACCATGATCTCCGATCTGTTGGCATCCAGCATACGCCCATGTCAACACA 256
 Qy 353 ATCAGCCCTGGGACAGACGAGCAGAGAGAGACAGAGAAAAACACAGCATGA 412
 Db 255 ATCAGCCCTGGGACAGACGAGCAGAGAGAGAGAGAGAAAAACACAGCATGA 196
 Qy 413 GAACACAGTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 472
 Db 195 GAACACAGTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 136
 Qy 473 CAGGAAATGTGACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTTGCACACAGCA 532
 Db 135 CAGGAAATGTGACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTTGCACACAGCA 76
 Qy 533 GAGAAATTAACAGCTTTTCAAAACCCGGGAGAGTTGGCTGTTAAAGAAACCATTA 592
 Db 75 GAGAAATTAACAGCTTTTCAAAACCCGGGAGAGTTGGCTGTTAAAGAAACCATTA 16
 Qy 593 TGCCTTAGACAGTG 606
 Db 15 TGCCTTAGACAGTG 2

RESULT 21
 ABL79431/c
 ID ABL79431 standard; cDNA: 349 BP.
 AC ABL79431;
 XX
 DT 17-MAY-2002 (first entry)
 DE Human ovarian cancer related cDNA clone SEQ ID NO:2409.
 XX
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 OS Homo sapiens.
 XX
 PN W0200192581-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US17756.
 XX
 PR 26-MAY-2000; 2000US-207484P.
 XX
 PA (CORI-) CORIXA CORP.
 PI Algate PA, Harlocker SL, Jones R;
 XX
 DR WPI: 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide

PT polypeptide -

XX
XX
PS Claim 1: SEQ ID 2409; 489pp; English.

CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.

XX
XX
SO Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other;

Query Match 49.1%; Score 307; DB 24; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.2e-112;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCAATGATCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTCAACAATCAGCC 359
DB 310 CCAATGATCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTCAACAATCAGCC 251
QY 360 CTGGGGACACGACGACGAGGAGAGACAGAGAAAAAACAACAGATGAGACACA 419
DB 250 CTGGGGACACGACGAGGAGGAGAGACAGAGAAAAAACAACAGATGAGACACA 191
QY 420 GTAAATGAATAAACCAATTAATTTAGCCCTCTGCTGCTTACTGGCCAGGAAA 479
DB 190 GTAAATGAATAAACCAATTAATTTAGCCCTCTGCTGCTTACTGGCCAGGAAA 131
QY 480 TGGTACCAATTTTCACTGTGACTTGACAGCTTCTTTTGCACAAGCAGAGAGATT 539
DB 130 TGGTACCAATTTTCACTGTGACTTGACAGCTTCTTTTGCACAAGCAGAGAGATT 71
QY 540 TAAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAATGCTTTA 599
DB 70 TAAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAATGCTTTA 11
QY 600 GACAGTG 606
DB 10 GACAGTG 4

RESULT 22
ABL81262/c
ID ABL81262 standard; cDNA; 409 BP.
XX
AC ABL81262;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:4240.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.

PD 06-DEC-2001.
XX
XX
PE 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
DR WPI; 2002-122075/16.
XX
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide -

PS Claim 1; SEQ ID 4240; 489pp; English.

XX
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of an ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.

XX
XX
SO Sequence 409 BP; 89 A; 106 C; 87 G; 127 T; 0 other;

Query Match 42.1%; Score 263; DB 24; Length 409;
Best Local Similarity 99.7%; Pred. No. 3.0e-95;
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 293 GCGGAGCCATGATCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTCAACA 352
DB 315 GCGGAGCCATGATCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTCAACA 256
QY 353 ATCAGCCCTGGGACACGACGAGGAGGAGAGACAGAGAAAAAACAACAGATGA 412
DB 255 ATCAGCCCTGGGACACGACGAGGAGGAGAGACAGAGAAAAAACAACAGATGA 196
QY 413 GAACACAGTAATTAATTAATTAATTAATTTAGCCCTCTGCTGCTTACTGGC 472
DB 195 GAACACAGTAATTAATTAATTAATTAATTTAGCCCTCTGCTGCTTACTGGC 136
QY 473 CAGGAATGTACCAATTTTCACTGTGACTTGACAGCTTCTTTTGCACAAGCAGAA 532
DB 135 CAGGAATGTACCAATTTTCACTGTGACTTGACAGCTTCTTTTGCACAAGCAGAA 76
QY 533 GAGAAATTTAAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAA 592
DB 75 GAGAAATTTAAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAA 16
QY 593 TGCCTTTAGACAGTG 606
DB 15 TGCCTTTAGACAGTG 2

RESULT 23

Db 209 GCGGCTGTCGGTGAGTGGCAGTATGACGC 240

RESULT 27

AL33985/C

ID AAL33985 standard; DNA; 50 BP.

AC AAL33985;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #7193.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3451; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;

XX Query Match 4.2%; Score 26; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 0.68;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 293 GCGGAGCATGATCTCGAATCTG 318

Db 26 GCGGAGCATGATCTCGAATCTG 1

RESULT 28

AL33986/C

ID AAL33986 standard; DNA; 50 BP.

AC AAL33986;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #7194.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3451; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 other;

XX Query Match 4.2%; Score 26; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 0.68;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 ACCTGTCAGTGTCTGTTGGTTTG 292

Db 50 ACCTGTCAGTGTCTGTTGGTTTG 25

RESULT 29
AAL27277/C
ID AAL27277 standard; DNA; 51 BP.

XX AL27277;
AC 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #485.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000MO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections.
XX
PS Claim 1; Page 1529; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid protein, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 9 A; 5 C; 10 G; 27 T; 0 other;
XX

Query Match 4.0%; Score 25; DB 22; Length 51;
Best Local Similarity 100.0%; Pred No. 1.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 401 AACACAGCATGAGACAGTAAT 425
DB 51 AACACAGCATGAGACAGTAAT 27

RESULT 30
ABAI8284
ID ABAI8284 standard; DNA; 263 BP.
XX
AC ABAI8284;
XX

DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 10615.
XX
KW Human; nocotropic; neuroprotective; cytostatic; dermatological; virocidic;
KW Immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnary;
KW antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer;
KW antiallergic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR
 XX
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure: SEQ ID NO 10615; 1701pp + Sequence listing; English.
 XX
 CC The invention relates to novel genes (ABAI1004-ABAI21534) and proteins
 CC (ABAI14678-ABAI18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 263 BP; 88 A; 36 C; 67 G; 71 T; 1 other;
 Query Match 3.7%; Score 23; DB 22; Length 263;
 Best Local Similarity 100.0%; Pred No. 8.7;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 603 AGTGNAAAAAAAAAAAAAAAAA 625
 Db 241 AGTGNAAAAAAAAAAAAAAAAA 263
 AAL10167/c
 ID AAL10167 standard; cDNA; 377 BP.
 XX
 AC AAL10167;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Human breast cancer expressed polynucleotide 2624.
 XX
 KW Human; breast cancer; cell marker; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200151628-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 10-JAN-2001; 2001WO-US00798.
 XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
CC
SQ Sequence 1539 BP; 577 A; 372 C; 435 G; 146 T; 9 other;

Query Match 3.7%; Score 23; DB 23; Length 1539;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 AGACAGAGAGAGAGAGAGAGAG 407
DB 878 AGACAGAGAGAGAGAGAGAGAG 900
|||||

RESULT 34
ABK53839
ID ABK53839 standard; cDNA; 256 BP.
XX
AC ABK53839;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human head and neck tumour CDNA, SEQ ID No 34.
XX
KM Human; head and neck cancer; tumour; cytostatic; immunogenic; vaccine;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212329-A2.
XX
PD 14-FEB-2002.
XX
PE 01-AUG-2001; 2001WO-US24226.
XX
PR 03-AUG-2000; 2000US-223281P.
PR 16-NOV-2000; 2000US-249933P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Fan L;
XX
DR WPI; 2002-257467/30.
XX
PT Novel polynucleotide encoding head and neck tumour polypeptides, useful
PT in pharmaceutical compositions, e.g. vaccines, for treating head and
PT neck cancers -
XX
PS Claim 1; Page 123; 200pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising
CC sequences selected from 273 sequences fully defined in the specification.
CC (I), including its encoded polypeptide (II), an antibody binding to (II),
CC a fusion protein comprising (II) and a T-cell population stimulated by
CC (I) or (II) are useful for stimulating an immune response in a patient
CC and treating head and neck cancer in a patient. An oligonucleotide (III)
CC that hybridizes to (I) is useful for determining the presence of cancer
CC in a patient, by obtaining a biological sample from the patient,
CC contacting the sample with (III), detecting in the sample an amount of a
CC polynucleotide that hybridizes to the oligonucleotide, and comparing the

CC amount of polynucleotide that hybridizes to the oligonucleotides to a
CC predetermined cut-off value. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis and
CC treatment of head and neck cancer. ABK53806-ABK54078 represent human head
CC and neck cancer cDNA sequences of the invention.
CC
SQ Sequence 256 BP; 83 A; 31 C; 52 G; 83 T; 7 other;

Query Match 3.5%; Score 22; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAAAAAA 625
DB 213 GTGNAAAAAAAAAAAAAAAAAA 234
|||||

RESULT 35
ABV08332/C
ID ABV08332 standard; cDNA; 377 BP.
XX
AC ABV08332;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker CDNA 8323.
XX
KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200150860-A2.
XX
PD 23-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 1324; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

RESULT 38
ABK65378
ID ABK65378 standard; cDNA: 1388 BP.
XX
XX ABK65378;
XX
DT 02-JUL-2002 (first entry)
XX
XX Arabidopsis cDNA encoding a transcription factor #230.
DE
XX
XX Plant; ss: gene; transcription factor; transgenic;
KW agriculture; metabolic chemical; environmental stress; drought;
KW microbial disease resistance; herbicide resistance; seed yield;
KW fruit yield; growth rate; leaf senescence; flower senescence.
XX
XX Arabidopsis thaliana.
OS
XX
XX MO200215675-A1.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001MO-US26189.
XX
XX 22-AUG-2000; 2000US-227439P.
PR 16-NOV-2000; 2000US-0713994.
PR 16-APR-2001; 2001US-0837944.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (PIUG/) PILGRIM M.
PA (DUBB/) CREELMAN R.
PA (DUBB/) DUBBELL A J.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (KEDD/) KEDDIE J.
PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFFE O.
PA (REUB/) REUBER J L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O.
XX
PI Pilgrim M, Creelman R, Dubell AJ, Heard J, Jiang C, Keddie J;
PI Adam L, Ratcliff O, Reuber JL, Riechmann JL, Yu G, Pineda O;
XX
XX WPI: 2002-292022/33.
XX P-PSDB: AA093192.
XX
XX An isolated or recombinant polynucleotide used to produce a transgenic
XX plant -
XX
XX Claim 4; Page 927-929; 941pp; English.
XX
XX The invention relates to 1 of 232 isolated or recombinant polynucleotides
XX encoding an Arabidopsis thaliana transcription factor, their variants,
XX complements, fragments, or related polynucleotide with 31% to 95%
XX sequence identity, where the plant possesses an altered trait as compared
XX to a wild-type or reference plant, or the plant exhibits an altered
XX phenotype as compared to a wild-type or reference plant, or the plant
XX exhibits ectopic expression or altered expression of one or more genes
XX associated with a plant trait as compared to a wild plant. Also included
XX are a transgenic plant comprising the polynucleotides, a computer
XX readable medium having stored sequence information, and identifying a
XX sequence comprising a database comprising a plurality of known plant
XX sequences comprising inputting sequence information selected from one of
XX 464 fully defined sequences given in the specification. The isolated or
XX recombinant polynucleotide is used for producing a plant having a
XX modified trait, the method comprising selecting a polynucleotide that
XX encodes a polypeptide or an antisense nucleic acid, inserting the
XX polynucleotide or antisense nucleic acid into an expression vector,
XX introducing the vector into a plant or a cell of a plant to overexpress
XX the polypeptide or antisense nucleic acid, thereby producing a modified
XX plant, and selecting for a modified trait (e.g. increased
XX production of agriculturally useful proteins or metabolic chemicals,

CC pest tolerance, environmental stress response (e.g. drought), microbial
CC disease resistance, herbicide resistance, seed and fruit yield, growth
CC rate, leaf and flower senescence and many other traits listed in the
CC specification). The present sequence is one of the 232 polynucleotides
CC encoding an A. thaliana transcription factor.
XX
XX SQ Sequence 1388 BP; 398 A; 282 C; 319 G; 389 T; 0 other;
XX
XX Query Match 3.5%; Score 22; DB 24; Length 1388;
XX Best Local Similarity 100.0%; Pred. No. 18;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 374 GCAGAGGAGAGACAGAGAAA 395
XX |||||||||||||||||||
XX Db 991 GCAGAGGAGAGACAGAGAAA 1012
XX
XX
XX RESULT 39
XX AAH34281
XX ID AAH34281 standard; cDNA: 1823 BP.
XX
XX AAH34281;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen encoding cDNA SEQ ID NO:1363.
DE
XX
XX Human: colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
XX Homo sapiens.
XX
XX MO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-US26524.
XX
XX 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI: 2001-235357/24.
XX P-PSDB: AAG74876.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 1; Page 3077-3078; 9803pp; English.
XX
XX AAH2993 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytosolic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Additionally, N may be used to produce the colon cancer-associated P,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P may be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAG77789 represent sequences used in the exemplification of the
XX present invention.
XX
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.

Sequence 1823 BP; 355 A; 609 C; 516 G; 335 T; 8 other;

Query Match 3.5%; Score 22; DB 22; Length 1823;

Best Local Similarity 100.0%; Pred. No. 17; Mismatches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAA 625

DB 1726 GTGNAAAAAAAAAAAAAA 1747

RESULT 40

ABL90818/c

ID ABL90818 standard; cDNA; 2049 BP.

AC ABL90818;

DE Human polynucleotide SEQ ID NO 1380.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antifungal;

XX antiviral; anticonvulsant; antibacterial; antifungal; antiparasitic;

XX cardiact; gene therapy; cancer; immune disorder; cardiovascular disorder;

XX neurological disease; infection; human; secreted protein; gene; ss.

OS Homo sapiens.

PN WO200190304-A2.

XX 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US16450.

PR 19-MAY-2000; 2000US-205515P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barse CE, Rosen CA;

XX WPI: 2002-122018/16.

DR P-PSDB; ABB90409.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

PT prevention of neural, immune system, muscular, reproductive,

PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

PT disorders -

PS Claim 4; SEQ ID NO 1380; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-AB190853) and proteins

CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (anti)agonists are useful

CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone

CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC disease, hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2049 BP; 383 A; 571 C; 686 G; 400 T; 9 other;

XX Query Match 3.5%; Score 22; DB 24; Length 2049;

Best Local Similarity 100.0%; Pred. No. 17; Mismatches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAA 625

DB 325 GTGNAAAAAAAAAAAAAA 304

RESULT 41

AAH69474/c

ID AAH69474 standard; cDNA; 259 BP.

AC AAH69474;

DE Human cervical cancer marker nucleic acid 748.

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

XX Homo sapiens.

XX WO200142467-A2.

XX 14-JUN-2001.

XX 08-DEC-2000; 2000WO-US33312.

XX 08-DEC-1999; 99US-0169681.

XX 21-DEC-1999; 99US-0171350.

XX 14-MAR-2000; 2000US-0189315.

XX 12-MAY-2000; 2000US-0203791.

XX 09-JUN-2000; 2000US-0210600.

XX 21-JUL-2000; 2000US-0220114.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Deeds J, Berger A, Zhao X;

XX WPI: 2001-375006/39.

XX New isolated nucleic acid for diagnosing and treating cervical cancer

XX and for assessing and detecting compounds for treating the cancer -

XX Claim 1; Page 232; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with

CC cervical cancer with cytostatic activity. The nucleic acids and encoded

CC polypeptides are useful: to assess if a patient is afflicted with

CC cervical cancer or has a pre-malignant condition; to monitor the

CC progression of cervical cancer or a premalignant condition in a patient;

CC and to select and/or assess the efficacy of a compound or therapy for

CC inhibiting cervical cancer in a patient. The nucleic acids may also be

CC useful for gene therapy.

XX Sequence 259 BP; 73 A; 33 C; 37 G; 87 T; 29 other;

XX Query Match 3.4%; Score 21; DB 22; Length 259;

XX Best Local Similarity 100.0%; Pred. No. 54;

XX Mismatches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAAAAA 625

DB 63 TGNAAAAAAAAAAAAAAAAA 43

RESULT 42

AA109957/c

ID AA109957 standard; cDNA; 288 BP.

XX AA109957;

XX 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 2414.
XX KM Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220354.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 462; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
CC (AAU07544-AAU26788) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX SQ Sequence 288 BP; 76 A; 53 C; 75 G; 79 T; 5 other;
Query Match 3.4%; Score 21; DB 22; Length 288;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 605 TGNAAAAAAAAAAAAAAAAA 625
DB 70 TGNAAAAAAAAAAAAAAAAA 50
RESULT 43
ABV05091/C
ID ABV05091 standard; CDNA; 288 BP.
XX AC ABV05091;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker CDNA 5082.
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX DR Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX PS Claim 1; Page 864; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 288 BP; 76 A; 37 C; 29 G; 112 T; 34 other;
Query Match 3.4%; Score 21; DB 23; Length 288;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 605 TGNAAAAAAAAAAAAAAAAA 625
DB 55 TGNAAAAAAAAAAAAAAAAA 35
RESULT 44
ABV05770/C
ID ABV05770 standard; CDNA; 294 BP.
XX AC ABV05770;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker CDNA 5761.
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.

451

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 XX MPI: 2001-662795/76.
 XX
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 962; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 SQ Sequence 294 BP; 79 A; 52 C; 34 G; 119 T; 10 other;

Query Match 3.4%; Score 21; DB 23; Length 294;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
 ||||||||||||||||||
 DB 31 TGNAAAAAAAAAAAAAAAAAAAA 11

RESULT 45
 AAH68974/C
 ID AAH68974 standard; CDNA; 359 BP.
 XX
 AC AAH68974;
 XX
 DT 19-SEP-2001 (first entry)
 XX
 DE Human cervical cancer marker nucleic acid 248.
 XX
 KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 OS
 XX
 FN WO200142467-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 08-DEC-2000; 2000WO-US33312.
 XX
 PR 08-DEC-1999; 99US-0169681.
 PR 21-DEC-1999; 99US-0171350.
 PR 14-MAR-2000; 2000US-0189315.
 PR 12-MAY-2000; 2000US-0203791.
 PR 09-JUN-2000; 2000US-0210600.
 PR 21-JUL-2000; 2000US-0220114.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Deeds J, Berger A, Zhao X;
 XX
 DR MPI: 2001-375006/39.
 XX

PT New isolated nucleic acid for diagnosing and treating cervical cancer
 PT and for assessing and detecting compounds for treating the cancer -
 XX
 XX
 PS Claim 1: Page 147; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
 CC cervical cancer with cytostatic activity. The nucleic acids and encoded
 CC polypeptides are useful: to assess if a patient is afflicted with
 CC cervical cancer or has a pre-malignant condition; to monitor the
 CC progression of cervical cancer or a premalignant condition in a patient;
 CC and to select and/or assess the efficacy of a compound or therapy for
 CC inhibiting cervical cancer in a patient. The nucleic acids may also be
 CC useful for gene therapy.
 CC
 SQ Sequence 359 BP; 96 A; 62 C; 48 G; 131 T; 22 other;

Query Match 3.4%; Score 21; DB 22; Length 359;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
 ||||||||||||||||||
 DB 82 TGNAAAAAAAAAAAAAAAAAAAA 62

Search completed: November 7, 2002, 18:15:34
 Job time : 142.06 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 23.4202 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agtctccttgcagagact.....gnaaaaaaaaaaaaaaaaaa 625

Scoring table: OLIGO_NDC
Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 10

Total number of hits satisfying chosen parameters: 97832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents: NA.*
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	3.4	377	3	US-08-946-026-41
2	21	3.4	407	4	US-09-385-982-519
3	21	3.4	631	4	US-09-149-476-67
4	21	3.4	804	4	US-09-149-476-125
5	21	3.4	2176	4	US-08-974-549A-3
6	21	3.2	2369	4	US-09-149-476-309
7	21	3.2	265	1	US-08-686-878A-46
8	20	3.2	265	4	US-09-175-928-45
9	20	3.2	296	2	US-09-032-684-13
10	20	3.2	500	2	US-08-967-101-82
11	20	3.2	500	2	US-08-592-541-82
12	20	3.2	500	3	US-09-124-698-82
13	20	3.2	500	4	US-09-127-480-82
14	20	3.2	500	4	US-08-496-841C-82
15	20	3.2	500	4	US-09-124-523-82
16	20	3.2	789	4	US-09-020-956-32
17	20	3.2	789	4	US-09-030-607-32
18	20	3.2	789	4	US-09-605-785-32
19	20	3.2	789	4	US-09-439-313-32
20	20	3.2	789	4	US-09-352-616A-32
21	20	3.2	789	4	US-08-232-149A-32
22	20	3.2	1062	4	US-09-149-476-108
23	20	3.2	1210	4	US-09-443-041A-29
24	19	3.0	30	4	US-09-648-040-4
25	19	3.0	40	2	US-08-859-106A-4
26	19	3.0	40	4	US-09-011-540-11
27	19	3.0	51	4	US-09-051-079-5

28	19	3.0	52	3	US-08-618-100B-9	Sequence 9, Appl
29	19	3.0	69	1	US-08-702-344-7	Sequence 7, Appl
30	19	3.0	69	1	US-08-702-344-72	Sequence 22, Appl
31	19	3.0	69	4	US-09-289-911A-7	Sequence 7, Appl
32	19	3.0	84	1	US-08-664-596B-3	Sequence 3, Appl
33	19	3.0	84	1	US-08-738-367-3	Sequence 266, App
34	19	3.0	193	4	US-09-991-789A-266	Sequence 37, Appl
35	19	3.0	193	4	US-09-062-451-266	Sequence 98, Appl
36	19	3.0	208	1	US-08-686-878A-37	Sequence 98, Appl
37	19	3.0	208	2	US-08-967-101-98	Sequence 98, Appl
38	19	3.0	208	3	US-09-124-698-98	Sequence 98, Appl
39	19	3.0	208	4	US-09-127-480-98	Sequence 37, Appl
40	19	3.0	208	4	US-08-496-841C-98	Sequence 98, Appl
41	19	3.0	208	4	US-09-175-928-37	Sequence 98, Appl
42	19	3.0	208	4	US-09-124-523-98	Sequence 43, Appl
43	19	3.0	244	1	US-08-686-878A-43	Sequence 715, App
44	19	3.0	310	4	US-09-328-111-715	
45	19	3.0				

ALIGNMENTS

RESULT 1
US-08-946-026-41
; Sequence 41, Application US/08946026
; Patent No. 6034218
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Markl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-026-41
Query Match 3.4%; Score 21; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 605 TGNAAAAAAAAAAAAAAAAA 625
349 TGNAAAAAAAAAAAAAAAAA 369

```

RESULT 2
US-09-385-982-519/c
; Sequence 519, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 519
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(407)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-519

Query Match          3.4%: Score 21; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAA 625
Db 33 TGNAAAAAAAAAAAAA 13

RESULT 3
US-09-149-476-67
; Sequence 67, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 166 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-08-22

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QY  605 TGNAAAAAAAAAAAAA 625
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RESULT 4
US-09-149-476-125
; Sequence 125, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
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EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
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EARLIER FILING DATE: 1997-10-02

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625
Db 767 TGNAAAAAAAAAAAAA 787

RESULT 5
US-08-974-549A-3
Sequence 3, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..2176
OTHER INFORMATION: /note="clone 712562"
NAME/KEY: CDS
LOCATION: 23..802
US-08-974-549A-3

Query Match 3.4%; Score 21; DB 4; Length 2176;
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Db 2148 TGNAAAAAAAAAAAAA 2168

RESULT 6
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Sequence 309, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 3.4%: Score 21; DB 4; Length 2369;
Best Local Similarity 100.0%: Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625
DB 28 TGNAAAAAAAAAAAAA 8

RESULT 7
US-08-686-878A-46
Sequence 46, Application US/08686878A
Patent No. 5708157
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Jacobs, Kenneth
APPLICANT: Lavalley, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-686-878A-46

Query Match 3.2%: Score 20; DB 1; Length 265;
Best Local Similarity 100.0%: Pred. No. 4.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 245 GNAAAAAAAAAAAAAA 264

RESULT 8
US-09-175-928-45
Sequence 45, Application US/09175928A
Patent No. 6312921
GENERAL INFORMATION:

APPLICANT: McCoy, John M.
APPLICANT: Lavalley, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Mi, Sha
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B,AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 265
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: unsure
LOCATION: (2)
FEATURE:
NAME/KEY: unsure
LOCATION: (67)
FEATURE:
NAME/KEY: unsure
LOCATION: (75)
FEATURE:
NAME/KEY: unsure
LOCATION: (79)
FEATURE:
NAME/KEY: unsure
LOCATION: (101)
FEATURE:
NAME/KEY: unsure
LOCATION: (104)
FEATURE:
NAME/KEY: unsure
LOCATION: (111)
FEATURE:
NAME/KEY: unsure
LOCATION: (121)
FEATURE:
NAME/KEY: unsure
LOCATION: (133)
FEATURE:

NAME/KEY: unsure
LOCATION: (136)
FEATURE:
NAME/KEY: unsure
LOCATION: (157)
FEATURE:
NAME/KEY: unsure
LOCATION: (162)
FEATURE:
NAME/KEY: unsure
LOCATION: (164)
FEATURE:
NAME/KEY: unsure
LOCATION: (172)
FEATURE:
NAME/KEY: unsure
LOCATION: (175)
FEATURE:
NAME/KEY: unsure
LOCATION: (183)
FEATURE:
NAME/KEY: unsure
LOCATION: (187)
FEATURE:
NAME/KEY: unsure
LOCATION: (192)
FEATURE:
NAME/KEY: unsure
LOCATION: (199)..(200)
FEATURE:
NAME/KEY: unsure
LOCATION: (208)
FEATURE:
NAME/KEY: unsure
LOCATION: (211)
FEATURE:
NAME/KEY: unsure
LOCATION: (223)
FEATURE:
NAME/KEY: unsure
LOCATION: (225)
FEATURE:
NAME/KEY: unsure
LOCATION: (227)
FEATURE:
NAME/KEY: unsure
LOCATION: (243)..(244)
FEATURE:
NAME/KEY: unsure
LOCATION: (246)
US-09-175-928-45

Query Match 3.2%; Score 20; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 245 GNAAAAAAAAAAAAAA 264

RESULT 9
US-09-032-684-13/c
Sequence 13, Application US/09032684
Patent No. 5882874
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: RECIPROCAL SUBTRACTION DIFFERENTIAL
TITLE OF INVENTION: DISPLAY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,684
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 55551/JPW/AMG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-032-684-13

Query Match 3.2%; Score 20; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 60 GNAAAAAAAAAAAAAA 41

RESULT 10
US-08-967-101-82/c
Sequence 82, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-967-101-82

Query Match 3.2%; Score 20; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAGAAAAAGAAAAAGAAAA 625
|||||
DB 34 GNAAGAAAAAGAAAAAGAAAA 15

RESULT 11
US-08-592-541-82/C

Sequence 82, Application US/08592541
Patent No. 5986054

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,541

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-592-541-82

Query Match 3.2%; Score 20; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAGAAAAAGAAAAAGAAAA 625
|||||
DB 34 GNAAGAAAAAGAAAAAGAAAA 15

RESULT 12
US-09-124-698-82/C

Sequence 82, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/124,698

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/592,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-124-698-82

Query Match 3.2%; Score 20; DB 3; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAGAAAAAGAAAAAGAAAA 625
|||||
DB 34 GNAAGAAAAAGAAAAAGAAAA 15

RESULT 13
US-09-127-480-82/C

Sequence 82, Application US/09127480
Patent No. 6194153

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/127,480

FILED DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-82

Query Match 3.2%; Score 20; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
Db 34 GNAAAAAAAAAAAAAA 15

RESULT 14

US-08-496-841C-82/C
Sequence 82, Application US/08496841C
Patent No. 6210919

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehner, Ph.D.

REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 527-7700

TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 82:

US-08-496-841C-82

Query Match 3.2%; Score 20; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
Db 34 GNAAAAAAAAAAAAAA 15

RESULT 15

US-09-124-523-82/C
Sequence 82, Application US/09124523
Patent No. 6395960

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

ROMMENS, JOHANNA M

ATTORNEY/AGENT INFORMATION:

NAME: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/124,523

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/592,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-124-523-82

Query Match 3.2%; Score 20; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
Db 34 GNAAAAAAAAAAAAAA 15

RESULT 16

US-09-020-956-32/C
Sequence 32, Application US/09020956
Patent No. 6261562

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

ATTORNEY/AGENT INFORMATION:

NAME: Dillin, David C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS

NUMBER OF SEQUENCES: 178

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020, 956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-020-956-32

Query Match 3.2%; Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
|||||
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 17
US-09-030-607-32/C
Sequence 32, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030, 607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-030-607-32

Query Match 3.2%; Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
|||||
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 18
US-09-605-785-32/C
Sequence 32, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John H.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605, 785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-32

Query Match 3.2%; Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625
|||||
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 19
US-09-439-313-32/C
Sequence 32, Application US/09439313
Patent No. 6325505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.

```
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: fastseq for windows version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-32
```

```
Query Match 3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 20
US-09-352-616A-32/C
Sequence 32, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jlangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: fastseq for windows version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-32
```

```
Query Match 3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 21
US-09-232-149A-32/C
Sequence 32, Application US/09232149A
Patent No. 6463611
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
```

```
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: fastseq for windows version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-32
```

```
Query Match 3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 22
US-09-149-476-108
Sequence 108, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
```



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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAGAAAAAGAAAAA 625
Db 1030 GNAAGAAAAAGAAAAA 1049

RESULT 23
US-09-443-041A-29
; Sequence 29, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Triflicum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1129
; OTHER INFORMATION: any nucleotide
US-09-443-041A-29

Query Match
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAGAAAAAGAAAAA 625
Db 1129 GNAAGAAAAAGAAAAA 1148

RESULT 24
US-09-648-040-4
; Sequence 4, Application US/09648040
; Patent No. 6436665
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/09/648,040
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,261
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
```

```

; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4

Query Match
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAGAAAAAGAAAAA 625
Db 10 NAAAAAGAAAAAGAAAAA 28

RESULT 25
US-08-859-106A-4/C
; Sequence 4, Application US/08859106A
; Patent No. 5965422
; GENERAL INFORMATION:
; APPLICANT: LOFFLER, Fridolin
; APPLICANT: NGUYEN, Quoc Khanh
; APPLICANT: SCHUSTER, Erwin
; APPLICANT: SPROBBER, Bruno
; APPLICANT: THOMAS, Lutz
; APPLICANT: WOLF, Sabine
; TITLE OF INVENTION: LYSOPHOSPHOLIPASE PRODUCED FROM
; TITLE OF INVENTION: ASPERGILLUS BY RECOMBINANT METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,106A
; FILING DATE: 20-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19620649.9
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 015200-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 40
; OTHER INFORMATION: /product= "N is A, C or G"
US-08-859-106A-4
```

Query Match 3.0%; Score 19; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 607 NAAAAAAAAAAAAAAAAA 625
DB 40 NAAAAAAAAAAAAAAAAA 22

RESULT 26
US-09-011-540-11/c
Sequence 11, Application US/09011540
Patent No. 6228632
GENERAL INFORMATION:
APPLICANT: SCHUSTER, Erwin
APPLICANT: SPROESSLER, Bruno
APPLICANT: TITZE, Kornelia
APPLICANT: GOTTSCHALK, Michael
APPLICANT: KHANH, Nguyen Quoc
APPLICANT: WOLF, Sabine
APPLICANT: PLAINER, Hermann
TITLE OF INVENTION: LEUCINE AMINOPEPTIDASES PRODUCED RECOMBINANTLY FROM
FILE REFERENCE: 015200-051
CURRENT FILING DATE: 1998-04-20
EARLIER FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: DE 19526485.1
EARLIER FILING DATE: 1995-07-20
EARLIER APPLICATION NUMBER: PCT/EP96/01430
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 11
LENGTH: 40
TYPE: DNA
ORGANISM: Aspergillus sojae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)..(440)
OTHER INFORMATION: N is A, C or G.
US-09-011-540-11

Query Match 3.0%; Score 19; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
DB 40 NAAAAAAAAAAAAAAAAA 22

RESULT 27
US-09-051-079-5/c
Sequence 5, Application US/09051079A
Patent No. 6214549
GENERAL INFORMATION:
APPLICANT: WEINDEL, Kurt
APPLICANT: SEIDEL, Cristoph
APPLICANT: LASSONCZYK, Gerhard
TITLE OF INVENTION: METHOD OF DETECTING A SUBSTANCE TO BE ANALYZED
FILE REFERENCE: 101614-07096
CURRENT FILING DATE: US/09/051,079A
EARLIER FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/EP96/04358
EARLIER FILING DATE: 1996-10-08
EARLIER APPLICATION NUMBER: DE/195 37 952.7
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 5
LENGTH: 51
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)
OTHER INFORMATION: n means DNP bound via DNP-TEG.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)
OTHER INFORMATION: n means DNP bound via DNP-TEG.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-051-079-5

Query Match 3.0%; Score 19; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
DB 21 NAAAAAAAAAAAAAAAAA 3

RESULT 28
US-08-618-1008-9/c
Sequence 9, Application US/086181008
Patent No. 6088976
GENERAL INFORMATION:
APPLICANT: Briggs, Michael R.
APPLICANT: Auwerx, Johan
APPLICANT: de Vos, Piet
APPLICANT: Steels, Bart
APPLICANT: Croston, Glenn E.
TITLE OF INVENTION: MODULATORS OF OB GENE AND
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,1008
FILING DATE: March 19, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,588
FILING DATE: October 30, 1995
APPLICATION NUMBER: 08/510,584
FILING DATE: August 2, 1995
APPLICATION NUMBER: 08/418,096
FILING DATE: April 5, 1995
APPLICATION NUMBER: 08/408,584
FILING DATE: March 20, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: "N" represents any base.

US-08-618-100B-9

Query Match 3.0%; Score 19; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
|||||
DB 51 NAAAAAAAAAAAAAAAAA 33

RESULT 29

US-08-702-344-7
Sequence 7, Application US/08702344
Patent No. 5723315

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/702,344
APPLICATION NUMBER: US/08/702,344
CLASSIFICATION: 536
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-08-702-344-7

Query Match 3.0%; Score 19; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
|||||
DB 5 NAAAAAAAAAAAAAAAAA 23

RESULT 30

US-08-702-344-22

Sequence 22, Application US/08702344
Patent No. 5723315

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/702,344
APPLICATION NUMBER: US/08/702,344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-08-702-344-22

Query Match 3.0%; Score 19; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
|||||
DB 22 NAAAAAAAAAAAAAAAAA 40

RESULT 31

US-09-269-911A-7/c

Sequence 7, Application US/09269911A
Patent No. 6228589

GENERAL INFORMATION:
APPLICANT: Brenner, Sydney
TITLE OF INVENTION: MEASUREMENT OF GENE EXPRESSION PROFILES
TITLE OF INVENTION: IN TOXICITY-DETERMINATION
FILE REFERENCE: 5525-0025.10
CURRENT APPLICATION NUMBER: US/09/269,911A
CURRENT FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 69
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: conjugate
NAME/KEY: misc_feature
LOCATION: (65)...(65)
OTHER INFORMATION: n = cDNA from library
NAME/KEY: misc_feature
LOCATION: (66)...(69)
OTHER INFORMATION: n = A,T,C or G
US-09-269-91A-7

Query Match 3.0%; Score 19; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 65 NAAAAAAAAAAAAAAAAA 47

RESULT 32

US-08-664-596B-3
Sequence 3, Application US/08664596B
Patent No. 5807703
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-664-596B-3

Query Match 3.0%; Score 19; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 8 NAAAAAAAAAAAAAAAAA 26

RESULT 33

US-08-738-367-3
Sequence 3, Application US/08738367
Patent No. 5827688
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-738-367-3

Query Match 3.0%; Score 19; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 8 NAAAAAAAAAAAAAAAAA 26

RESULT 34
US-08-991-789A-266/C
Sequence 266, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington


```
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-967-101-98

Query Match          3.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
DB 159 NAAAAAAAAAAAAAAAAA 141

RESULT 38
US-08-592-541-98/C
; Sequence 98, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-592-541-98

Query Match          3.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
DB 159 NAAAAAAAAAAAAAAAAA 141

RESULT 39
US-09-124-698-98/C
; Sequence 98, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-124-698-98

Query Match          3.0%; Score 19; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 14;
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	Matches	19; Conservative	0; Mismatches	0; Indels	0; Gaps
Qy	607	NNNNNNNNNNNNNNNNNNNN	625		
Db	159	NNNNNNNNNNNNNNNNNNNN	141		

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RESULT 40
US-09-127-480-98/c
Sequence 98 Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSTOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: TESTA, HUMWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-98

Query Match 3.0%; Score 19; DB 4; Length 208;
Best Local Similarity 100.0%; Pred.No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
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Db 159 NAAAAAAAAAAAAAAAAAAAAA 141

RESULT 41
US-08-496-841C-98/C
Sequence 98 Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSTOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Darby & Darby, PC
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1 STREET: 805 Third Avenue
2 CITY: New York
3 STATE: New York
4 COUNTRY: U.S.A.
5 ZIP: 10022
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patentln Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/496,841C
15 FILING DATE: 28-Jun-1995
16 CLASSIFICATION: <unknown>
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Paul F. Fehlner, Ph.D.
20 REGISTRATION NUMBER: 35,135
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (212) 527-7700
23 TELEFAX: (212) 753-6237
24
25 INFORMATION FOR SEQ ID NO: 98:
26
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 208 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32
33 MOLECULE TYPE: DNA (genomic)
34
35 SEQUENCE DESCRIPTION: SEQ ID NO: 98:
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37 US-08-496-841C-98
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US-09-175-928-37

Query Match 3.0%; Score 19; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 161 NAAAAAAAAAAAAAAAAAAAA 179

RESULT 43
US-09-124-523-98/C
Sequence 98; Application US/09124523
Patent No. 6395960
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CURRENT APPLICATION DATA:
ADDRESS: TESTA, HURWITZ & THIBRAULT
STREET: High Street Tower - 125 High Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ. ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-124-523-98

Query Match 3.0%; Score 19; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 159 NAAAAAAAAAAAAAAAAAAAA 141

RESULT 44
US-08-686-878A-43
Sequence 43; Application US/08686878A
Patent No. 5708157
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racine, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 71
CURRENT APPLICATION DATA:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-686-878A-43

Query Match

3.0%; Score 19; DB 1; Length 244;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 226 GNAAAAAAAAAAAAAA 244

RESULT 45

US-09-328-111-715

Sequence 715; Application US/09328111

Patent No. 6262333

GENERAL INFORMATION:

APPLICANT: Endege, Wilson O.

APPLICANT: Steinmann, Kathleen E.

APPLICANT: Astle, Jon H.

APPLICANT: Burgess, Christopher C.

APPLICANT: Bushnell, Steven E.

APPLICANT: Carroll III, Eddie

APPLICANT: Carino, Theodore J.

APPLICANT: Derli, Adnan

APPLICANT: Ford, Donna M.

APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 715

LENGTH: 310

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc-feature

LOCATION: (1)..(310)

OTHER INFORMATION: n = A,T,C or G

US-09-328-111-715

Query Match

3.0%; Score 19; DB 4; Length 310;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
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 DB 280 NAAAAAAAAAAAAAAAAA 298

Search completed: November 7, 2002, 23:12:21
 Job time : 31.4202 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 23:08:43 : Search time 27.1619 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agttctctctgcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 10

Total number of hits satisfying chosen parameters: 149939

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	625	100.0	625	US-09-867-701-10876	Sequence 10876, A
3	606	97.0	1897	US-09-825-294-214	Sequence 214, App
4	486	77.8	1619	US-09-825-294-205	Sequence 205, App
5	486	77.8	1619	US-09-825-294-211	Sequence 211, App
6	359	57.4	1362	US-09-825-294-208	Sequence 208, App
7	314	50.2	373	US-09-867-701-1516	Sequence 1516, App
8	307	49.1	349	US-09-867-701-2409	Sequence 2409, App
9	263	42.1	409	US-09-867-701-4240	Sequence 4240, App
10	166	26.6	201	US-09-867-701-8894	Sequence 8894, App
11	154	24.6	390	US-09-867-701-1532	Sequence 1532, App
12	120	19.2	558	US-09-867-701-2375	Sequence 2375, App
13	92	14.7	381	US-09-867-701-7826	Sequence 7826, App
14	22	3.5	819	US-09-938-842A-1283	Sequence 1283, App
15	21	3.4	322	US-09-783-590-6936	Sequence 6936, App
16	21	3.4	508	US-09-925-299-698	Sequence 698, App
17	21	3.4	547	US-09-834-975-379	Sequence 379, App
18	21	3.4	600	US-09-783-590-7037	Sequence 7037, App
19	21	3.4	1350	US-09-925-301-539	Sequence 539, App

20	21	3.4	1402	US-09-925-297-171	Sequence 171, App
c 21	20	3.2	58	US-09-783-590-2406	Sequence 2406, App
c 22	20	3.2	60	US-09-919-580-419	Sequence 419, App
c 23	20	3.2	66	US-09-925-301-759	Sequence 759, App
c 24	20	3.2	57	US-09-815-343-241	Sequence 241, App
c 25	20	3.2	217	US-09-895-828-248	Sequence 248, App
c 26	20	3.2	226	US-10-046-935-291	Sequence 291, App
c 27	20	3.2	265	US-10-040-916-46	Sequence 46, App
c 28	20	3.2	291	US-09-834-975-374	Sequence 374, App
c 29	20	3.2	451	US-09-777-564-625	Sequence 625, App
c 30	20	3.2	456	US-09-783-590-10830	Sequence 10830, App
c 31	20	3.2	648	US-09-925-301-819	Sequence 819, App
c 32	20	3.2	789	US-09-759-143-32	Sequence 32, App
c 33	20	3.2	789	US-09-780-669-32	Sequence 32, App
c 34	20	3.2	789	US-09-030-606-32	Sequence 32, App
c 35	20	3.2	789	US-09-822-827-32	Sequence 32, App
c 36	20	3.2	789	US-09-115-453-32	Sequence 32, App
c 37	20	3.2	368004	US-09-949-654-3	Sequence 3, App
c 38	19	3.0	51	US-09-783-590-8086	Sequence 8086, App
c 39	19	3.0	52	US-09-783-590-5881	Sequence 5881, App
c 40	19	3.0	53	US-09-919-580-705	Sequence 705, App
c 41	19	3.0	53	US-09-783-590-3220	Sequence 3220, App
c 42	19	3.0	56	US-09-919-580-171	Sequence 171, App
c 43	19	3.0	56	US-09-919-580-677	Sequence 677, App
c 44	19	3.0	56	US-09-919-580-713	Sequence 713, App
c 45	19	3.0	60	US-09-925-301-758	Sequence 758, App

ALIGNMENTS

RESULT 1
US-09-825-294-210
Sequence 210, Application US/09825294
Patent No. US2002004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 210
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(625)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match 100.0%; Score 625; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.4e-242;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTGCAGAGAGTGGCGCGGAGCGCAAGCAAGGCGCTGCACAAACG 60
DB 1 AGTTCTCCTTGCAGAGAGTGGCGCGGAGCGCAAGCAAGGCGCTGCACAAACG 60
QY 61 GGGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGCGCTTCTCGTGTGGTGGTCTG 120
DB 61 GGGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGCGCTTCTCGTGTGGTGGTCTG 120
QY 121 CACGCGACGGCGGCGAGCAGACCTTGCAGACACCGCGGAAATGCTCTCGAGAGAC 180
DB 121 CACGCGACGGCGGCGAGCAGACCTTGCAGACACCGCGGAAATGCTCTCGAGAGAC 180

```

OY 181 CGTGTACAGAGGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTGCCGAGAGGGAG 240
    |||||||
DB 181 CGTGTACAGAGGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTGCCGAGAGGGAG 240
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCGTCTGGGTTTGGCCGAGC 300
    |||||||
DB 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCGTCTGGGTTTGGCCGAGC 300
OY 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCCAAATGTCAACAATTCAGCCC 360
    |||||||
DB 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCCAAATGTCAACAATTCAGCCC 360
OY 361 TGGGACAGACGACGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
    |||||||
DB 361 TGGGACAGACGACGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
OY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGAAAT 480
    |||||||
DB 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGAAAT 480
OY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCCACAGCAGAGAAATT 540
    |||||||
DB 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCCACAGCAGAGAAATT 540
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
DB 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
OY 601 ACAGTGNAAAAAAGAAAAA 625
    |||||||
DB 601 ACAGTGNAAAAAAGAAAAA 625

```

RESULT 2

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US-09-867-701-10876
; Sequence 10876, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10876
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

```

Query Match 100.0%; Score 625; DB 10; Length 625;

Best Local Similarity 100.0%; Pred. No. 1.4e-242;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCTCTTTCAGAGAGCTGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGC 60
    |||||||
DB 1 AGTTCTCTTTCAGAGAGCTGCGCGGAGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGC 60
OY 61 GCGGCTGTGCGTGTGAGTGTGCGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 120
    |||||||
DB 61 GCGGCTGTGCGTGTGAGTGTGCGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 120
OY 121 CAGCGACAGGCGGCGACAGCAGCACTGTGACGAACACCCCGGAAAGTGTGCGAGGACAC 180
    |||||||
DB 121 CAGCGACAGGCGGCGACAGCAGCACTGTGACGAACACCCCGGAAAGTGTGCGAGGACAC 180

```

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OY 181 CGTGTACAGAGGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTGCCGAGAGGGAG 240
    |||||||
DB 181 CGTGTACAGAGGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTGCCGAGAGGGAG 240
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCGTCTGGGTTTGGCCGAGC 300
    |||||||
DB 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCGTCTGGGTTTGGCCGAGC 300
OY 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCCAAATGTCAACAATTCAGCCC 360
    |||||||
DB 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCCAAATGTCAACAATTCAGCCC 360
OY 361 TGGGACAGACGACGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
    |||||||
DB 361 TGGGACAGACGACGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
OY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGAAAT 480
    |||||||
DB 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGAAAT 480
OY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCCACAGCAGAGAAATT 540
    |||||||
DB 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCCACAGCAGAGAAATT 540
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
DB 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
OY 601 ACAGTGNAAAAAAGAAAAA 625
    |||||||
DB 601 ACAGTGNAAAAAAGAAAAA 625

```

RESULT 3

```

US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolke, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

```

Query Match 97.0%; Score 606; DB 10; Length 1897;

Best Local Similarity 100.0%; Pred. No. 5.7e-235;

Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCTCTTTCAGAGAGCTGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGC 60
    |||||||
DB 1271 AGTTCTCTTTCAGAGAGCTGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGC 1330
OY 61 GCGGCTGTGCGTGTGAGTGTGCGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 120
    |||||||
DB 1331 GCGGCTGTGCGTGTGAGTGTGCGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 1390
OY 121 CAGCGACAGGCGGCGACAGCAGCACTGTGACGAACACCCCGGAAAGTGTGCGAGGACAC 180
    |||||||

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```
Db 1391 CAGCGACAGCGGCGACGACACACCTGACAGACACCGCGAAACCTGCTGGAGAGAC 1450
|
|
|
Qy 181 CGGTACAGAGCGCGGTGTGATGACGAGCTAGAGTAAAAAGTCTCCGAGAGAGGAG 240
|
|
|
Db 1451 CGGTACAGAGCGCGGTGTGATGACGAGCTAGAGTAAAAAGTCTCCGAGAGAGGAG 1510
|
|
|
Qy 241 GAGGATCATGTACGCCCGGAAAGTAGACCTGCTCCAGTCTGCTTGGTTGGCCGACG 300
|
|
|
Db 1511 GAGGATCATGTACGCCCGGAAAGTAGACCTGCTCCAGTCTGCTTGGTTGGCCGACG 1570
|
|
|
Qy 301 CAGGATCTCCGAAATCTGTTGGGCAATGACGATGACGCAATGACAAATCAGCCC 360
|
|
|
Db 1571 CAGGATCTCCGAAATCTGTTGGGCAATGACGATGACGCAATGACAAATCAGCCC 1630
|
|
|
Qy 361 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACAGAGATGAGAACAG 420
|
|
|
Db 1631 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACAGAGATGAGAACAG 1690
|
|
|
Qy 421 TAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAT 480
|
|
|
Db 1691 TAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAT 1750
|
|
|
Qy 481 GGTACCAATTTTCAAGTGTGACCTTGACCTCTTTTGGCACAAGAGAGAAATTT 540
|
|
|
Db 1751 GGTACCAATTTTCAAGTGTGACCTTGACCTCTTTTGGCACAAGAGAGAAATTT 1810
|
|
|
Qy 541 AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 600
|
|
|
Db 1811 AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 1870
|
|
|
Qy 601 ACAAGT 606
|
|
|
Db 1871 ACAAGT 1876
|
|
|
```

RESULT 4

```
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stol, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205
```

```
Query Match 77.8%; Score 486; DB 10; Length 1619;
Best Local Similarity 99.8%; Pred. No. 9.7e-187;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAGAGACAGCGGCGCTGCACAAAGCG 60
|
|
|
Db 992 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAGAGACAGCGGCGCTGCACAAAGCG 1051
|
|
|
Qy 61 GCGGCTGTGCTGTGAGAGTGGCATGTAGCGGAGCGGCTTCGTCGTCGTCGTCGTCG 120
|
|
|
Db 1052 GCGGCTGTGCTGTGAGAGTGGCATGTAGCGGAGCGGCTTCGTCGTCGTCGTCGTCG 1111
|
|
|
Qy 121 CAGCGACAGCGGCGCAGACAGACAC--TGACAGAAACACCCCGGAAACTGTCGAGAGACA 179
|
|
|
Db 1112 CAGCGACAGCGGCGCAGACAGACACCTTGCAGAAACACCCCGGAAACTGTCGAGAGACA 1171
|
|
|
```

```
Qy 180 CCGTGTACAGAGCGGCTTGATGACCGAGCTAGAGTAAAAACGCTCCGAGAGGGA 239
|
|
|
Db 1172 CCGTGTACAGAGCGGCTTGATGACCGAGCTAGAGTAAAAACGCTCCGAGAGGGA 1231
|
|
|
Qy 240 GAGGATCATGTACGCCCGGAAAGTAGACCTGCTCCAGTCTGCTTGGGTTGGCCGAG 299
|
|
|
Db 1232 GAGGATCATGTACGCCCGGAAAGTAGACCTGCTCCAGTCTGCTTGGGTTGGCCGAG 1291
|
|
|
Qy 300 CCAATGATCTCCGAAATCTGTTGGGCAATGACGATGACGCAATGACAAATCAGCC 359
|
|
|
Db 1292 CCAATGATCTCCGAAATCTGTTGGGCAATGACGATGACGCAATGACAAATCAGCC 1351
|
|
|
Qy 360 CTGGGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACAGACATGAGAACACA 419
|
|
|
Db 1352 CTGGGACAGACGAGCAGAGGAGAGACAGAGAAAAAGAAAAACAGACATGAGAACACA 1411
|
|
|
Qy 420 GTAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAA 479
|
|
|
Db 1412 GTAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTGCTTACTGGCCAGGAAA 1471
|
|
|
Qy 480 TGGTACCAATTTTCAAGTGTGACCTTGACCTCTTTTGGCACAAGAGAGAAATTT 539
|
|
|
Db 1472 TGGTACCAATTTTCAAGTGTGACCTTGACCTCTTTTGGCACAAGAGAGAAATTT 1531
|
|
|
Qy 540 TAAACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 599
|
|
|
Db 1532 TAAACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 1591
|
|
|
Qy 600 GACAGT 606
|
|
|
Db 1592 GACAGT 1598
|
|
|
```

RESULT 5

```
US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stol, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211
```

```
Query Match 77.8%; Score 486; DB 10; Length 1619;
Best Local Similarity 99.8%; Pred. No. 9.7e-187;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAGAGACAGCGGCGCTGCACAAAGCG 60
|
|
|
Db 992 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAGAGACAGCGGCGCTGCACAAAGCG 1051
|
|
|
Qy 61 GCGGCTGTGCTGTGAGAGTGGCATGTAGCGGAGCGGCTTCGTCGTCGTCGTCGTCG 120
|
|
|
Db 1052 GCGGCTGTGCTGTGAGAGTGGCATGTAGCGGAGCGGCTTCGTCGTCGTCGTCGTCG 1111
|
|
|
Qy 121 CAGCGACAGCGGCGCAGACAGACAC--TGACAGAAACACCCCGGAAACTGTCGAGAGACA 179
|
|
|
Db 1112 CAGCGACAGCGGCGCAGACAGACACCTTGCAGAAACACCCCGGAAACTGTCGAGAGACA 1171
|
|
|
Qy 180 CCGTGTACAGAGCGGCTTGATGACCGAGCTAGAGTAAAAACGCTCCGAGAGGGA 239
|
|
|
```

```
|||||
Db 1172 CCGTATACAGAGCGGGTTGATGATACCGAGCTAGTAGAAAAACCTCTCCGAGAAAGGGA 1231
QY 240 GGAGGATCATGTAGCCCGGAGTAGAGACCTGTCAGTGTGCTGGTTGGCCGCGAG 299
Db 1232 GGAGGATCATGTAGCCCGGAGTAGAGACCTGTCAGTGTGCTGGTTGGCCGCGAG 1291
QY 300 CCATATCTCCGAACTGCTGGTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 359
Db 1292 CCATATCTCCGAACTGCTGGTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 1351
QY 360 CTGGGACAGACAGCAGAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAACACA 419
Db 1352 CTGGGACAGACAGCAGAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAACACA 1411
QY 420 GTAATGAAATAAACCAATAAATATTAGCCCTCTGTTCTGCTTACTGCCAGAGAAA 479
Db 1412 GTAATGAAATAAACCAATAAATATTAGCCCTCTGTTCTGCTTACTGCCAGAGAAA 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGCTGTGACCTCTTTGGCACAGACAGAGAAAT 539
Db 1472 TGGTACCAATTTTTCAGTGTGAGCTGTGACCTCTTTGGCACAGAGAGAAAT 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAAGACCAATTAATGCTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAAGACCAATTAATGCTTA 1591
QY 600 GACAGTG 606
Db 1592 GACAGTG 1598
|||||
```

RESULT 6

```
US-09-825-294-208/c
; Sequence 208, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-208
```

Query Match 57.4%; Score 359; DB 10; Length 1362;

Best Local Similarity 100.0%; Pred. No. 1.1e-135;

Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGACGGCGCTGCACAAAGG 60
Db 1215 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGACGGCGCTGCACAAAGG 1156
QY 61 GCGGCTGTGCTGTGAGTGTGCGCATGTACGGCGACAGCGCTTCTGTGTTGGCTGTG 120
Db 1155 GCGGCTGTGCTGTGAGTGTGCGCATGTACGGCGAGCGCTTCTGTGTTGGCTGTG 1096
QY 121 CAGCGACAGCGCGACAGACAGCACTGACGAACACCCCGAACTGCTGCGAGGACAC 180
Db 1095 CAGCGACAGCGCGACAGACAGCACTGACGAACACCCCGAACTGCTGCGAGGACAC 1036
QY 181 CGTGTACAGAGCGGGTGTATGACGAGCTGAGAGTGAAGAAAAGCTGCCGAGAGGGAG 240
Db 1035 CGTGTACAGAGCGGGTGTATGACGAGCTGAGGTAGAAAAGCTGCCGAGAGGGAG 976
|||||
```

```
QY 241 GAGATCATGTACGCCCGGAGTAGAGACCTGTCAGTGTGCTGGTTGGCCGCGAGC 300
Db 975 GAGATCATGTACGCCCGGAGTAGAGACCTGTCAGTGTGCTGGTTGGCCGCGAGC 916
QY 301 CATGATCTCCGAACTGCTGGTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 359
Db 915 CATGATCTCCGAACTGCTGGTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 857
|||||
```

RESULT 7

```
US-09-867-701-1516/c
; Sequence 1516, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867, 701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1516
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-1516
```

Query Match 50.2%; Score 314; DB 10; Length 373;

Best Local Similarity 100.0%; Pred. No. 1.4e-117;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 293 GCCGACGACATGATCCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTACACA 352
Db 315 GCCGACGACATGATCCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTACACA 256
QY 353 ATCAGCCCTGGGAGACAGACAGAGAGGAGAGACAGAAAAAGAAAAACAGCATGA 412
Db 255 ATCAGCCCTGGGAGACAGACAGAGAGGAGAGAGAGAAAAAGAAAAACAGCATGA 196
QY 413 GACACAGTAATGAATTAACCATTAATATTAGCCCTCTGTTCTGTGCTTACTGCG 472
Db 195 GACACAGTAATGAATTAACCATTAATATTAGCCCTCTGTTCTGTGCTTACTGCG 136
QY 473 CAGGAATGTGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCA 532
Db 135 CAGGAATGTGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAAGCA 76
QY 533 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAAGACATTAA 592
Db 75 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAAGACATTAA 16
QY 593 TGCTTTAGACAGTG 606
Db 15 TGCTTTAGACAGTG 2
|||||
```

RESULT 8

```
US-09-867-701-2409/c
; Sequence 2409, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867, 701
; CURRENT FILING DATE: 2001-05-29
```

```
;; NUMBER OF SEQ ID NOS: 10912
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2409
;; LENGTH: 349
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-867-701-2409
```

```
Query Match          49.1%; Score 307; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.4e-115;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 300 CCATATCTCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAAATCAGCC 359
D 310 CCATATCTCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAAATCAGCC 251
QY 360 CTGGCAGACAGCAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
D 250 CTGGCAGACAGCAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 420 GTAATGATATAAACCATTAAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGT 479
D 190 GTAATGATATAAACCATTAAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGT 131
QY 480 TGTGACCAATTTTTCAGTGTGTGACTTGACAGCTTTCTTTGCCACAAGCAGAGAA 539
D 130 TGTGACCAATTTTTCAGTGTGTGACTTGACAGCTTTCTTTGCCACAAGCAGAGAA 71
QY 540 TAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTA 599
D 70 TAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTA 11
QY 600 GACAGTG 606
D 10 GACAGTG 4
```

```
RESULT 9
US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240
```

```
Query Match          42.1%; Score 263; DB 10; Length 409;
Best Local Similarity 99.7%; Pred. No. 4.5e-97;
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 293 GCGGACCCATGATCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAA 352
D 315 GCGGACCCATGATCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAA 256
QY 353 ATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
D 255 ATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 413 GAACACAGTAAATATAAACCATTAAATATTTAGCCCTCTGTCTGTCTGTCTGT 472
D 195 GAACACAGTAAATATAAACCATTAAATATTTAGCCCTCTGTCTGTCTGTCTGT 136
```

```
QY 473 CAGAAATGTATCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGACA 532
D 135 CAGAAATGTATCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGACA 76
QY 533 GAGATTTAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAGCATTAA 592
D 75 GAGATTTAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAGCATTAA 16
QY 593 TGCCTTACAGAGTG 606
D 15 TGCCTTACAGAGTG 2
```

```
RESULT 10
US-09-867-701-8894/c
; Sequence 8894, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8894
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8894
```

```
Query Match          26.6%; Score 166; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.5e-58;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 231 AGAAGGGAGAGAGATCTATGACGCCCGGAAGTAGACCTGTCAGTCTGTTGGGTT 290
D 181 AGAAGGGAGAGAGATCTATGACGCCCGGAAGTAGACCTGTCAGTCTGTTGGGTT 122
QY 291 TGGCCGACCATGATCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAA 350
D 121 TGGCCGACCATGATCTCCGATTCGTGGGTCATCCAGCATACGGCCAAATGTACAA 62
QY 351 CAATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
D 61 CAATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 16
```

```
RESULT 11
US-09-867-701-1532
; Sequence 1532, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1532
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
```



```

; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6936
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (165)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (166)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (176)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (216)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (241)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (241)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (258)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (292)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (311)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (316)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-6936

Query Match
Best Local Similarity 100.0%; DB 10; Length 322;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
DB 290 TGNAAAAAAAAAAAAAAAAAAAA 310

RESULT 16
US-09-925-299-698
; Sequence 698, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 698
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (449)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (480)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (496)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (499)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (505)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-698

Query Match
Best Local Similarity 100.0%; DB 10; Length 508;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 AGTGNAAAAAAAAAAAAAAAAAAAA 623
DB 445 AGTGNAAAAAAAAAAAAAAAAAAAA 465

RESULT 17
US-09-834-975-379
; Sequence 379, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hufel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: OF HUMAN CANCERS
; CURRENT APPLICATION NUMBER: US/09/834,975
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 379
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(547)
; OTHER INFORMATION: n = A,T,C or G
; US-09-834-975-379

Query Match
Best Local Similarity 100.0%; DB 10; Length 547;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
DB 527 TGNAAAAAAAAAAAAAAAAAAAA 547
```

```
RESULT 18
US-09-783-590-7037
; Sequence 7037, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7037
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (133)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (185)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (408)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (409)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (418)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (428)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
; NAME/KEY: misc feature
; LOCATION: (447)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (449)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (458)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (497)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (499)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (510)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (514)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (544)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (562)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (571)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (575)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-7037
```

```
Query Match 3.4%; Score 21; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 605 TGNAAAAAAAAAAAAA 625
Db 573 TGNAAAAAAAAAAAAA 593

RESULT 19
US-09-925-301-539
; Sequence 539, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 539
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1305)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1344)
```

```
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc-feature
LOCATION: (1349)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-539
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 10; Length 1350;
Pred. No. 7.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
Db 1303 TGNAAAAAAAAAAAAAAAAAAAA 1323
```

```
RESULT 20
US-09-925-297-171
Sequence 171, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
PRIORITY FILING DATE: 2001-08-10
PRIORITY FILING DATE: 2000-03-08
PRIORITY FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 171
LENGTH: 1402
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1370)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: (1400)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-171
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 10; Length 1402;
Pred. No. 7.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 605 TGNAAAAAAAAAAAAAAAAAAAA 625
Db 1368 TGNAAAAAAAAAAAAAAAAAAAA 1368
```

```
RESULT 21
US-09-783-590-2406/c
Sequence 2406, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: FO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIORITY FILING DATE: 2000-02-15
PRIORITY FILING DATE: 1995-04-12
PRIORITY FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 2406
LENGTH: 58
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (34)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc-feature
LOCATION: (41)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc-feature
LOCATION: (47)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc-feature
LOCATION: (52)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc-feature
LOCATION: (58)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2406
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 58;
Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 606 GNAAAAAAAAAAAAAAAAAAAAA 625
Db 35 GNAAAAAAAAAAAAAAAAAAAAA 16
```

```
RESULT 22
US-09-919-580-419/c
Sequence 419, Application US/09919580
Patent No. US20020110832A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
PRIORITY FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 419
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: 54
OTHER INFORMATION: n = A,T,C or G
US-09-919-580-419
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 60;
Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 606 GNAAAAAAAAAAAAAAAAAAAAA 625
Db 55 GNAAAAAAAAAAAAAAAAAAAAA 36
```

```
RESULT 23
US-09-925-301-759/c
Sequence 759, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
```

```

; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 759
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (6)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (66)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-301-759
```

```

Query Match          3.2%: Score 20; DB 10; Length 66;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 606 GNAAGAAAAAGAAAAAGAAAAA 625
    |||
DB 60 GNAAGAAAAAGAAAAAGAAAAA 41
```

```

RESULT 24
US-09-815-343-241/C
; Sequence 241, Application US/09815343
; Patent No. US2001005596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(97)
; OTHER INFORMATION: n = A,T,C or G
; US-09-815-343-241
```

```

Query Match          3.2%: Score 20; DB 10; Length 97;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 606 GNAAGAAAAAGAAAAAGAAAAA 625
    |||
DB 88 GNAAGAAAAAGAAAAAGAAAAA 69
```

```

RESULT 25
US-09-895-828-248
; Sequence 248, Application US/09895828
; Patent No. US20020099012A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Carter, Darriek
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.539
; CURRENT APPLICATION NUMBER: US/09/895,828
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 217
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 201
; OTHER INFORMATION: n = A,T,C or G
; US-09-895-828-248
```

```

Query Match          3.2%: Score 20; DB 10; Length 217;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 604 GTGNAAGAAAAAGAAAAAGAAAA 623
    |||
DB 198 GTGNAAGAAAAAGAAAAAGAAAA 217
```

```

RESULT 26
US-10-046-935-291/C
; Sequence 291, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 291
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 20, 57, 141, 184, 206
; OTHER INFORMATION: n = A,T,C or G
; US-10-046-935-291
```

```

Query Match          3.2%: Score 20; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 606 GNAAGAAAAAGAAAAAGAAAAA 625
    |||
DB 21 GNAAGAAAAAGAAAAAGAAAAA 2
```

RESULT 27
US-10-040-916-46
; Sequence 46, Application US/10040916
; Patent No. US20020146769A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John
; Lavallee, Edward
; Racie, Lisa
; Merberg, David
; Treacy, Maurice
; Evans, Cheryl
; Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,916
FILING DATE: 07-Jan-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,029
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 08/686,878
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-040-916-46
Query Match 3.2%; Score 20; DB 12; Length 265;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 606 GNAAAAAAAAAAAAAA 625
DB 245 GNAAAAAAAAAAAAAA 264
RESULT 28
US-09-834-975-374/c
; Sequence 374, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; Applicant: Brown, Jeffrey
; Applicant: Bolt, Andrew
; Applicant: Van Hufel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

;; TITLE OF INVENTION: OF HUMAN CANCERS
;; FILE REFERENCE: MRI-016B
;; CURRENT APPLICATION NUMBER: US/09/834,975
;; CURRENT FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: 60/197,538
;; PRIOR FILING DATE: 2000-04-14
;; NUMBER OF SEQ ID NOS: 1046
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 374
;; LENGTH: 291
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: (1)...(291)
;; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-374
Query Match 3.2%; Score 20; DB 10; Length 291;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 605 TGNAAAAAAAAAAAAA 624
DB 41 TGNAAAAAAAAAAAAA 22
RESULT 29
US-09-777-564-625/c
; Sequence 625, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; Applicant: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 625
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(451)
OTHER INFORMATION: n = A,T,C or G
US-09-777-564-625
Query Match 3.2%; Score 20; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 606 GNAAAAAAAAAAAAAA 625
DB 373 GNAAAAAAAAAAAAAA 354
RESULT 30
US-09-783-590-10830
; Sequence 10830, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; Applicant: Haseltine, William A.
; Applicant: Li, Haodong
; Applicant: Rosen, Craig A.
; Applicant: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590

CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10830
LENGTH: 496
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (8)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (161)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (182)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (209)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (210)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (216)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (237)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (278)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (279)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (283)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (304)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (310)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (318)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (321)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (357)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (364)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (392)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (396)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (404)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (416)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (419)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (445)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (447)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (448)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (461)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (493)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10830
Query Match
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3.2%; Score 20; DB 10; Length 496;
Qy 606 GNAAGAAAAAGAAAAAGAAAA 625
Db 7 GNAAGAAAAAGAAAAAGAAAA 26
RESULT 31
US-09-925-301-819
Sequence 819, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 819
LENGTH: 648
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (369)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (518)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (544)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (547)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (565)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (584)
OTHER INFORMATION: n equals a,t,g, or c

```

; NAME/KEY: misc.feature
; LOCATION: (626)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-819

Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 648;
Matches 20; Conservative 0; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 625 GNAAAAAAAAAAAAAA 644

RESULT 32
US-09-759-143-32/C
; Sequence 32, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-32

Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 789;
Matches 20; Conservative 0; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 33
US-09-780-669-32/C
; Sequence 32, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurrell, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-780-669-32
```

```

Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 789;
Matches 20; Conservative 0; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47
```

```

RESULT 34
US-09-030-606-32/C
; Sequence 32, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-606-32

Query Match 3.2%; Score 20; DB 10; Length 789;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 35
US-09-822-827-32/C
Sequence 32, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-822-827-32

Query Match 3.2%; Score 20; DB 10; Length 789;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 36
US-09-115-453-32/C
Sequence 32, Application US/09115453B
Patent No. US20020090372A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-115-453-32

Query Match 3.2%; Score 20; DB 10; Length 789;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 37
US-09-949-654-3/C
Sequence 3, Application US/09949654
Patent No. US20020127644A1
GENERAL INFORMATION:
APPLICANT: VAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: C1000817
CURRENT APPLICATION NUMBER: US/09/949,654
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/231,572
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 368004
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(368004)
OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3

Query Match 3.2%; Score 20; DB 10; Length 368004;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 GAAAAACACAGCATGAGAAC 416
DB 350891 GAAAAACACAGCATGAGAAC 350872

RESULT 38
US-09-783-590-8086/C
Sequence 8086, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8086
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature


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; LOCATION: (51)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-8086
```

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Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 51 NAAAAAAAAAAAAAAAAAAAA 33
```

```
RESULT 39
US-09-783-590-5881/c
; Sequence 5881, Application US/09783590
```

```
; Patent No. US20020110850A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
```

```
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
```

```
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
```

```
; FILE REFERENCE: PO-16.2C1
```

```
; CURRENT APPLICATION NUMBER: US/09/783,590
```

```
; PRIOR FILING DATE: 2000-02-15
```

```
; PRIOR APPLICATION NUMBER: 08/420,856
```

```
; PRIOR FILING DATE: 1995-04-12
```

```
; PRIOR APPLICATION NUMBER: 08/346,731
```

```
; NUMBER OF SEQ ID NOS: 12485
```

```
; SOFTWARE: Patentln Ver. 2.0
```

```
; SEQ ID NO 5881
```

```
; LENGTH: 52
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; LOCATION: (48)
```

```
; OTHER INFORMATION: n equals a,t,g, or c
```

```
US-09-783-590-5881
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
```

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Db 48 NAAAAAAAAAAAAAAAAAAAA 30
```

```
RESULT 40
US-09-919-580-705/c
; Sequence 705, Application US/09919580
```

```
; Patent No. US20020110832A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Pyle, Ruth
```

```
; APPLICANT: Xu, Jiangchun
```

```
; APPLICANT: Secrist, Heather
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; FILE REFERENCE: 210121.552
```

```
; CURRENT APPLICATION NUMBER: US/09/919,580
```

```
; PRIOR FILING DATE: 2001-07-30
```

```
; NUMBER OF SEQ ID NOS: 934
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 705
```

```
; LENGTH: 53
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: misc-feature
```

```
; LOCATION: 34, 42, 46
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-705
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 34 NAAAAAAAAAAAAAAAAAAAA 16
```

```
RESULT 41
US-09-783-590-3220/c
; Sequence 3220, Application US/09783590
```

```
; Patent No. US20020110850A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
```

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; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
```

```
; APPLICANT: Ruben, Steven M.
```

```
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
```

```
; FILE REFERENCE: PO-16.2C1
```

```
; CURRENT APPLICATION NUMBER: US/09/783,590
```

```
; PRIOR FILING DATE: 2000-02-15
```

```
; PRIOR APPLICATION NUMBER: 08/420,856
```

```
; PRIOR FILING DATE: 1995-04-12
```

```
; PRIOR APPLICATION NUMBER: 08/346,731
```

```
; NUMBER OF SEQ ID NOS: 12485
```

```
; SOFTWARE: Patentln Ver. 2.0
```

```
; SEQ ID NO 3220
```

```
; LENGTH: 53
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; LOCATION: (16)
```

```
; OTHER INFORMATION: n equals a,t,g, or c
```

```
US-09-783-590-3220
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
```

```
Db 53 NAAAAAAAAAAAAAAAAAAAA 35
```

```
RESULT 42
US-09-919-580-171/c
; Sequence 171, Application US/09919580
```

```
; Patent No. US20020110832A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Pyle, Ruth
```

```
; APPLICANT: Xu, Jiangchun
```

```
; APPLICANT: Secrist, Heather
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; FILE REFERENCE: 210121.552
```

```
; CURRENT APPLICATION NUMBER: US/09/919,580
```

```
; PRIOR FILING DATE: 2001-07-30
```

```
; NUMBER OF SEQ ID NOS: 934
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 171
```

```
; LENGTH: 56
```

```
; TYPE: DNA
```

ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 LOCATION: 49
 OTHER INFORMATION: n = A,T,C or G
 US-09-919-580-171

Query Match
 Best Local Similarity 100.0%; Score 19; DB 10; Length 56;
 Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
 |||
 Db 49 NAAAAAAAAAAAAAAAAAAAA 31

RESULT 43
 US-09-919-580-677/c
 ; Sequence 677, Application US/09919580
 ; Patent No. US20020110832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 210121.552
 ; CURRENT APPLICATION NUMBER: US/09/919,580
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 677
 ; LENGTH: 56
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 53
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-919-580-677

Query Match
 Best Local Similarity 100.0%; Score 19; DB 10; Length 56;
 Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
 |||
 Db 53 NAAAAAAAAAAAAAAAAAAAA 35

RESULT 44
 US-09-919-580-713/c
 ; Sequence 713, Application US/09919580
 ; Patent No. US20020110832A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 210121.552
 ; CURRENT APPLICATION NUMBER: US/09/919,580
 ; CURRENT FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 713
 ; LENGTH: 56
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 35, 37, 42, 56
 ; OTHER INFORMATION: n = A,T,C or G

US-09-919-580-713

Query Match
 Best Local Similarity 100.0%; Score 19; DB 10; Length 56;
 Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
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 Db 35 NAAAAAAAAAAAAAAAAAAAA 17

RESULT 45
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 ; Sequence 758, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 758
 ; LENGTH: 60
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (36)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (38)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (40)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (45)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (46)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-301-758

Query Match
 Best Local Similarity 100.0%; Score 19; DB 10; Length 60;
 Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
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 Db 36 NAAAAAAAAAAAAAAAAAAAA 18

Search completed: November 8, 2002, 02:06:25
 Job time : 100.162 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:02:33 ; Search time 1399.81 Seconds
(without alignments)
11225.881 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
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Sequence: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Scoring table: 24791104 seqs, 12571243825 residues

Searched:

Word size : 10

Total number of hits satisfying chosen parameters: 10637023

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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Result	Score	Match	Length	ID	Description
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2	625	100.0	625	1	Sequence 210, App
3	625	100.0	625	1	Sequence 210, App
4	625	100.0	625	1	Sequence 210, App
5	625	100.0	625	1	Sequence 210, App
6	606	97.0	1897	1	Sequence 214, App
7	606	97.0	1897	1	Sequence 214, App
8	606	97.0	1897	1	Sequence 214, App
9	606	97.0	1897	1	Sequence 214, App
10	606	97.0	1897	1	Sequence 214, App
11	606	97.0	1897	1	Sequence 214, App
12	555	88.8	1608	43	Sequence 111, App
13	555	88.8	1608	43	Sequence 111, App
14	555	88.8	1608	43	Sequence 111, App
15	555	88.8	1608	43	Sequence 111, App
16	555	88.8	1608	43	Sequence 111, App
17	555	88.8	1608	43	Sequence 111, App
18	555	88.8	1608	43	Sequence 111, App
19	555	88.8	1608	43	Sequence 111, App
20	555	88.8	1608	43	Sequence 111, App
21	555	88.8	1608	43	Sequence 111, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 555 88.8 1917 25 US-09-652-355-9112 Sequence 9112, Ap
23 555 88.8 1917 25 US-09-652-914-8473 Sequence 8473, Ap
24 555 88.8 1917 25 US-09-652-917-2477 Sequence 2477, Ap
25 555 88.8 1917 31 US-09-801-833-7188 Sequence 7188, Ap
26 555 88.8 1918 17 US-09-397-022-4454 Sequence 4454, Ap
27 555 88.8 1918 31 US-09-808-383-4454 Sequence 4454, Ap
28 555 88.8 1925 25 US-09-652-121-7293 Sequence 7293, Ap
29 555 88.8 1925 25 US-09-652-128-9375 Sequence 9375, Ap
30 555 88.8 1925 25 US-09-652-917-3346 Sequence 3346, Ap
31 555 88.8 1925 27 US-09-652-917-3346 Sequence 3346, Ap
32 555 88.8 1925 27 US-09-699-997-11085 Sequence 11085, A
33 555 88.8 1925 29 US-09-710-281-4458 Sequence 4458, Ap
34 555 88.8 1953 1 PCT-US00-09066-38 Sequence 1608, Ap
35 555 88.8 1953 36 US-09-950-083-1914 Sequence 38, Appl
36 555 88.8 1953 40 US-10-105-299-2414 Sequence 1914, Ap
37 555 88.8 1956 1 PCT-US00-14973-23 Sequence 2414, Ap
38 555 88.8 1956 36 US-09-950-083-1915 Sequence 23, Appl
39 555 88.8 1956 40 US-10-105-299-2415 Sequence 1915, Ap
40 555 88.8 1967 1 PCT-US02-29964-16 Sequence 2415, Ap
41 549 87.8 1890 23 US-09-611-523-203 Sequence 16, Appl
42 545 87.2 716 61 US-60-172-373-15734 Sequence 203, App
43 486 77.8 1619 1 PCT-US01-45395-205 Sequence 15734, A
44 486 77.8 1619 1 PCT-US01-45395-211 Sequence 205, App
45 486 77.8 1619 28 US-09-713-550-205 Sequence 211, App
Sequence 205, App
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ALIGNMENTS

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RESULT 1
PCT-US01-45395-210
: Sequence 210, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-210
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Query Match 100.0% Score 625; DB 1; Length 625;

Best Local Similarity 100.0%; Pred. No. 6.3e-125; Mismatches 0; Indels 0; Gaps 0;

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Matches 625: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTCTCTTGGAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGC 60
DB 1 AGTTCTCTTGGAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGC 60
QY 61 GCGCGTGTGGTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGTTGGCTGCTG 120
DB 61 GCGCGTGTGGTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGTTGGCTGCTG 120
QY 121 CAGCGACAGCGGCGGACAGACAGCACTGTGACGAACACCCCGGCAAACTGCTGCGAGACAC 180
DB 121 CAGCGACAGCGGCGGACAGACAGCACTGTGACGAACACCCCGGCAAACTGCTGCGAGACAC 180
QY 181 CGTGTACAGAGAGCGGCTGTATGACGAGCTGAGTGAAGAAACGTTCTCGAGAGAGGAG 240
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DB 181 CGTGTACAGAGAGCGGCTGTATGACGAGCTGAGTGAAGAAACGTTCTCGAGAGAGGAG 240
QY 241 GAGGATCATGTACAGCGCGGAGAGTAGACCTGTCTCAGTGTCTTGGTTGGCCGAC 300
DB 241 GAGGATCATGTACAGCGCGGAGAGTAGACCTGTCTCAGTGTCTTGGTTGGCCGAC 300
QY 301 CATGATCTCTCGAATCTGTGGGATCATGACGATCGGCAATGTACAAACATGAGCC 360
DB 301 CATGATCTCTCGAATCTGTGGGATCATGACGATCGGCAATGTACAAACATGAGCC 360
QY 361 TGGGACAGACAGCAGAGAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACAG 420
DB 361 TGGGACAGACAGCAGAGAGAGGAGAGAGACAGAGAAAGAAACACAGCATGAGAACAG 420
QY 421 TAAATGAATTAACCAATAATATTTAGCCCTGTCTGTCTGTACTGCCAGGAAT 480
DB 421 TAAATGAATTAACCAATAATATTTAGCCCTGTCTGTCTGTACTGCCAGGAAT 480
QY 481 GGTACCAATTTTTCAGTGTGTGACTGTGACGCTTCTTTGCCACAGCAGAGAAAT 540
DB 481 GGTACCAATTTTTCAGTGTGTGACTGTGACGCTTCTTTGCCACAGCAGAGAAAT 540
QY 541 AACACTGTTTCAACCCCGGGAGGTTGGCTGTGTTAAAGAAAGACATTAATGCTTAG 600
DB 541 AACACTGTTTCAACCCCGGGAGGTTGGCTGTGTTAAAGAAAGACATTAATGCTTAG 600
QY 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
DB 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
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RESULT 2
US-09-825-294-210
: Sequence 210, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.4845
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: fastseq for Windows Version 3.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (1)...(625)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210
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Query Match 100.0% Score 625; DB 31; Length 625;

Best Local Similarity 100.0%; Pred. No. 6.3e-125; Mismatches 0; Indels 0; Gaps 0;

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Matches 625: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTCTCTTGGAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGC 60
DB 1 AGTTCTCTTGGAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGC 60
QY 61 GCGCGTGTGGTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGTTGGCTGCTG 120
DB 61 GCGCGTGTGGTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGTTGGCTGCTG 120
QY 121 CAGCGACAGCGGCGGACAGACAGCACTGTGACGAACACCCCGGCAAACTGCTGCGAGACAC 180
DB 121 CAGCGACAGCGGCGGACAGACAGCACTGTGACGAACACCCCGGCAAACTGCTGCGAGACAC 180
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QY 181 CGTGTACAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAGAAAGGGAG 240
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QY 241 GAGGATCATGTACGCCCGGAAAGTAGACCTGTCCAGTCGTGCTGGGTTGGCCGACG 300
Db 241 GAGGATCATGTACGCCCGGAAAGTAGACCTGTCCAGTCGTGCTGGGTTGGCCGACG 300
QY 301 CATGATCTCCGAAATCTGTTGGGCATCCAGCAATACGCCAATGTACAAACATCAGCCC 360
Db 301 CATGATCTCCGAAATCTGTTGGGCATCCAGCAATACGCCAATGTACAAACATCAGCCC 360
QY 361 TGGGACACACGAGCAGAGGAGAGACAGAAAAAACAACAGCATGAGAACACAG 420
Db 361 TGGGACACACGAGCAGAGGAGAGACAGAAAAAACAACAGCATGAGAACACAG 420
QY 421 TAAATGAATAAACCAATAAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT 480
Db 421 TAAATGAATAAACCAATAAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT 480
QY 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCACAAGCAGAGAAATT 540
Db 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCACAAGCAGAGAAATT 540
QY 541 AACACTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTAG 600
Db 541 AACACTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTAG 600
QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
Db 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
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RESULT 3

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US-09-867-701-10876
; Sequence 10876, Application US/09867701
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10876
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876
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Query Match 100.0%; Score 625; DB 33; Length 625;

Best Local Similarity 100.0%; Pred. No. 6,3e-125; Indels 0; Gaps 0;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGTTTCCTTGACAGAGACTGGCGCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAAGCG 60
QY 61 GGGGCTGTGGTGGTAGAGTGCATGTACGCGGAGGCGCTTCTGCTGGTGGCTGCTG 120
Db 61 GGGGCTGTGGTGGTAGAGTGCATGTACGCGGAGGCGCTTCTGCTGGTGGCTGCTG 120
QY 121 CAGCGACAGCGCGGACAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 180
Db 121 CAGCGACAGCGCGGACAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 180
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QY 241 GAGGATCATGTACGCCCGGAAAGTAGACCTGTCCAGTCGTGCTGGGTTGGCCGACG 300
Db 241 GAGGATCATGTACGCCCGGAAAGTAGACCTGTCCAGTCGTGCTGGGTTGGCCGACG 300
QY 301 CATGATCTCCGAAATCTGTTGGGCATCCAGCAATACGCCAATGTACAAACATCAGCCC 360
Db 301 CATGATCTCCGAAATCTGTTGGGCATCCAGCAATACGCCAATGTACAAACATCAGCCC 360
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Db 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCACAAGCAGAGAAATT 540
QY 541 AACACTTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTAG 600
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RESULT 4

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US-09-970-966-210
; Sequence 210, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.4846
; CURRENT APPLICATION NUMBER: US/09/970,966
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-210
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Query Match 100.0%; Score 625; DB 36; Length 625;

Best Local Similarity 100.0%; Pred. No. 6,3e-125; Indels 0; Gaps 0;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGTTTCCTTGACAGAGACTGGCGCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAAGCG 60
QY 61 GGGGCTGTGGTGGTAGAGTGCATGTACGCGGAGGCGCTTCTGCTGGTGGCTGCTG 120
Db 61 GGGGCTGTGGTGGTAGAGTGCATGTACGCGGAGGCGCTTCTGCTGGTGGCTGCTG 120
QY 121 CAGCGACAGCGCGGACAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 180
Db 121 CAGCGACAGCGCGGACAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 180
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181 CGGTACAGAGGCGGTGATGACCGAGCTGAGTAAACGTTCTCCGAGAGGGAG 240
181 CGGTACAGAGGCGGTGATGACCGAGCTGAGTAAACGTTCTCCGAGAGGGAG 240
241 GAGGATCATGTACGCCGGAAGTAGAGCTGCTGAGTGTGGTGGTGGCCGAGC 300
241 GAGGATCATGTACGCCGGAAGTAGAGCTGCTGAGTGTGGTGGTGGCCGAGC 300
301 CATGATCCTCCGAAATCTGTTGGGATCCAGCATAGCCCAATGTACAAATCAGCCC 360
301 CATGATCCTCCGAAATCTGTTGGGATCCAGCATAGCCCAATGTACAAATCAGCCC 360
361 TGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAACACAGCATGAGACACAG 420
361 TGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAACACAGCATGAGACACAG 420
421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
481 GGATACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGAGAAATT 540
481 GGATACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGAGAAATT 540
541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625

RESULT 5

US-10-212-677-210
; Sequence 210, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jlangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-210

Query Match 100.0%; Score 625; DB 42; Length 625;
Best Local Similarity 100.0%; Pred. No. 6,3e-125;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTTCCTCTTGCAGAGAGATGCGCGCGGAGCGGAAGACACAGGCGCTGCACAAAGC 60
1 AGTTCCTCTTGCAGAGAGATGCGCGCGGAGCGGAAGACACAGGCGCTGCACAAAGC 60
61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGAGGCGCTTCTGTTGGTGGCGTGG 120
61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGAGGCGCTTCTGTTGGTGGCGTGG 120
121 CAGCGACAGGCGGACAGCAGCACTGACGAAACCCCGGAAACTGCTGCGAGGACAC 180

121 CAGCGACAGGCGGACAGCAGCACTGACGAAACCCCGGAAACTGCTGCGAGGACAC 180
181 CGGTACAGAGGCGGTGATGACCGAGCTGAGTAAACGTTCTCCGAGAGGGAG 240
181 CGGTACAGAGGCGGTGATGACCGAGCTGAGTAAACGTTCTCCGAGAGGGAG 240
241 GAGGATCATGTACGCCGGAAGTAGAGCTGCTGAGTGTGGTGGTGGCCGAGC 300
241 GAGGATCATGTACGCCGGAAGTAGAGCTGCTGAGTGTGGTGGTGGCCGAGC 300
301 CATGATCCTCCGAAATCTGTTGGGATCCAGCATAGCCCAATGTACAAATCAGCCC 360
301 CATGATCCTCCGAAATCTGTTGGGATCCAGCATAGCCCAATGTACAAATCAGCCC 360
361 TGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAACACAGCATGAGACACAG 420
361 TGGGCGACAGCAGCAGGAGGAGAGACAGAGAAAACACAGCATGAGACACAG 420
421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
481 GGATACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGAGAAATT 540
481 GGATACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTGCCAAGCAAGAGAAATT 540
541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625

RESULT 6

PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214

Query Match 97.0%; Score 606; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 5,3e-121;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTTCCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACACAGGCGCTGCACAAAGC 60
1271 AGTTCCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACACAGGCGCTGCACAAAGC 1330
61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGAGGCGCTTCTGTTGGTGGCGTGG 120
1331 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGAGGCGCTTCTGTTGGTGGCGTGG 1390
121 CAGCGACAGGCGGACAGCAGCACTGACGAAACCCCGGAAACTGCTGCGAGGACAC 180

Db	1391	CAGCCAGACGGCGGACACAGACGACCTGACAGAACACCCCGGAAACTGTCGGAGACAC	1450
Qy	181	CCTGTACAGACAGCGGTTGTATGACCCAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGAG	240
Db	1451	CCTGTACAGAGACCGGGTTGTATGATACCGAGCTGAGGTAGAAAAACGTCTCCAGAAAGGAG	1510
Qy	241	GAGGATCATGTACGCCCGGAGAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCCGAGC	300
Db	1511	GAGGATCATGTACGCCCGGAGAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCCGAGC	1570
Qy	301	CATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCAACAATACAGCC	360
Db	1571	CATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCAACAATACAGCC	1630
Qy	361	TGGGAGACAGACGAGCAGGAGGAGACAGAGAAAGAAACACAGCATGAGAACACAG	420
Db	1631	TGGGAGACAGCAGCAGGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAG	1690
Qy	421	TAAATGAATAAAAACCATAAATATTTAGCCCTCTGCTTCTGTGCTTACTGCGCAGAAAT	480
Db	1691	TAAATGAATAAAAACCATAAATATTTAGCCCTCTGCTTCTGTGCTTACTGCGCAGAAAT	1750
Qy	481	GGTACCAATTTTTCAGTGTGGAGCTGCACAGCTTCTTTTGGCCACAGCAGAGAAATTT	540
Db	1751	GGTACCAATTTTTCAGTGTGGAGCTGCACAGCTTCTTTTGGCCACAGCAGAGAAATTT	1810
Qy	541	AACACTGTTTCAAAACCCGGGGGAGTGGCTGTGTATTAGAAAGAACCTTAAATGCTTTAG	600
Db	1811	AACACTGTTTCAAAACCCGGGGGAGTGGCTGTGTATTAGAAAGAACCTTAAATGCTTTAG	1870
Qy	601	ACAGTG 606	
Db	1871	ACAGTG 1876	

```

RESULT 7
US-09-825-294-214
Sequence 214, Application US/09825294
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 214
LENGTH: 1897
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1897)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

```

Query Match	97.0%	Score 606	DB 31	Length 1897
Best Local Similarity	100.0%	Pred. No. 5,3e-12		
Matches 606	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	AGTCTCCTTTCGACAGAGACTCTGGGCGCGGAGCGCAACCGGGCGTGTGGCAAAAGG	60
Db	1271	AGTCTCCTTTCGACAGAGACTCTGGGCGCGGAGCGCAACCGGGCGTGTGGCAAAAGG	1330
Qy	61	GGGCGCTTCGCTGTGGAGTGTCCGCAATGACGCCAGCGCTTCTCGTGTGGCGTCTGG	120
Db	1331	GGGCGCTTCGCTGTGGAGTGTCCGCAATGACGCCAGCGCTTCTCGTGTGGCGTCTGG	1390
Qy	121	CAGCGACAGCGGCGACACAGCACTGTGCACGAACACCGCGGAACTGTGTGGAGGACAC	180

Db	1391	CGCGCGACGGCGGCACACACGACCTTCGACGAACACCGCGGAAACGTCTCGAGGAC	1450
QY	181	CGTGTACAGAGGCGGGTGTATGACGAGCTGAGGTAGAAAAACGCTCCGAGAGGGAG	240
Db	1451	CGTGTACAGAGGCGGGTGTATGACGAGCTGAGGTAGAAAAACGCTCTCCGAGAGGGAG	1510
QY	241	GAGGATCATGTACGCGCGGAAGTAGAGCCTGTCACATCGTGCTTGGGTTTGGCCGAGC	300
Db	1511	GAGGATCATGTACGCGCGGAAGTAGAGCCTGTCACATCGTGCTTGGGTTTGGCCGAGC	1570
QY	301	CATGATCCCTCCGAATGTGGTTGGGCAATCCAGCATACGGCCAAATGTCAACAATACGCC	360
Db	1571	CATGATCCCTCCGAATGTGGTTGGGCAATCCAGCATACGGCCAAATGTCAACAATACGCC	1630
QY	361	TGGGCAGACAGCAGCAGGAGGAGAGACAGAGAAAAACACACATGAGAAACAG	420
Db	1631	TGGGCAGACAGCAGGAGGAGAGAGACAGAGAAAAACACACATGAGAAACAG	1690
QY	421	TAAATGAAATAAAAACCTAAAAATTTTAGCCCTGTCTGTGCTTACTGCGCCAGAAAT	480
Db	1691	TAAATGAAATAAAAACCTAAAAATTTTAGCCCTGTCTGTGCTTACTGCGCCAGAAAT	1750
QY	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAACGAGAGGAATTT	540
Db	1751	GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAAACGAGAGGAATTT	1810
QY	541	AAACACTGTTTCAAAACCGGGGGAGTTGGCTGTTTAAAGAAAGCATTTAAATGCTTTAG	600
Db	1811	AAACACTGTTTCAAAACCGGGGGAGTTGGCTGTTTAAAGAAAGCATTTAAATGCTTTAG	1870
QY	601	ACAGTG 606	
Db	1871	ACAGTG 1876	

```

RESULT 8
US-09-970-966-214
: Sequence 214, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesch, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.4846
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-970-966-214

```

Query Match	97.0%	Score 606	DB 36	Length 1897
Best Local Similarly	100.0%	Pred. No. 5.3e-12		
Matches 606	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]


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OY 181 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 240
    |||||||
Db 1451 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 1510
OY 241 GAGGATCATGTACGCCCGGGAAGTAGACCTCGTCCAGTGTGCTGGTTGGCCGACG 300
    |||||||
Db 1511 GAGGATCATGTACGCCCGGGAAGTAGACCTCGTCCAGTGTGCTGGTTGGCCGACG 1570
OY 301 CATGATCTCCGAATCTGTTGGGATTCACGATACGGCCAAATGTACACAAATCAGCCC 360
    |||||||
Db 1571 CATGATCTCCGAATCTGTTGGGATTCACGATACGGCCAAATGTACACAAATCAGCCC 1630
OY 361 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAAACAACGATGAGAACACAG 420
    |||||||
Db 1631 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAAACAACGATGAGAACACAG 1690
OY 421 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 480
    |||||||
Db 1691 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 1750
OY 481 GGTACCAATTTTTCAGTGTGACCTGTGACAGCTCTTTTCCACAAGACAGAAATTT 540
    |||||||
Db 1751 GGTACCAATTTTTCAGTGTGACCTGTGACAGCTCTTTTCCACAAGACAGAAATTT 1810
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
    |||||||
Db 1811 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1870
OY 601 ACAGTG 606
    |||||||
Db 1871 ACAGTG 1876

```

RESULT 9 US-10-212-677-214

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; Sequence 214, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenuault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-677-214

```

Query Match 97.0%; Score 606; DB 42; Length 1897;
Best Local Similarity 100.0%; Pred. No. 5,3e-121;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCTCTTGAGAGAGACTGGCGCCGGAGAGCAAGCAAGCGGCGCTGCACAAAGCG 60
    |||||||
Db 1271 AGTTCTCTTGAGAGAGACTGGCGCCGGAGAGCAAGCAAGCGGCGCTGCACAAAGCG 1330
OY 61 GCGGCTGTGCTGTGAGTGTGCGCATGTACGCCAGGCGCTTCTGCTGTTGGCTGCTG 120
    |||||||
Db 1331 GCGGCTGTGCTGTGAGTGTGCGCATGTACGCCAGGCGCTTCTGCTGTTGGCTGCTG 1390
OY 121 CAGCGACAGGCGGACAGACAGCAGTGCAGAACACCGCCGAAATGCTGCGAGGACAC 180
    |||||||
Db 1391 CAGCGACAGGCGGACAGACAGCAGTGCAGAACACCGCCGAAATGCTGCGAGGACAC 1450
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 240
    |||||||

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Db 1451 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 1510
OY 241 GAGGATCATGTACGCCCGGGAAGTAGACCTCGTCCAGTGTGCTGGTTGGCCGACG 300
    |||||||
Db 1511 GAGGATCATGTACGCCCGGGAAGTAGACCTCGTCCAGTGTGCTGGTTGGCCGACG 1570
OY 301 CATGATCTCCGAATCTGTTGGGATTCACGATACGGCCAAATGTACACAAATCAGCCC 360
    |||||||
Db 1571 CATGATCTCCGAATCTGTTGGGATTCACGATACGGCCAAATGTACACAAATCAGCCC 1630
OY 361 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAAACAACGATGAGAACACAG 420
    |||||||
Db 1631 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAAACAACGATGAGAACACAG 1690
OY 421 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 480
    |||||||
Db 1691 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 1750
OY 481 GGTACCAATTTTTCAGTGTGACCTGTGACAGCTCTTTTCCACAAGACAGAAATTT 540
    |||||||
Db 1751 GGTACCAATTTTTCAGTGTGACCTGTGACAGCTCTTTTCCACAAGACAGAAATTT 1810
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
    |||||||
Db 1811 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1870
OY 601 ACAGTG 606
    |||||||
Db 1871 ACAGTG 1876

```

RESULT 10 US-60-261-974-9/C

```

; Sequence 9, Application US/60261974
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001096-PROV
; CURRENT APPLICATION NUMBER: US/60/261,974
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 43729
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(43729)
; OTHER INFORMATION: n = A,T,C or G
; US-60-261-974-9

```

Query Match 97.0%; Score 606; DB 70; Length 43729;
Best Local Similarity 100.0%; Pred. No. 2,2e-121;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCTCTTGAGAGAGACTGGCGCCGGAGAGCAAGCAAGCGGCGCTGCACAAAGCG 60
    |||||||
Db 41583 AGTTCTCTTGAGAGAGACTGGCGCCGGAGAGCAAGCAAGCGGCGCTGCACAAAGCG 41524
OY 61 GCGGCTGTGCTGTGAGTGTGCGCATGTACGCCAGGCGCTTCTGCTGTTGGCTGCTG 120
    |||||||
Db 41523 GCGGCTGTGCTGTGAGTGTGCGCATGTACGCCAGGCGCTTCTGCTGTTGGCTGCTG 41464
OY 121 CAGCGACAGGCGGACAGACAGCAGTGCAGAACACCGCCGAAATGCTGCGAGGACAC 180
    |||||||
Db 41463 CAGCGACAGGCGGACAGACAGCAGTGCAGAACACCGCCGAAATGCTGCGAGGACAC 41404
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 240
    |||||||
Db 41403 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGAG 41344

```


Db 1201 GCGCGTGTGGTGTGGAGTGTGGCATGTACGGGCAGAGCGCTTCTGCTGGTGTGGCCGTGCT 1260

QY 121 CAGCCACAGAGCGGGCAGCACACGACACTTGACAGCAACCCCGCAAACTGCTGCGAGACAC 180

Db 1261 CAGCCACAGAGCGGGCAGCACACGACACTTGACAGCAACCCCGCAAACTGCTGCGAGACAC 1320

QY 181 CGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAAAGGGGAG 240

Db 1321 CGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAAAGGGGAG 1380

QY 241 GAGGATCATGTACGCCCGGAGTAGGACCTGCTCCAGTGTGCTTGGTTTGGCCGACG 300

Db 1381 GAGGATCATGTACGCCCGGAGTAGGACCTGCTCCAGTGTGCTTGGTTTGGCCGACG 1440

QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCCAATGTGCACAACATCAGCCC 360

Db 1441 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCCAATGTGCACAACATCAGCCC 1500

QY 361 TGGGACAGACAGCAGGAGGAGGAGAGACAGAAAAAGAAAACACAGCATGAGAACACAG 420

Db 1501 TGGGACAGACAGCAGGAGGAGGAGAGACAGAAAAAGAAAACACAGCATGAGAACACAG 1560

QY 421 TAAATGAATAAAAACATAAATATTTAGCCCTCTGTCTGTCTTACTGCGCCAGGAAT 480

Db 1561 TAAATGAATAAAAACATAAATATTTAGCCCTCTGTCTGTCTTACTGCGCCAGGAAT 1620

QY 481 GGTACCATTCTTTCAGTGTGTGACTTGACAGCTTCTTTTCCACAAGCAGAGAAATTT 540

Db 1621 GGTACCATTCTTTCAGTGTGTGACTTGACAGCTTCTTTTCCACAAGCAGAGAAATTT 1680

QY 541 AACACTGTTTCAAAACCCGGGAGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTTAG 600

Db 1681 AACACTGTTTCAAAACCCGGGAGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTTAG 1740

QY 601 ACAGTGTG 606

Db 1741 ACAGTGTG 1746

RESULT 16

US-60-308-868-26

Sequence 26, Application US/60308868

GENERAL INFORMATION:

APPLICANT: Schebye, Xiao Min

TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR

FILE REFERENCE: PA-0048-1 P

CURRENT APPLICATION NUMBER: US/60/308,868

CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PERL Program

SEQ ID NO 26

LENGTH: 1866

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No: 227484.13

US-60-308-868-26

Query Match 88.8%, Score 555, DB 74, Length 1866,
Best Local Similarity 99.8%, Pred. No. 4,4e-110,
Matches 605, Conservativity 0, Mismatches 1,
Totals 0, Gaps 0.

	Query Match	88.8%	Score 555:	DB 74:	Length 1866:
	Best Local Similarity	99.8%:	Pred.	No. 4,4e-110:	
	Matches 605:	Conservative	0:	Mismatches 1:	Indels 0; Gaps 0;
OY	1 AGTCTCCTTCAGAGGACTGGCGCCGGAGCGCAAGCAACGGCGCTGCACAACGG				60
Db	1141 AGTTCTCCTTCAGAGGACTGGCGCCGGAGCGCAAGCAACGGCGCTGCACAACGG				1200
OY	61 GGCGGTGTCGTGGTGSGAGTGGCATTAACGGGCAAGGGCGTTCGTGTTGGCTCTGG				120
Db	1201 GGCGGTGTCGTGGTGSGAGTGGCATTAACGGGCAAGGGCGTTCGTGTTGGCTCTGG				1260
OY	121 CAGGACAGGGGGAAGCACACACCTGGACGAACCCGGCGAAMCTCTGGAGAGAAC				180

Db 1261 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGGAGAGAC 1320
Qy 181 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 240
Db 1321 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 1380
Qy 241 GAGGATCATGATGACCGCGGAGTAGAGCTGCTCCAGTGTGCTGGTTGGCCGACG 300
Db 1381 GAGGATCATGATGACCGCGGAGTAGAGCTGCTCCAGTGTGCTGGTTGGCCGACG 1440
Qy 301 CATGATCTCCGAATCTGGTGGGATCCAGATGACAGATGACAGATGACAGCC 360
Db 1441 CATGATCTCCGAATCTGGTGGGATCCAGATGACAGATGACAGATGACAGCC 1500
Qy 361 TGGGACAGACAG 420
Db 1501 TGGGACAGACAG 1560
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTGCTGCTGCTTACGCGCAGAGAAAT 480
Db 1561 TAAATGAATAAACATTAATATTTAGCCCTGCTGCTGCTTACGCGCAGAGAAAT 1620
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCAGAGAGAGAAAT 540
Db 1621 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCAGAGAGAGAAAT 1680
Qy 541 AACACGTGTTCAACCCCGGGGAGTGGCTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 1681 AACACGTGTTCAACCCCGGGGAGTGGCTGTTAAAGAAAGACATTAATGCTTTAG 1740
Qy 601 ACAAGT 606
Db 1741 ACAAGT 1746

RESULT 17
US-09-371-168-7188
; Sequence 7188, Application US/09371168
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, M. Alexandra
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN BRAIN LIBRARY
; CURRENT APPLICATION NUMBER: US/09/371,168
; EARLIER FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: 60/095,907
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/103,145
; NUMBER OF SEQ ID NOS: 8285
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7188
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-168-7188

Query Match 88.8%; Score 555; DB 17; Length 1917;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCTCTTGAGAGAGACTGGCGCGGAGACGGAAGAGCAAGGCGCTGACAAAGCG 60
Db 1286 AGTTCTCTTGAGAGAGACTGGCGCGGAGACGGAAGAGCAAGGCGCTGACAAAGCG 1345
Qy 61 GCGGCTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTGTG 120
Db 1346 GCGGCTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTGTG 1405
Qy 121 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGCGAGAGAC 180
Db 1406 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGCGAGAGAC 1465

Qy 181 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 240
Db 1466 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 1525
Qy 241 GAGGATCATGATGACCGCGGAGTAGAGCTGCTCCAGTGTGCTGGTTGGCCGACG 300
Db 1526 GAGGATCATGATGACCGCGGAGTAGAGCTGCTCCAGTGTGCTGGTTGGCCGACG 1585
Qy 301 CATGATCTCCGAATCTGGTGGGATCCAGATGACAGATGACAGATGACAGCC 360
Db 1586 CATGATCTCCGAATCTGGTGGGATCCAGATGACAGATGACAGATGACAGCC 1645
Qy 361 TGGGACAGACAG 420
Db 1646 TGGGACAGACAG 1705
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTGCTGCTGCTTACGCGCAGAGAAAT 480
Db 1706 TAAATGAATAAACATTAATATTTAGCCCTGCTGCTGCTTACGCGCAGAGAAAT 1765
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCAGAGAGAAAT 540
Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCAGAGAGAAAT 1825
Qy 541 AACACGTGTTCAACCCCGGGGAGTGGCTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 1826 AACACGTGTTCAACCCCGGGGAGTGGCTGTTAAAGAAAGACATTAATGCTTTAG 1885
Qy 601 ACAAGT 606
Db 1886 ACAAGT 1891

RESULT 18
US-09-644-873-9077
; Sequence 9077, Application US/09644873
; GENERAL INFORMATION:
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600,1169-001
; CURRENT APPLICATION NUMBER: US/09/644,873
; EARLIER FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,064
; EARLIER FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 11286
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9077
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-644-873-9077

Query Match 88.8%; Score 555; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCTCTTGAGAGAGACTGGCGCGGAGACGGAAGAGCAAGGCGCTGACAAAGCG 60
Db 1286 AGTTCTCTTGAGAGAGACTGGCGCGGAGACGGAAGAGCAAGGCGCTGACAAAGCG 1345
Qy 61 GCGGCTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTGTG 120
Db 1346 GCGGCTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTGTG 1405
Qy 121 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGCGAGAGAC 180
Db 1406 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGCGAGAGAC 1465
Qy 181 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 240
Db 1466 CGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAGAGAAACGTCCTCGAAGAGGGAG 1525

QY 241 GAGATCATGTACCCCGGAGTAGAGACCTGTCCTTGGTTGGCCGACG 300
| | | | |
Db 1526 GAGATCATGTACCCCGGAGTAGAGACCTGTCCTTGGTTGGCCGACG 1585
QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360
| | | | |
Db 1586 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 1645
QY 361 TGGGACAGACGAGAGGAGAGACAGAGAAAGAAACAGAGCTGAGAACAG 420
| | | | |
Db 1646 TGGGACAGACGAGAGGAGAGAGACAGAGAAAGAAACAGAGCTGAGAACAG 1705
QY 421 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
| | | | |
Db 1706 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 1765
QY 481 GGTACCAATTTTCAGTTGGAGTGTGACAGCTTCTTTGGCCAGAGAGAAATTT 540
| | | | |
Db 1766 GGTACCAATTTTCAGTTGGAGTGTGACAGCTTCTTTGGCCAGAGAGAAATTT 1825
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
| | | | |
Db 1826 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 1885
QY 601 ACAGTG 606
| | | | |
Db 1886 ACAGTG 1891

RESULT 19
US-09-652-109-9370
; Sequence 9370, Application US/09652109
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1180-001
; CURRENT APPLICATION NUMBER: US/09/652.109
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151.128
; NUMBER OF SEQ ID NOS: 1999-08-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9370
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-109-9370

Query Match 88.8%; Score 555; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTTCTCCTTGCAGAGACTGGCCCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGCG 60
| | | | |
Db 1286 AGTTCTCCTTGCAGAGACTGGCCCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGCG 1345
QY 61 GGGCGTGTGCGTGTGAGTGCAGATGTACGCGAGGCGCTTCGCGTGGTGGCGTGTG 120
| | | | |
Db 1346 GGGCGTGTGCGTGTGAGTGCAGATGTACGCGAGGCGCTTCGCGTGGTGGCGTGTG 1405
QY 121 CAGCGACAGCGCGAGCAGACACCTGCAGAACACCCCGCGAAATCTGCTGAGAGAC 180
| | | | |
Db 1406 CAGCGACAGCGCGAGCAGACACCTGCAGAACACCCCGCGAAATCTGCTGAGAGAC 1465
QY 181 CGGTACAGAGAGGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCTCGAGAGGAG 240
| | | | |
Db 1466 CGGTACAGAGAGGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCTCGAGAGGAG 1525
QY 241 GAGGATCATGTACGCCCGGAGAGTAGACCTGTCAGTCTGTTGGTTGGCCGACG 300
| | | | |
Db 1526 GAGGATCATGTACGCCCGGAGAGTAGACCTGTCAGTCTGTTGGTTGGCCGACG 1585

QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360
| | | | |
Db 1586 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 1645
QY 361 TGGGACAGACGAGAGGAGAGACAGAGAAAGAAACAGAGCTGAGAACAG 420
| | | | |
Db 1646 TGGGACAGACGAGAGGAGAGAGACAGAGAAAGAAACAGAGCTGAGAACAG 1705
QY 421 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
| | | | |
Db 1706 TAAATGAATAAACCATTAATATTATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 1765
QY 481 GGTACCAATTTTCAGTTGGAGTGTGACAGCTTCTTTGGCCAGAGAGAAATTT 540
| | | | |
Db 1766 GGTACCAATTTTCAGTTGGAGTGTGACAGCTTCTTTGGCCAGAGAGAAATTT 1825
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
| | | | |
Db 1826 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 1885
QY 601 ACAGTG 606
| | | | |
Db 1886 ACAGTG 1891

RESULT 20
US-09-652-121-6191
; Sequence 6191, Application US/09652121
; GENERAL INFORMATION:
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1188-001
; CURRENT APPLICATION NUMBER: US/09/652.121
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151.129
; NUMBER OF SEQ ID NOS: 1999-08-30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6191
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-121-6191

Query Match 88.8%; Score 555; DB 25; Length 1917;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTTCTCCTTGCAGAGACTGGCCCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGCG 60
| | | | |
Db 1286 AGTTCTCCTTGCAGAGACTGGCCCGGAGCGCAAGAGCAAGGGCGCTGCACAAAGCG 1345
QY 61 GGGCGTGTGCGTGTGAGTGCAGATGTACGCGAGGCGCTTCGCGTGGTGGCGTGTG 120
| | | | |
Db 1346 GGGCGTGTGCGTGTGAGTGCAGATGTACGCGAGGCGCTTCGCGTGGTGGCGTGTG 1405
QY 121 CAGCGACAGCGCGAGCAGACACCTGCAGAACACCCCGCGAAATCTGCTGAGAGAC 180
| | | | |
Db 1406 CAGCGACAGCGCGAGCAGACACCTGCAGAACACCCCGCGAAATCTGCTGAGAGAC 1465
QY 181 CGGTACAGAGAGGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCTCGAGAGGAG 240
| | | | |
Db 1466 CGGTACAGAGAGGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCTCGAGAGGAG 1525
QY 241 GAGGATCATGTACGCCCGGAGAGTAGACCTGTCAGTCTGTTGGTTGGCCGACG 300
| | | | |
Db 1526 GAGGATCATGTACGCCCGGAGAGTAGACCTGTCAGTCTGTTGGTTGGCCGACG 1585
QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360
| | | | |
Db 1586 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 1645

Db 1706 TAAATTAATTAACCATTAATTAATTTAGCCCTCTGTCTGTCTTACTGTGGCCAGGAAT 1765
Qy 481 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 540
Db 1766 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 1825
Qy 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAACCATTAATGCTTTAG 600
Db 1826 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAACCATTAATGCTTTAG 1885
Qy 601 ACACTG 606
Db 1886 ACACTG 1891

RESULT 23

US-09-652-914-8473
; Sequence 8473, Application US/09652914
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1193-001
; CURRENT APPLICATION NUMBER: US/09/652,914
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 9677
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8473
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-914-8473

Query Match 88.8% Score 555; DB 25; Length 1917;
Best Local Similarity 99.8% Pred. No. 4,4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 60
Db 1286 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 1345
Qy 61 GGCCCTGTGGTGGTGGAGTGCATGTAACGCGACGGCGCTTCTGTGGTGGCGTGTG 120
Db 1346 GGCCCTGTGGTGGTGGAGTGCATGTAACGCGACGGCGCTTCTGTGGTGGCGTGTG 1405
Qy 121 CAGGAGAGCGGCGGAGCAGACACCTGACAGAACCCGGCGAACTGTGGAGAGACAC 180
Db 1406 CAGGAGAGCGGCGGAGCAGACACCTGACAGAACCCGGCGAACTGTGGAGAGACAC 1465
Qy 181 CGGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCTCCGAAAGGGAG 240
Db 1466 CGGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCTCCGAAAGGGAG 1525
Qy 241 GAGGATCATGTACCCCGGGAAGTAGACCTGTCCAGTGTCTGTGGTGGCGGACG 300
Db 1526 GAGGATCATGTACCCCGGGAAGTAGACCTGTCCAGTGTCTGTGGTGGCGGACG 1585
Qy 301 CATGATCTCCGATCTGGTGGGAGTACAGCATACGGCAATGTCCACAACATCAGCCC 360
Db 1586 CATGATCTCCGATCTGGTGGGAGTACAGCATACGGCAATGTCCACAACATCAGCCC 1645
Qy 361 TGGGACAGACAG 420
Db 1646 TGGGACAGACAG 1705
Qy 421 TAAATGAATTAACCATTAATTAATTTAGCCCTCTGTCTGTGTACTGTGGCCAGGAAT 480
Db 1706 TAAATGAATTAACCATTAATTAATTTAGCCCTCTGTGTGTACTGTGGCCAGGAAT 1765
Qy 481 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 540
Db 1766 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 1825

Db 1766 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 1825
Qy 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAACCATTAATGCTTTAG 600
Db 1826 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAACCATTAATGCTTTAG 1885
Qy 601 ACACTG 606
Db 1886 ACACTG 1891

RESULT 24

US-09-652-917-2477
; Sequence 2477, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652,917
; PRIOR FILING DATE: 2000-08-30
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2477
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-917-2477

Query Match 88.8% Score 555; DB 25; Length 1917;
Best Local Similarity 99.8% Pred. No. 4,4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 60
Db 1286 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 1345
Qy 61 GGCCCTGTGGTGGTGGAGTGCATGTAACGCGACGGCGCTTCTGTGGTGGCGTGTG 120
Db 1346 GGCCCTGTGGTGGTGGAGTGCATGTAACGCGACGGCGCTTCTGTGGTGGCGTGTG 1405
Qy 121 CAGGAGAGCGGCGGAGCAGACACCTGACAGAACCCGGCGAACTGTGGAGAGACAC 180
Db 1406 CAGGAGAGCGGCGGAGCAGACACCTGACAGAACCCGGCGAACTGTGGAGAGACAC 1465
Qy 181 CGGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCTCCGAAAGGGAG 240
Db 1466 CGGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCTCCGAAAGGGAG 1525
Qy 241 GAGGATCATGTACCCCGGGAAGTAGACCTGTCCAGTGTCTGTGGTGGCGGACG 300
Db 1526 GAGGATCATGTACCCCGGGAAGTAGACCTGTCCAGTGTCTGTGGTGGCGGACG 1585
Qy 301 CATGATCTCCGATCTGGTGGGAGTACAGCATACGGCAATGTCCACAACATCAGCCC 360
Db 1586 CATGATCTCCGATCTGGTGGGAGTACAGCATACGGCAATGTCCACAACATCAGCCC 1645
Qy 361 TGGGACAGACAG 420
Db 1646 TGGGACAGACAG 1705
Qy 421 TAAATGAATTAACCATTAATTAATTTAGCCCTCTGTGTGTACTGTGGCCAGGAAT 480
Db 1706 TAAATGAATTAACCATTAATTAATTTAGCCCTCTGTGTGTACTGTGGCCAGGAAT 1765
Qy 481 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 540
Db 1766 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTTGCACAGCAAGAGAGAATT 1825

OY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 480
| | | | |
DB 216 TAAATTAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 157
| | | | |
OY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTCTTTTCCACAAGAGAGAAATT 540
| | | | |
DB 156 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTCTTTTCCACAAGAGAGAAATT 97
| | | | |
OY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAACATTAAATGCTTTAG 600
| | | | |
DB 96 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAACATTAAATGCTTTAG 37
| | | | |
OY 601 ACAGTG 606
| | | | |
DB 36 ACAGTG 31

RESULT 29

US-09-652-128-9375/c
; Sequence 9375, Application US/09652128
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1171-001
; CURRENT APPLICATION NUMBER: US/09/652,128
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,133
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10265
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-128-9375

Query Match 88.8%; Score 555; DB 25; Length 1925;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGTTTCCTTGGAGAGAGCTGGCGCGGAGCGGAAGCAACGGCGCTGCACAAAGCG 60
| | | | |
DB 636 AGTTTCCTTGGAGAGAGCTGGCGCGGAGCGGAAGCAACGGCGCTGCACAAAGCG 577
| | | | |
OY 61 GCGCGTGTGGTGTGAGTGGCATGTACGCGCAGCGCTTCTGCTGTTGGCGTGTG 120
| | | | |
DB 576 GCGCGTGTGGTGTGAGTGGCATGTACGCGCAGCGCTTCTGCTGTTGGCGTGTG 517
| | | | |
OY 121 CAGCGACAGCGCGCAGCAGCACTGCAAGAACACCGCGCAAACTGCTGGGAGACAC 180
| | | | |
DB 516 CAGCGACAGCGCGCAGCAGCACTGCAAGAACACCGCGCAAACTGCTGGGAGACAC 457
| | | | |
OY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAACGTCGAGAAAGGAG 240
| | | | |
DB 456 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAACGTCGAGAAAGGAG 397
| | | | |
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTTGGGTTTGGCCGACG 300
| | | | |
DB 396 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTTGGGTTTGGCCGACG 337
| | | | |
OY 301 CATGATCTCTCCGAATCTGTTGGGATTCAGCATGAGGCAATGTACAAACATTCAGCCG 360
| | | | |
DB 336 CATGATCTCTCCGAATCTGTTGGGATTCAGCATGAGGCAATGTACAAACATTCAGCCG 277
| | | | |
OY 361 TGGGCGACACGAGCGAGGAGAGACAGAGAAAACACAGCATGAGAACACAG 420
| | | | |
DB 276 TGGGCGACACGAGCGAGGAGAGACAGAGAAAACACAGCATGAGAACACAG 217
| | | | |
OY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 480
| | | | |
DB 216 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 157
| | | | |

OY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTCTTTTCCACAAGAGAGAAATT 540
| | | | |
DB 156 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTCTTTTCCACAAGAGAGAAATT 97
| | | | |
OY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAACATTAAATGCTTTAG 600
| | | | |
DB 96 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAACATTAAATGCTTTAG 37
| | | | |
OY 601 ACAGTG 606
| | | | |
DB 36 ACAGTG 31

RESULT 30

US-09-652-917-3346/c
; Sequence 3346, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Distefero, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652,917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3346
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-917-3346

Query Match 88.8%; Score 555; DB 25; Length 1925;
Best Local Similarity 99.8%; Pred. No. 4.4e-110;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGTTTCCTTGGAGAGAGCTGGCGCGGAGCGGAAGCAACGGCGCTGCACAAAGCG 60
| | | | |
DB 636 AGTTTCCTTGGAGAGAGCTGGCGCGGAGCGGAAGCAACGGCGCTGCACAAAGCG 577
| | | | |
OY 61 GCGCGTGTGGTGTGAGTGGCATGTACGCGCAGCGCTTCTGCTGTTGGCGTGTG 120
| | | | |
DB 576 GCGCGTGTGGTGTGAGTGGCATGTACGCGCAGCGCTTCTGCTGTTGGCGTGTG 517
| | | | |
OY 121 CAGCGACAGCGCGCAGCAGCACTGCAAGAACACCGCGCAAACTGCTGGGAGACAC 180
| | | | |
DB 516 CAGCGACAGCGCGCAGCAGCACTGCAAGAACACCGCGCAAACTGCTGGGAGACAC 457
| | | | |
OY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAACGTCGAGAAAGGAG 240
| | | | |
DB 456 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAACGTCGAGAAAGGAG 397
| | | | |
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTTGGGTTTGGCCGACG 300
| | | | |
DB 396 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTTGGGTTTGGCCGACG 337
| | | | |
OY 301 CATGATCTCTCCGAATCTGTTGGGATTCAGCATGAGGCAATGTACAAACATTCAGCCG 360
| | | | |
DB 336 CATGATCTCTCCGAATCTGTTGGGATTCAGCATGAGGCAATGTACAAACATTCAGCCG 277
| | | | |
OY 361 TGGGCGACACGAGCGAGGAGAGACAGAGAAAACACAGCATGAGAACACAG 420
| | | | |
DB 276 TGGGCGACACGAGCGAGGAGAGACAGAGAAAACACAGCATGAGAACACAG 217
| | | | |
OY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 480
| | | | |
DB 216 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGCTTACTGCGAGGAAT 157
| | | | |
OY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTCTTTTCCACAAGAGAGAAATT 540
| | | | |

Db 156 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCCACAAGCAGAGAAATTT 97
|
QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
|
Db 96 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 37
|
QY 601 ACACTG 606
|
Db 36 ACACTG 31

RESULT 31

US-09-997-11085/c
; Sequence 11085, Application US/09699997
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Sinos-Santiago, Immaculada
; APPLICANT: Stefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2020-001
; CURRENT APPLICATION NUMBER: US/09/699,997
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,359
; NUMBER OF SEQ ID NOS: 12714
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11085
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-11085

Query Match 88.8%: Score 555; DB 27; Length 1925;
Best Local Similarity 99.8%: Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTCAGAGAGACTGGCCGGGAGCGGAAAGCAAGCGGCGCTGCACAAAGCG 60
|
Db 636 AGTTCCTCTTCAGAGAGACTGGCCGGGAGCGGAAAGCAAGCGGCGCTGCACAAAGCG 577
|
QY 61 GGGCCTGCGGTGGTGGAGTGGCATGTAACGGCAGGCGCTTCTGTGGTGGCGTCTG 120
|
Db 576 GGGCCTGCGGTGGTGGAGTGGCATGTAACGGCAGGCGCTTCTGTGGTGGCGTCTG 517
|
QY 121 CAGGAGAGGCGGAGCAGACACCTGACAGAACACCCGCCGAACTGGTGAGAGACAC 180
|
Db 516 CAGGAGAGGCGGAGCAGACACCTGACAGAACACCCGCCGAACTGGTGAGAGACAC 457
|
QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAGAAAAGCTCTCCGAGAGGGAG 240
|
Db 456 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAGAAAAGCTCTCCGAGAGGGAG 397
|
QY 241 GAGGATCATGTAGCCCGGAGTAGAGACTGGTCCAGTGTGCTGGTGGTGGCGGACG 300
|
Db 396 GAGGATCATGTAGCCCGGAGTAGAGACTGGTCCAGTGTGCTGGTGGTGGCGGACG 337
|
QY 301 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATGAGCCC 360
|
Db 336 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATGAGCCC 277
|
QY 361 TGGGCAACACAG 420
|
Db 276 TGGGCAACACAG 217
|
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTGCTGTGCTGTACTGGCCAGGAAT 480
|
Db 216 TAAATGAATAAACCATTAATATTTAGCCCTGCTGTGCTGTACTGGCCAGGAAT 157
|
QY 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAAGAGAGAAATTT 540
|
Db 156 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAAGAGAGAAATTT 97

QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
|
Db 96 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 37
|
QY 601 ACACTG 606
|
Db 36 ACACTG 31

RESULT 32

US-09-710-281-4458/c
; Sequence 4458, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Sebda, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710,281
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,254
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4458
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-281-4458

Query Match 88.8%: Score 555; DB 28; Length 1925;
Best Local Similarity 99.8%: Pred. No. 4.4e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTCAGAGAGACTGGCCGGGAGCGGAAAGCAAGCGGCGCTGCACAAAGCG 60
|
Db 636 AGTTCCTCTTCAGAGAGACTGGCCGGGAGCGGAAAGCAAGCGGCGCTGCACAAAGCG 577
|
QY 61 GGGCCTGCGGTGGTGGAGTGGCATGTAACGGCAGGCGCTTCTGTGGTGGCGTCTG 120
|
Db 576 GGGCCTGCGGTGGTGGAGTGGCATGTAACGGCAGGCGCTTCTGTGGTGGCGTCTG 517
|
QY 121 CAGGAGAGGCGGAGCAGACACCTGACAGAACACCCGCCGAACTGGTGAGAGACAC 180
|
Db 516 CAGGAGAGGCGGAGCAGACACCTGACAGAACACCCGCCGAACTGGTGAGAGACAC 457
|
QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAGAAAAGCTCTCCGAGAGGGAG 240
|
Db 456 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAGAAAAGCTCTCCGAGAGGGAG 397
|
QY 241 GAGGATCATGTAGCCCGGAGTAGAGACTGGTCCAGTGTGCTGGTGGTGGCGGACG 300
|
Db 396 GAGGATCATGTAGCCCGGAGTAGAGACTGGTCCAGTGTGCTGGTGGTGGCGGACG 337
|
QY 301 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATGAGCCC 360
|
Db 336 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATGAGCCC 277
|
QY 361 TGGGCAACACAG 420
|
Db 276 TGGGCAACACAG 217
|
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTGCTGTGCTGTACTGGCCAGGAAT 480
|
Db 216 TAAATGAATAAACCATTAATATTTAGCCCTGCTGTGCTGTACTGGCCAGGAAT 157
|
QY 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAAGAGAGAAATTT 540
|
Db 156 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAAGAGAGAAATTT 97
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QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600

QY 601 ACAGTG 606
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 Db 84 ACAGTG 79

RESULT 35
 US-09-950-083-1914/c
 ; Sequence 1914, Application US/09950083
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, et. al
 ; TITLE OF INVENTION: Human Secreted Proteins
 ; FILE REFERENCE: PS805
 ; CURRENT APPLICATION NUMBER: US/09/950, 083
 ; PRIOR FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: 60/278,650
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/833,245
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/11988
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/06043
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06012
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06058
 ; PRIOR FILING DATE: 2000-03-09
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 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06059
 ; PRIOR FILING DATE: 2000-03-09
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 ; PRIOR FILING DATE: 2000-03-09
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 ; PRIOR FILING DATE: 2000-03-09
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 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06057
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06824
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 ; PRIOR FILING DATE: 2000-03-16
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 ; PRIOR FILING DATE: 2000-03-16
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 ; PRIOR APPLICATION NUMBER: PCT/US00/06791
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: PCT/US00/06828
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 ; PRIOR FILING DATE: 2000-03-22
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 ;; PRIOR APPLICATION NUMBER: PCT/US00/14973
 ;; PRIOR FILING DATE: 2000-06-01
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14964
 ;; PRIOR FILING DATE: 2000-06-01
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26376
 ;; PRIOR FILING DATE: 2000-09-26
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26371
 ;; PRIOR FILING DATE: 2000-09-26
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26324

1	PRIOR FILING DATE: 2000-09-26	
2	PRIOR APPLICATION NUMBER: PCT/US00/26323	
3	PRIOR FILING DATE: 2000-09-26	
4	PRIOR APPLICATION NUMBER: PCT/US00/26337	
5	PRIOR FILING DATE: 2000-09-26	
6	PRIOR APPLICATION NUMBER: PCT/US01/13318	
7	PRIOR FILING DATE: 2001-04-27	
8	PRIOR APPLICATION NUMBER: US 60/124,146	
9	PRIOR FILING DATE: 1999-03-12	
10	PRIOR APPLICATION NUMBER: US 60/167,061	
11	PRIOR FILING DATE: 1999-11-23	
12	PRIOR APPLICATION NUMBER: US 60/124,093	
13	PRIOR FILING DATE: 1999-03-12	
14	PRIOR APPLICATION NUMBER: US 60/166,989	
15	PRIOR FILING DATE: 1999-11-23	
16	PRIOR APPLICATION NUMBER: US 60/124,145	
17	PRIOR FILING DATE: 1999-03-12	
18	PRIOR APPLICATION NUMBER: US 60/168,654	
19	PRIOR FILING DATE: 1999-12-03	
20	PRIOR APPLICATION NUMBER: US 60/124,099	
21	PRIOR FILING DATE: 1999-03-12	
22	PRIOR APPLICATION NUMBER: US 60/168,661	
23	PRIOR FILING DATE: 1999-12-03	
24	PRIOR APPLICATION NUMBER: US 60/124,096	
25	PRIOR FILING DATE: 1999-03-12	
26	PRIOR APPLICATION NUMBER: US 60/168,622	
27	PRIOR FILING DATE: 1999-12-03	
28	PRIOR APPLICATION NUMBER: US 60/124,143	
29	PRIOR FILING DATE: 1999-03-12	
30	PRIOR APPLICATION NUMBER: US 60/168,663	
31	PRIOR FILING DATE: 1999-12-03	
32	PRIOR APPLICATION NUMBER: US 60/124,095	
33	PRIOR FILING DATE: 1999-03-12	
34	PRIOR APPLICATION NUMBER: US 60/138,598	
35	PRIOR FILING DATE: 1999-06-11	
36	PRIOR APPLICATION NUMBER: US 60/168,665	
37	PRIOR FILING DATE: 1999-12-03	
38	PRIOR APPLICATION NUMBER: US 60/125,360	
39	PRIOR FILING DATE: 1999-03-19	
40	PRIOR APPLICATION NUMBER: US 60/138,626	
41	PRIOR FILING DATE: 1999-06-11	
42	PRIOR APPLICATION NUMBER: US 60/168,662	
43	PRIOR FILING DATE: 1999-12-03	
44	PRIOR APPLICATION NUMBER: US 60/124,144	
45	PRIOR FILING DATE: 1999-03-12	
46	PRIOR APPLICATION NUMBER: US 60/138,574	
47	PRIOR FILING DATE: 1999-06-11	
48	PRIOR APPLICATION NUMBER: US 60/168,667	
49	PRIOR FILING DATE: 1999-12-03	
50	PRIOR APPLICATION NUMBER: US 60/124,142	
51	PRIOR FILING DATE: 1999-03-12	
52	PRIOR APPLICATION NUMBER: US 60/138,597	
53	PRIOR FILING DATE: 1999-06-11	
54	PRIOR APPLICATION NUMBER: US 60/168,666	
55	PRIOR FILING DATE: 1999-12-03	
56	PRIOR APPLICATION NUMBER: US 60/125,359	
57	PRIOR FILING DATE: 1999-03-19	
58	PRIOR APPLICATION NUMBER: US 60/168,664	
59	PRIOR FILING DATE: 1999-12-03	
60	PRIOR APPLICATION NUMBER: US 60/126,051	
61	PRIOR FILING DATE: 1999-03-23	
62	PRIOR APPLICATION NUMBER: US 60/169,906	

Dd	624	GCCCGCTGTCGGTGAGTGGAGTGGCATGTACGGCGCAGGCGCTCTCTGTGGTTGGCGTGC	565
Qy	121	CAGCACACAGCGCGCAGCAGCAGCACTGTGACGAACAACCCGCCGAATCTGTGGAGACAC	180
Dd	564	CAGCACACAGCGCGCAGCAGCAGCACTGTGACGAACAACCCGCCGAATCTGTGGAGACAC	505
Qy	181	CGTGTACAGAGACCGGTTGATGATGACCAGCTGTGAGTAGAAAAAAGTCTCCGAAAGGGAG	240
Dd	504	CGTGTACAGAGACCGGTTGATGATGACCAGCTGTGAGTAGAAAAAAGTCTCCGAAAGGGAG	445
Qy	241	GAGGATCATGTACGCCCGGAGAGTACGACTCTCCAGTGTGCTTTGGTTTTGGCCGACG	300
Dd	444	GAGGATCATGTACGCCCGGAGAGTACGACTCTCCAGTGTGCTTTGGTTTTGGCCGACG	385
Qy	301	CATGATCCMCCGAATCTGTGGTTGGGATCCAGATCATCGGCGCAATGTACAAACATCAGCC	360
Dd	384	CATGATCCMCCGAATCTGTGGTTGGGATCCAGATCATCGGCGCAATGTACAAACATCAGCC	325
Qy	361	TGGGACAGACAGCAGCAGGAGGAGAGACAGAAAAAAGAAAACACAGCATGAGAACAG	420
Dd	324	TGGGACAGACAGCAGCAGGAGGAGAGACAGAAAAAAGAAAACACAGCATGAGAACAG	265
Qy	421	TAAATGAATAAACCATTAATAATTATTAGCCCCCTGTGTCTGTGCTTACTGGCCAGAAAT	480
Dd	264	TAAATRAATAAACCATTAATAATTATTAGCCCCCTGTGTCTGTGCTTACTGGCCAGAAAT	205
Qy	481	GGTACCAATTTTTCAGTGTGTGACTTGTGACAGCTCTTTTGGCCACAAGCAGAGAAATTT	540
Dd	204	GGTACCAATTTTTCAGTGTGTGACTTGTGACAGCTCTTTTGGCCACAAGCAGAGAAATTT	145
Qy	541	AACACTGTTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAATTAATGCTTAG	600
Dd	144	AACACTGTTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAATTAATGCTTAG	85
Qy	601	ACAGTG 606 	
Dd	84	ACAGTG 79	
RESULT 36			
US-10-105-299-2414/C			
; Sequence 2414, Application US/10105299			
; GENERAL INFORMATION:			
; APPLICANT: Rosen, et. al			
; TITLE OF INVENTION: Human Secreted Proteins			
; FILE REFERENCE: PS950			
; CURRENT APPLICATION NUMBER: US/10/105_299			
; CURRENT FILING DATE: 2002-03-26			
; NUMBER OF SEQ ID NOS: 15197			
; Prior Application removed - See File Wrapper or Palm			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 2414			
; LENGTH: 1953			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1362)..(1362)			
; OTHER INFORMATION: n equals a,t,g, or c			
US-10-105-299-2414			

	Query Match	Similarity	88.8%	Score 555	DB 36	Length 1953
Best Local	Similarity	99.8%	Pred. No. 4.3e-110			
Matches	605	Conservative	0	Mismatches	1	Indels 0; Gaps 0
QY	1	AGTTCCTCTTGAGAGAGACTGGCCGCCGAGCCGAGAAAGCAACGGGCGCTGTGACAAAGCG	60			
Db	684	AGTTCCTCTTGAGAGAGACTGGCCGCCGAGCCGAGAAAGCAACGGGCGCTGTGACAAAGCG	625			
QY	61	GGCGCTGCGGTGTGTGAGTGGCAATGTAACGGCAGCGCTTCTGTGAGTTGGCGTGTG	120			

	Matches	605;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	AGTTCTCCTTGAGAGACTGGCGCGGAGCGAGCAAGACAAGCGCGCTGCACAAAGCG	60							
Db	684	AGTTCTTCCTTGAGAGAGACTGGCGCGGAGCGAGCAAGACAAGCGCGCTGCACAAAGCG	625							
QY	61	GGCGGTGTCGGTGGAGAGAGTGGCAATGTATCGCGAGCGCCTCTGTGTGGTGGCGGCTG	120							
Db	624	GGCGCTGTGGTGGAGAGTGGCAATGTATCGCGAGCGCCTCTGTGTGGTGGCGTGGT	565							

OY	121	CAGCAGCAGGGGGCAGCAGCAGCAGCTGGACAGAACCCGGCGGAATGCTGCGAGGACAC	180
Db	564	CAGCGACAGGGGGCAGCAGCAGCAGCTGCACAGAACCCCGGAACTGCTGCGGGACAC	505
OY	181	CGTGTACAGAGACGGGTTGATGACCCAGCTGAGGTAGAAAAACGTCCTCGAGAAAGGGAG	240
Db	504	CGTGTACAGAGACGGGTTGATGACCCAGCTGAGGTAGAAAAACGTCCTCGAGAAAGGGAG	445
OY	241	GAGGATTCATGACGCGCGCGAAGTAGAGACCTGTCAGTCGTCGTGGGTTTGGCGGAGC	300
Db	444	GAGGATTCATGACGCGCGCGAAGTAGAGACCTGTCAGTCGTCGTGGGTTTGGCGGAGC	385
OY	301	CATGATCTCTCCGAATCTGTGTGGGCATTCACAGCATACGGCCATGTCAACAACATCAGCCC	360
Db	384	CATGATCTCTCCGAATCTGTGTGGGCATTCACAGCATACGGCCATGTCAACAACATCAGCCC	325
OY	361	TGGCGACAGCAGGACGAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAAACACAG	420
Db	324	TGGCGACAGCAGGACGAGGAGGAGAGAGAGAAAAAACAACAGCATGAGAAACACAG	265
OY	421	TAAATGAATAAACCATAAAAATATTTAGCCCCCTCTGTTCTGTACTGCGCCAGGAAT	480
Db	264	TAAATRAATAAACCATAAAAATATTTAGCCCCCTCTGTTCTGTACTGCGCCAGGAAT	205
OY	481	GGTACCAATTTTTCAGTGTGGAATTTGACAGCCTCTTTGGCCACAGCAAGAGAAATTT	540
Db	204	GGTACCAATTTTTCAGTGTGGAATTTGACAGCCTCTTTGGCCACAGCAAGAGAAATTT	145
OY	541	AACACTGTTTAAACCCCGGGAGAGTTGGCTGTGTTAAAGAAAGACATTAATACCTTTAG	600
Db	144	AACACTGTTTAAACCCCGGGAGAGTTGGCTGTGTTAAAGAAAGACATTAATACCTTTAG	85
OY	601	ACACGTG 606	
Db	84	ACAGTG 79	

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RESULT 37
PCT-US00-14973-23/c
Sequence 23, Application PC/TUS0014973
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PS559PCm
CURRENT APPLICATION NUMBER: PCT/US00/14973
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,630
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1362)
OTHER INFORMATION: n equals a,t,g, or c
PCT-US00-14973-23

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Query Match	88.8%	Score 555	DB 1	Length 1956
Best Local Similarity	99.8%	Pred. NO. 4.3e-110		
Matches 605; Conservative		0; Mismatches 1;	Indels 0;	Gaps 0

QY	1	AGTTCCTCTTTCAGAGGACCTGGCCCGGAGCCGACAGACCGCGCTGCACAAAGCG	60
Db	684	AGTTCCTCTTTCAGAGGACCTGGCCCGGAGCCGACAGACCGCGCTGCACAAAGCG	6235
QY	61	GGCGCTGTCGGTGGTGAGTGGCATATGAGCGGACGGCGCTTCTCGTGTGTTGGCGTCGTG	120
Db	634	GGCGCTGTCGGTGGTGAGTGGCATATGAGCGGACGGCGCTTCTCGTGTGTTGGCGTCGTG	5655
QY	121	CAGCGACAGCGCGACGACACGACCTGCACAAACCCCGCGGAAACTGTCGAGGAGCAC	180

Db	564	CAGCGACAGGGGGGACGACACACCTGAGCAACACCGCGAAACTGCTGCAGAGCAC	505
OY	181	CGTGTACAGGACGGGTTGATGACCCGACCTGAGTAGAAAAAGCTCTCCAGAAAGGGAG	240
Db	504	CGTGTACAGGGACGGGTTGATGACCCGACCTGAGTAGAAAAAGCTCTCCGAAAGGGAG	445
OY	241	GAGGATCATGTACGCCGGGAAGTATGAGACCTGTCAGTCGGTGGTGGGTTTGGCGCCAGC	300
Db	444	GAGGATCATGTACGCCGGGAAGTATGAGACCTGTCAGTCGGTGGTGGGTTTGGCGCGAGC	385
OY	301	CATGATCCTCCGAATCTGTGTGGGCATTCACGATACGGCCCAATGTCAACAATACAGCCC	368
Db	384	CATGATCCTCCGAATCTGTGTGGGCATTCACGATACGGCCCAATGTCAACAATACAGCCC	325
OY	361	TGGGCACACACGACGAGGAGGGAGACAGACAGAAAAAACAACACCATGAGAACACAG	420
Db	324	TGGGCACACACGACGAGGAGGGAGACAGACAGAAAAAACAACACCATGAGAACACAG	265
OY	421	TAAATGATTAATAACCATTAATATTTAGCCCCCTGTGTCTGTACTGTGACCGAGAAAT	480
Db	264	TAAATRAATTAATAACCATTAATATTTAGCCCCCTGTGTCTGTGTACTGTGACCGAGAAAT	205
OY	481	GGTACCAATTTTTCAGTGTGTGGACTTACACGCTTCTTTCACACACAGAGAGAAATTT	540
Db	204	GGTACCAATTTTTCAGTGTGTGGACTTACACGCTTCTTTCGCAACACAGAGAGAAATTT	145
OY	541	AACACTGTTTCAAAACCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG	600
Db	144	AACACTGTTTCAAAACCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG	85
OY	601	ACAGTG 606	
Db	84	ACAGTG 79	

RESULT 38
US-09-950-083-1915/C

Sequence 1915, Application US/09950083

GENERAL INFORMATION:

APPLICANT: Rosen, et. al

TITLE OF INVENTION: Human Secreted Proteins

FILE REFERENCE: PS805

CURRENT APPLICATION NUMBER: US/09/950,.083

CURRENT FILING DATE: 2001-09-12

PRIOR APPLICATION NUMBER: 66/278,650

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 09/833,245

PRIOR FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: PCT/US01/11988

PRIOR FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: PCT/US00/06043

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06012

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06058

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06044

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06059

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06042

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06014

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06013

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06049

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06057

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: PCT/US00/06824

PRIOR FILING DATE: 2000-03-16


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; PRIOR APPLICATION NUMBER: US 60/124,144
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/138,574
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: US 60/168,667
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/124,142
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/138,597
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: US 60/168,666
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/125,359
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: US 60/168,664
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/126,051
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/169,906

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Query Match 88.8%; Score 555; DB 36; Length 1956;
 Best Local Similarity 99.8%; Pred. No. 4.3e-110;
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGTTCTCTTGCAGAGAGCTGGGCGGAGCGAGAGACGAGCGGCTGCACAAACG 60
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DB 684 AGTTCTCTTGCAGAGAGCTGGGCGGAGCGAGAGACGAGCGGCTGCACAAACG 625
QY 61 GGGCGTGTGGTGTGGAGTGGCATGTAGCGCAGCGGCTTCTGTTGGGTGGCTGT 120
    |||||||
DB 624 GGGCGTGTGGTGTGGAGTGGCATGTAGCGCAGCGGCTTCTGTTGGGTGGCTGT 565
QY 121 CAGCGAGAGCGGCGAGCAGACACCTGACGAAACCCGCGAACTGTGCGAGAGAC 180
    |||||||
DB 564 CAGCGAGAGCGGCGAGCAGACACCTGACGAAACCCGCGAACTGTGCGAGAGAC 505
QY 181 CGGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTCTCCAGAGAG 240
    |||||||
DB 504 CGGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTCTCCAGAGAG 445
QY 241 GAGGATCATGTAGCGCCGGAAGTAGACCTGTCAGTCTGCTGGGTGGCCGAGC 300
    |||||||
DB 444 GAGGATCATGTAGCGCCGGAAGTAGACCTGTCAGTCTGCTGGGTGGCCGAGC 385
QY 301 CAGGATCTCTCGAATCTGTTGGGCATCCAGCATAGCGCCATGTCAACAATCAGCCC 360
    |||||||
DB 384 CAGGATCTCTCGAATCTGTTGGGCATCCAGCATAGCGCCATGTCAACAATCAGCCC 325
QY 361 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAG 420
    |||||||
DB 324 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAG 265
QY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTGCTTACTGCGCAGGAAT 480
    |||||||
DB 264 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTGCTTACTGCGCAGGAAT 205
QY 481 GGTACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAAATTT 540
    |||||||
DB 204 GGTACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAAATTT 145
QY 541 AACACTGTTTCAAAACCGGGGAGATTGGCTGTAAAGAAACCATTAATGCTTTAG 600
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DB 144 AACACTGTTTCAAAACCGGGGAGATTGGCTGTAAAGAAACCATTAATGCTTTAG 85
QY 601 ACAAGTG 606
    |||||
DB 84 ACAAGTG 79

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; APPLICANT: Rosen, et. al
; TITLE OR INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See file Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2415
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1362)..(1362)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-105-299-2415

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Query Match 88.8%; Score 555; DB 40; Length 1956;
 Best Local Similarity 99.8%; Pred. No. 4.3e-110;
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGTTCTCTTGCAGAGAGCTGGGCGGAGCGGAGAGACGAGCGGCTGCACAAACG 60
    |||||||
DB 684 AGTTCTCTTGCAGAGAGCTGGGCGGAGCGGAGAGACGAGCGGCTGCACAAACG 625
QY 61 GGGCGTGTGGTGTGGAGTGGCATGTAGCGCAGCGGCTTCTGTTGGGTGGCTGT 120
    |||||||
DB 624 GGGCGTGTGGTGTGGAGTGGCATGTAGCGCAGCGGCTTCTGTTGGGTGGCTGT 565
QY 121 CAGCGAGAGCGGCGAGCAGACACCTGACGAAACCCGCGAACTGTGCGAGAGAC 180
    |||||||
DB 564 CAGCGAGAGCGGCGAGCAGACACCTGACGAAACCCGCGAACTGTGCGAGAGAC 505
QY 181 CGGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAGCTCTCCAGAGAG 240
    |||||||
DB 504 CGGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAGCTCTCCAGAGAG 445
QY 241 GAGGATCATGTAGCGCCGGAAGTAGACCTGTCAGTCTGCTGGGTGGCCGAGC 300
    |||||||
DB 444 GAGGATCATGTAGCGCCGGAAGTAGACCTGTCAGTCTGCTGGGTGGCCGAGC 385
QY 301 CAGGATCTCTCGAATCTGTTGGGCATCCAGCATAGCGCCATGTCAACAATCAGCCC 360
    |||||||
DB 384 CAGGATCTCTCGAATCTGTTGGGCATCCAGCATAGCGCCATGTCAACAATCAGCCC 325
QY 361 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAG 420
    |||||||
DB 324 TGGGACAGACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAG 265
QY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTGCTTACTGCGCAGGAAT 480
    |||||||
DB 264 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTGCTTACTGCGCAGGAAT 205
QY 481 GGTACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAAATTT 540
    |||||||
DB 204 GGTACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAAATTT 145
QY 541 AACACTGTTTCAAAACCGGGGAGATTGGCTGTAAAGAAACCATTAATGCTTTAG 600
    |||||||
DB 144 AACACTGTTTCAAAACCGGGGAGATTGGCTGTAAAGAAACCATTAATGCTTTAG 85
QY 601 ACAAGTG 606
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DB 84 ACAAGTG 79

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RESULT 39
 US-10-105-299-2415/c
 ; Sequence 2415, Application US/10105299
 ; GENERAL INFORMATION:

RESULT 40
 PCT-US02-29964-16
 ; Sequence 16, Application PC/TUS0229964
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Ren, Feiyang

APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Dunrui
APPLICANT: Ghosh, Malabika
APPLICANT: Asundi, Vinod
APPLICANT: Wehrman, Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle W.
APPLICANT: Meng, Gezhi
APPLICANT: Haley-Vicente, Dana
APPLICANT: Drmanac, Radote J.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 809ACIP PCT
CURRENT APPLICATION NUMBER: PCT/US02/29964
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,739
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 992
SOFTWARE: PC_FIL_genes Version 6.0
SEQ ID NO 16
LENGTH: 1967
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (338)..(763)
PCT-US02-29964-16

Query Match 88.8%; Score 555; DB 1; Length 1967;
Best Local Similarity 99.8%; Pred. No. 4,3e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTTCTCTTCGACAGAGACTGGCGCGGACGCGAAGACGAGCGGCGCTGCACAAAGCG 60
DB 1349 AGTTCTCTTCGACAGAGACTGGCGCGGACGCGAAGACGAGCGGCGCTGCACAAAGCG 1408
QY 61 GCGCGTGTGCTGTGAGTGTGCGCATGTACGCGACGCGCTTCTGCTGTGCGCTGCTG 120
DB 1409 GCGCGTGTGCTGTGAGTGTGCGCATGTACGCGACGCGCTTCTGCTGTGCGCTGCTG 1468
QY 121 GAGCGACGAGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
DB 1469 GAGCGACGAGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1528
QY 181 CCGTACAGAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAACGTTCTCCGAGAGGAGAG 240
DB 1529 CCGTACAGAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAACGTTCTCCGAGAGGAGAG 1588
QY 241 GAGGATCATGTACGCGCGGAGAGTACGCTGCTCCAGTGTGCTGTGCTGTGCTGTGCTG 300
DB 1589 GAGGATCATGTACGCGCGGAGAGTACGCTGCTCCAGTGTGCTGTGCTGTGCTGTGCTG 1648

QY 301 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCAAATGTACAAATCAGCCCC 360
DB 1649 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCAAATGTACAAATCAGCCCC 1708
QY 361 TGGGACAGACGACGAG 420
DB 1709 TGGGACAGACGAG 1768
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTTGCCAGGAAT 480
DB 1769 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTTGCCAGGAAT 1828
QY 481 GGTACCAATTTTTCAGTGTGTGAGCTTGAAGCTTTTCCACAAAGAGAGATTT 540
DB 1829 GGTACCAATTTTTCAGTGTGTGAGCTTGAAGCTTTTCCACAAAGAGAGATTT 1888
QY 541 AACACGTGTTCAACCCGCGGAGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
DB 1889 AACACGTGTTCAACCCGCGGAGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1948
QY 601 ACAGTG 606
DB 1949 ACAGTG 1954

RESULT 41
US-09-611-523-203
Sequence 203, Application US/09611523
GENERAL INFORMATION:
APPLICANT: OTA, TOSHIO
APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: KAMAI, YUKI
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: HAYASHI, KOJI
TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
FILE REFERENCE: 084335/0121
CURRENT APPLICATION NUMBER: US/09/611,523
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: JP 1999-194179
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: JP 2000-118775
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183766
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/159,586
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/183,323
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 679
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 203
LENGTH: 1890
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (274)..(768)
US-09-611-523-203

Query Match 87.8%; Score 549; DB 23; Length 1890;
Best Local Similarity 99.8%; Pred. No. 8.4e-109;
Matches 599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 CCTTCAGAGAGACTGGCGCGGAGCGGAGAGCAAGAGCGGCGCTGCACAAAGCGGCGCT 66
DB 1290 CCTTCAGAGAGACTGGCGCGGAGCGGAGAGCAAGAGCGGCGCTGCACAAAGCGGCGCT 1349
QY 67 GTCGCTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGCTGTGCTGTGCTGTGCTG 126
DB 1350 GTCGCTGTGAGTGTGCGCATGTACGCGCAGGCGCTTCTGCTGTGCTGTGCTGTGCTG 1409

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 ; Search time 17.4612 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agtctctcttcagagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size : 10

Total number of hits satisfying chosen parameters: 43951

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	62.9	1524	6 US-10-230-437-15	Sequence 15, Appl
2	3	3.5	1329	6 US-10-264-237-1044	Sequence 1044, Ap
3	3	3.5	2049	6 US-10-264-237-1380	Sequence 1380, Ap
4	21	3.4	2062	6 US-10-264-237-464	Sequence 464, Ap
5	21	3.4	2176	5 US-09-721-456-3	Sequence 0, Appl
6	20	3.2	457	6 US-10-240-425-208	Sequence 208, Appl
7	19	3.0	163	5 US-09-513-999C-21763	Sequence 21763, A
8	19	3.0	496	6 US-10-131-813A-533	Sequence 533, App
9	19	3.0	496	6 US-10-131-819A-533	Sequence 533, App
10	19	3.0	496	6 US-10-131-823A-533	Sequence 533, App
11	19	3.0	496	6 US-10-131-824A-533	Sequence 533, App
12	19	3.0	496	6 US-10-131-826A-533	Sequence 533, App
13	19	3.0	496	6 US-10-131-829A-533	Sequence 533, App
14	19	3.0	496	6 US-10-127-829A-533	Sequence 533, App
15	19	3.0	496	6 US-10-127-831A-533	Sequence 533, App
16	19	3.0	496	6 US-10-127-835A-533	Sequence 533, App
17	19	3.0	496	6 US-10-127-837A-533	Sequence 533, App
18	19	3.0	496	6 US-10-127-842A-533	Sequence 533, App
19	19	3.0	496	6 US-10-127-850A-533	Sequence 533, App
20	19	3.0	496	6 US-10-127-850A-533	Sequence 533, App
21	19	3.0	496	6 US-10-128-889A-533	Sequence 533, App
22	19	3.0	496	6 US-10-128-889A-533	Sequence 533, App
23	19	3.0	496	6 US-10-131-830A-533	Sequence 533, App
24	19	3.0	496	6 US-10-131-833A-533	Sequence 533, App
25	19	3.0	496	6 US-10-131-837A-533	Sequence 533, App
26	19	3.0	496	6 US-10-125-930A-533	Sequence 533, App

ALIGNMENTS

27	19	3.0	496	6 US-10-127-825A-533	Sequence 533, App
28	19	3.0	496	6 US-10-127-838B-533	Sequence 533, App
29	19	3.0	496	6 US-10-127-843A-533	Sequence 533, App
30	19	3.0	496	6 US-10-127-849A-533	Sequence 533, App
31	19	3.0	496	6 US-10-128-664A-533	Sequence 533, App
32	19	3.0	496	6 US-10-128-665A-533	Sequence 533, App
33	19	3.0	496	6 US-10-128-665A-533	Sequence 533, App
34	19	3.0	496	6 US-10-128-666A-533	Sequence 533, App
35	19	3.0	496	6 US-10-128-666A-533	Sequence 533, App
36	19	3.0	496	6 US-10-128-666A-533	Sequence 533, App
37	19	3.0	496	6 US-10-131-821A-533	Sequence 533, App
38	19	3.0	496	6 US-10-131-821A-533	Sequence 533, App
39	19	3.0	496	6 US-10-137-872A-533	Sequence 533, App
40	19	3.0	531	4 US-08-250-795A-19	Sequence 19, Appl
41	19	3.0	692	4 US-10-264-237-662	Sequence 662, App
42	19	3.0	1330	6 US-10-264-237-1069	Sequence 1069, Ap
43	19	3.0	2069	6 US-10-264-237-447	Sequence 447, App
44	19	3.0	3196	6 US-10-264-237-1221	Sequence 1221, Ap
45	19	3.0	15832	6 US-10-240-453-117	Sequence 117, App

RESULT 1
US-10-230-437-15
; Sequence 15, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P35301C94
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 62.9%; Score 393; DB 6; Length 1524;

Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAA 625
DB 1996 TGNAAAAAAAAAAAAAA 2016

RESULT 5

US-09-721-456-3

Sequence 0 Application US/09721456

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721.456

FILING DATE: 22-NOV-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974.549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724.643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844.419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846.017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851.843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854.050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911.312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912.951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915.503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: /note= "clone 712562"

SEQUENCE CHARACTERISTICS:

LENGTH: 2176 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY:

LOCATION: 1..2176

SEQUENCE DESCRIPTION: SEQ ID NO: 3;

US-09-721-456-3

Query Match

Best Local Similarity 3.4%; Score 21; DB 5; Length 2176;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAA 625

DB 2148 TGNAAAAAAAAAAAAAA 2168

RESULT 6

US-10-240-425-208

Sequence 208 Application US/10240425

GENERAL INFORMATION:

APPLICANT: Williams, Amanda

APPLICANT: Boland, Joseph F.

APPLICANT: Lord, Reginald V.

APPLICANT: Alvarez, Chris

APPLICANT: Wetzel, Jon C.

APPLICANT: Scherf, Uwe

APPLICANT: Vockley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

FILE REFERENCE: 44921-5026

CURRENT APPLICATION NUMBER: US/10/240.425

CURRENT FILING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: PCT/US01/09847

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/193.446

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 1588

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 208

LENGTH: 457

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. AA631399

US-10-240-425-208

Query Match

Best Local Similarity 3.2%; Score 20; DB 6; Length 457;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 GAAAAACACAGCATGAGAAC 416

DB 334 GAAAAACACAGCATGAGAAC 353

RESULT 7

US-09-513-999C-21763

Sequence 21763 Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclet, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59 US2 REG

CURRENT APPLICATION NUMBER: US/09/513.999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122.487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 21763

LENGTH: 163

TYPE: DNA

ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 134
; OTHER INFORMATION: w-a or t
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 135
; OTHER INFORMATION: n-a, g, c or t
; US-09-513-999C-21763

Query Match      3.0%; Score 19; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 135 NAAAAAAAAAAAAAAAAAAAA 153

RESULT 8
US-10-131-813A-533
; Sequence 533, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131, 813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-131-813A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 9
US-10-131-819A-533
; Sequence 533, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C134
; CURRENT APPLICATION NUMBER: US/10/131, 819A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-131-819A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
```

Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
 DB 396 NAAAAAAAAAAAAAAAAA 414

RESULT 10

US-10-131-823A-533
 ; Sequence 533, Application US/10131823A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P330R1C143
 ; CURRENT APPLICATION NUMBER: US/10/131,823A
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 533
 ; LENGTH: 496
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 396
 ; OTHER INFORMATION: unknown base
 ; US-10-131-823A-533

Query Match 3.0%; Score 19; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
 DB 396 NAAAAAAAAAAAAAAAAA 414

RESULT 11

US-10-131-824A-533
 ; Sequence 533, Application US/10131824A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P330R1C126
 ; CURRENT APPLICATION NUMBER: US/10/131,824A
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 533
 ; LENGTH: 496
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 396
 ; OTHER INFORMATION: unknown base
 ; US-10-131-824A-533

Query Match 3.0%; Score 19; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625
 DB 396 NAAAAAAAAAAAAAAAAA 414

RESULT 12
 US-10-131-826A-533
 ; Sequence 533, Application US/10131826A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.

```

: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C128
: CURRENT APPLICATION NUMBER: US/10/131,826A
: PRIOR FILING DATE: 1997-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: TYPE: DNA
: LENGTH: 496
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-826A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
      ||||||||||||||||
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 13
: Sequence 533, Application US/10131829A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C128
: CURRENT APPLICATION NUMBER: US/10/131,826A
: PRIOR FILING DATE: 1997-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: TYPE: DNA
: LENGTH: 496
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-829A-533
```

```

: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,829A
: PRIOR FILING DATE: 2002-04-27
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: TYPE: DNA
: LENGTH: 496
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-829A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
      ||||||||||||||||
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 14
: Sequence 533, Application US/10125926A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,829A
: PRIOR FILING DATE: 2002-04-27
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: TYPE: DNA
: LENGTH: 496
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-829A-533
```

```

; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-125-926A-533

Query Match
Best Local Similarity 3.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 15
US-10-127-829A-533
; Sequence 533, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
```

```

; FILE REFERENCE: P3330R1C85
; CURRENT APPLICATION NUMBER: US/10/127,829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-127-829A-533

Query Match
Best Local Similarity 3.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 16
US-10-127-831A-533
; Sequence 533, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C107
; CURRENT APPLICATION NUMBER: US/10/127,831A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
```

```
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-831A-533
```

```
Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414
```

```
RESULT 17
US-10-127-835A-533
```

```
; Sequence 533, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C102
; CURRENT APPLICATION NUMBER: US/10/127, 835A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
```

```
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-835A-533
```

```
Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414
```

```
RESULT 18
US-10-127-837A-533
```

```
; Sequence 533, Application US/10127837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C96
; CURRENT APPLICATION NUMBER: US/10/127, 837A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
```

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-837A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 19
US-10-127-842A-533
; Sequence 533, Application US/10127842A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C100
; CURRENT APPLICATION NUMBER: US/10/127,842A
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-842A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 20
US-10-127-850A-533
; Sequence 533, Application US/10127850A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C110
; CURRENT APPLICATION NUMBER: US/10/127,850A
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
```

```

; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-850A-533

```

Query Match	3.0%	Score 19	DB 6	Length 496
Best Local Similarity	100.0%	Pred. No. 2.7		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	607	NAAAAAAAAAAAAAAAAA	625
Db	396	NAAAAAAAAAAAAAAAAA	414

RESULT 21
US-10-127-901A-533
; sequence 533, Application US/10127901A
; contact information:

```

1 APPLICANT: Baker, Kevin P.
2 APPLICANT: Beresini, Maureen
3 APPLICANT: DeForge, Laura
4 APPLICANT: Desnoyers, Luc
5 APPLICANT: Filvaroff, Ellen
6 APPLICANT: Gao, Mel-Qiang
7 APPLICANT: Gerritsen, Mary E.
8 APPLICANT: Goddard, Audrey
9 APPLICANT: Godowski, Paul J.
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Sherwood, Steven
12 APPLICANT: Smith, Victoria
13 APPLICANT: Stewart, Timothy A.
14 APPLICANT: Tumas, Daniel
15 APPLICANT: Watanabe, Collin K
16 APPLICANT: Wood, William
17 APPLICANT: Zhang, Zhenli
18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
19 TITLE OF INVENTION: ACIDS ENCODING THE SAME
20 FILE REFERENCE: P3330R1C86
21 CURRENT APPLICATION NUMBER: US/10/127,901A
22 CURRENT FILING DATE: 2002-10-15
23 PRIOR APPLICATION NUMBER: 60/049911
24 PRIOR FILING DATE: 1997-06-18
25 PRIOR APPLICATION NUMBER: 60/056974
26 PRIOR FILING DATE: 1997-08-26
27 PRIOR APPLICATION NUMBER: 60/059113
28 PRIOR FILING DATE: 1997-09-17
29 PRIOR APPLICATION NUMBER: 60/059115
30 PRIOR FILING DATE: 1997-09-17
31 PRIOR APPLICATION NUMBER: 60/059117
32 PRIOR FILING DATE: 1997-09-17
33 PRIOR APPLICATION NUMBER: 60/059122
34 PRIOR FILING DATE: 1997-09-17
35 PRIOR APPLICATION NUMBER: 60/059184
36 PRIOR FILING DATE: 1997-09-17
37 PRIOR APPLICATION NUMBER: 60/059263
38 PRIOR FILING DATE: 1997-09-18
39 PRIOR APPLICATION NUMBER: 60/059352
40 PRIOR FILING DATE: 1997-09-19
41 PRIOR APPLICATION NUMBER: 60/059588
42 PRIOR FILING DATE: 1997-09-19
43 Remaining Prior Application data removed - See File Wrapper or PALM.
44 NUMBER OF SEQ ID NOS: 550
45 SEQ ID NO 533
46 LENGTH: 496

```

Query Match 3.0%; Score 19; DB 6; Length 496;

[illegible]

QY	607	NAAAAAAAAAAAAAAAAA	625
Db	396	NAAAAAAAAAAAAAAAAA	414

RESULT 22
US-10-128-689A-533
; Sequence 533, Application US/10128689A
; Patent Information:

```

1 APPLICANT: Baker, Kevin P.
2 APPLICANT: Beresini, Maureen
3 APPLICANT: DeForge, Laura
4 APPLICANT: Desnoyers, Luc
5 APPLICANT: Filvaroff, Ellen
6 APPLICANT: Gao, Wei-Qiang
7 APPLICANT: Gerritsen, Mary E.
8 APPLICANT: Goddard, Audrey
9 APPLICANT: Godowski, Paul J.
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Sherwood, Steven
12 APPLICANT: Smith, Victoria
13 APPLICANT: Stewart, Timothy A.
14 APPLICANT: Tumas, Daniel
15 APPLICANT: Watanabe, Colin K
16 APPLICANT: Wood, William
17 APPLICANT: Zhang, Zemin
18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
19 TITLE OF INVENTION: ACIDS ENCODING THE SAME
20 FILE REFERENCE: P3330R1C117
21 CURRENT APPLICATION NUMBER: US/10/128, 689A
22 CURRENT FILING DATE: 2002-10-15
23 PRIOR APPLICATION NUMBER: 60/049911
24 PRIOR FILING DATE: 1997-06-18
25 PRIOR APPLICATION NUMBER: 60/056974
26 PRIOR FILING DATE: 1997-08-26
27 PRIOR APPLICATION NUMBER: 60/059113
28 PRIOR FILING DATE: 1997-09-17
29 PRIOR APPLICATION NUMBER: 60/059115
30 PRIOR FILING DATE: 1997-09-17
31 PRIOR APPLICATION NUMBER: 60/059117
32 PRIOR FILING DATE: 1997-09-17
33 PRIOR APPLICATION NUMBER: 60/059122
34 PRIOR FILING DATE: 1997-09-17
35 PRIOR APPLICATION NUMBER: 60/059184
36 PRIOR FILING DATE: 1997-09-17
37 PRIOR APPLICATION NUMBER: 60/059263
38 PRIOR FILING DATE: 1997-09-18
39 PRIOR APPLICATION NUMBER: 60/059352
40 PRIOR FILING DATE: 1997-09-19
41 PRIOR APPLICATION NUMBER: 60/059588
42 PRIOR FILING DATE: 1997-09-19
43 Remaining Prior Application data removed - See File Wrapper or PALM.
44 NUMBER OF SEQ ID NOS: 550
45 SEQ ID NO 533
46 LENGTH: 496
47 TYPE: DNA
48 ORGANISM: Homo Sapien
49 FEATURE:
50 NAME/KEY: unsure
51 LOCATION: 396
52 OTHER INFORMATION: unknown base
53
54 US-10-128-689A-533

```

Query Match	3.0%	Score 19:	DB 6:	Length 496:
Best Similarity	100.0%	Pred. No. 2.7:		
Matches 19:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

```
QY      607  NAAAAAAAAAAAAAAAAA  625
        |||||
Db      396  NAAAAAAAAAAAAAAAAA  414
```



```

RESULT 23
US-10-131-830A-533
; Sequence 533, Application US/10131830A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C137
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/059974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 530
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-830A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 24
US-10-131-833A-533
; Sequence 533, Application US/10131833A
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C142
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-833A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 25
US-10-131-837A-533
; Sequence 533, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

```

```

; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey J.
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C131
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Saplen
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-131-837A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 26
US-10-125-930A-533
; Sequence 533, Application US/10125930A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
```

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C78
; CURRENT APPLICATION NUMBER: US/10/125,930A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Saplen
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-125-930A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 27
US-10-127-825A-533
; Sequence 533, Application US/10127825A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3330R1C84
;; CURRENT APPLICATION NUMBER: US/10/127,825A
;; PRIOR FILING DATE: 2002-04-22
;; PRIOR APPLICATION NUMBER: 60/049911
;; PRIOR FILING DATE: 1997-06-18
;; PRIOR APPLICATION NUMBER: 60/056974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059115
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059117
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-825A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 28
US-10-127-838B-533
;; Sequence 533, Application US/10127838B
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: Deforge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3330R1C98
;; CURRENT APPLICATION NUMBER: US/10/127,838B
;; PRIOR FILING DATE: 2002-04-22
;; PRIOR APPLICATION NUMBER: 60/049911
;; PRIOR FILING DATE: 1997-06-18
```

```
;; PRIOR APPLICATION NUMBER: 60/056974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059115
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059117
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-838B-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 29
US-10-127-843A-533
;; Sequence 533, Application US/10127843A
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: Deforge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3330R1C99
;; CURRENT APPLICATION NUMBER: US/10/127,843A
;; PRIOR FILING DATE: 2002-04-22
;; PRIOR APPLICATION NUMBER: 60/049911
;; PRIOR FILING DATE: 1997-06-18
;; PRIOR APPLICATION NUMBER: 60/056974
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059115
;; PRIOR FILING DATE: 1997-09-17
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;; PRIOR APPLICATION NUMBER: 60/059117
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO: 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-843A-533
```

```
Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414
```

```
RESULT 30
US-10-127-849A-533
; Sequence 533, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C103
; CURRENT APPLICATION NUMBER: US/10/127, 849A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
```

```
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO: 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-849A-533
```

```
Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414
```

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RESULT 31
US-10-128-684A-533
; Sequence 533, Application US/10128684A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C118
; CURRENT APPLICATION NUMBER: US/10/128, 684A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
```

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-128-684A-533

Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 32
US-10-128-685A-533
; Sequence 533, Application US/10128685A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C116
; CURRENT APPLICATION NUMBER: US/10/128, 685A
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien

FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-128-685A-533

Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 33
US-10-128-686A-533
; Sequence 533, Application US/10128686A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C119
; CURRENT APPLICATION NUMBER: US/10/128, 686A
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-128-686A-533

	Query Match	3.0%	Score 19;	DB 6;	Length 496;
	Best Local Similarity	100.0%;	Pred. No. 2.7;		
	Matches 19; Conservative	0;	Mismatches	0;	Gaps 0;
Qy	607 NAAAAAAAAAAAAAAAAA	625			
Db	396 NAAAAAAAAAAAAAAAAA	414			

RESULT 34
US-10-128-690A-533

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C122
 CURRENT APPLICATION NUMBER: US/10/128,690A

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/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 533
/ LENGTH: 496
/ TYPE: DNA
/ ORGANISM: Homo Saplen
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: 396
/ OTHER INFORMATION: unknown base
/
/
/ US-10-1-128-690A-533

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	Query Match	3.0%	Score 19:	DB 6:	Length 496:	
	Best Local Similarity	100.0%	Pred. No. 2.7:			
	Matches 19: Conservative	0:	Mismatches	0:	Gaps	0
QY	607	AAAAAAAAAAAAAAAAAAAA	625			

Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 35
US-10-128-693A-533

```

1  sequence 5357, Application: US/10128693A
2  GENERAL INFORMATION:
3  APPLICANT: Baker, Kevin P.
4  APPLICANT: Beresini, Maureen
5  APPLICANT: DeForge, Laura
6  APPLICANT: Desnoyers, Luc
7  APPLICANT: Filvaroff, Ellen
8  APPLICANT: Gao, Wei-Qiang
9  APPLICANT: Gerritsen, Mary E.
10 APPLICANT: Goddard, Audrey
11 APPLICANT: Godowski, Paul J.
12 APPLICANT: Gurney, Austin L.
13 APPLICANT: Sherwood, Steven
14 APPLICANT: Smith, Victoria
15 APPLICANT: Stewart, Timothy A.
16 APPLICANT: Tunas, Daniel
17 APPLICANT: Watanabe, Colin K
18 APPLICANT: Wood, William
19 APPLICANT: Zhang, Zemin
20 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
21 TITLE OF INVENTION: ACIDS ENCODING THE SAME
22 FILE REFERENCE: P333081C120
23 CURRENT APPLICATION NUMBER: US/10/128,693A

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1 PRIOR APPLICATION NUMBER: 60/049911
2 PRIOR FILING DATE: 1997-06-18
3 PRIOR APPLICATION NUMBER: 60/056974
4 PRIOR FILING DATE: 1997-08-26
5 PRIOR APPLICATION NUMBER: 60/059113
6 PRIOR FILING DATE: 1997-09-17
7 PRIOR APPLICATION NUMBER: 60/059115
8 PRIOR FILING DATE: 1997-09-17
9 PRIOR APPLICATION NUMBER: 60/059117
10 PRIOR FILING DATE: 1997-09-17
11 PRIOR APPLICATION NUMBER: 60/059122
12 PRIOR FILING DATE: 1997-09-17
13 PRIOR APPLICATION NUMBER: 60/059184
14 PRIOR FILING DATE: 1997-09-17
15 PRIOR APPLICATION NUMBER: 60/059263
16 PRIOR FILING DATE: 1997-09-18
17 PRIOR APPLICATION NUMBER: 60/059352
18 PRIOR FILING DATE: 1997-09-19
19 PRIOR APPLICATION NUMBER: 60/059588
20 PRIOR FILING DATE: 1997-09-19
21 Remaining prior Application data removed - See file Wrapper or PALM.
22 NUMBER OF SEQ ID NOS: 550
23 SEQ ID NO 533
24
25 LENGTH: 496
26
27 TYPE: DNA
28 ORGANISM: Homo Sapien
29
30 FEATURE:
31 NAME/KEY: unsure
32 LOCATION: 396
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34 OTHER INFORMATION: unknown base
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[illegible]

RESULT 36
US-10-131-821A-533
; Sequence 533, Application US/10131821A


```

; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Matanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C150
; CURRENT APPLICATION NUMBER: US/10/137,872A
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-137-872A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 39
US-10-137-873A-533
; Sequence 533, Application US/10137873A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Mei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

```

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C149
; CURRENT APPLICATION NUMBER: US/10/137,873A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-137-873A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 40
US-08-250-795A-19
; Sequence 19, Application US/08250795A
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Isabel
; TITLE OF INVENTION: Immunosuppressant Target Proteins
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ROPES & GRAY
; STREET: 1 International Place
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,795A
; FILING DATE: 27-May-1994
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709

```



```
REFERENCE/DOCKET NUMBER: APBI-P01-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7000
TELEFAX: (617) 951-7050
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 531 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-250-795A-19
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 4; Length 531;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 492 NAAAAAAAAAAAAAAAAAAAA 510
```

```
RESULT 41
US-10-264-237-662
; Sequence 662, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 662
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (651)..(651)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (684)..(684)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (692)..(692)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-662
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 692;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 651 NAAAAAAAAAAAAAAAAAAAA 669
```

```
RESULT 42
US-10-264-237-1069
; Sequence 1069, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1069
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1265)..(1265)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1069
```

```
Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 1330;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 1265 NAAAAAAAAAAAAAAAAAAAA 1283
```

```
RESULT 43
US-10-264-237-447
; Sequence 447, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 447
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2046)..(2046)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-447
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Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 2069;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 2046 NAAAAAAAAAAAAAAAAAAAA 2064
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```
RESULT 44
US-10-264-237-1221
; Sequence 1221, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
```

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1221
LENGTH: 3196
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (668)..(668)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3170)..(3170)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1221

Query Match 3.0%; Score 19; DB 6; Length 3196;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 3170 NAAAAAAAAAAAAAAAAA 3188

RESULT 45
US-10-240-453-117/c
Sequence 117, Application US/10240453
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 117
LENGTH: 15832
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (791, 2400, 3281, 4994, 5001..5002, 5006, 5012, 5016, 5024)
FEATURE:
NAME/KEY: unsure
LOCATION: (5221, 5244, 6508, 12917, 12968, 12987..12988, 13055)
US-10-240-453-117

Query Match 3.0%; Score 19; DB 6; Length 15832;

Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 791 NAAAAAAAAAAAAAAAAA 773

Search completed: November 8, 2002, 02:02:48
Job time : 48.4612 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 837.445 seconds

(without alignments)
12086.984 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agtctccttcgacagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 10

Total number of hits satisfying chosen parameters: 10588158

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
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12: gb_est3:*
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15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	555	88.8	702	14	B0006545
C 2	546	87.4	678	9	AI9336826
C 3	546	87.4	686	12	BF439382
C 4	537	85.9	537	12	BF594242
C 5	529	84.6	616	9	AI990500
C 6	526	84.2	627	13	BM669397

Result	Score	Query Match	Length	ID	Description
C 7	525	84.0	696	13	BM547680
C 8	516	82.6	649	10	AM590950
C 9	499	79.8	551	12	BE858216
C 10	489	78.2	540	12	BF939693
C 11	471	75.4	530	12	BF726459
C 12	462	73.9	527	10	AM338938
C 13	459	73.4	515	9	AI336858
C 14	442	70.7	690	10	AM149665
C 15	437	69.9	500	10	AM075598
C 16	425	68.0	591	9	AI884686
C 17	425	68.0	676	10	BE385990
C 18	423	67.7	467	9	AI150931
C 19	421	67.4	538	13	BM667957
C 20	415	66.4	537	9	AI018769
C 21	396	63.4	396	9	AA613995
C 22	393	62.9	452	9	AI391683
C 23	390	62.4	396	9	AI499630
C 24	390	62.4	534	10	BE350014
C 25	380	60.8	456	9	AT765236
C 26	369	59.0	381	12	BF054837
C 27	368	58.9	371	12	BF054680
C 28	365	58.4	378	9	AI742092
C 29	347	55.5	432	10	AM087372
C 30	339	54.2	759	12	BF126050
C 31	339	54.2	843	12	BF125134
C 32	338	54.1	387	9	AI272281
C 33	332	53.1	454	10	AM191974
C 34	315	50.4	480	9	AI423162
C 35	314	50.2	337	9	AA665640
C 36	314	50.2	354	9	AA970361
C 37	314	50.2	373	9	AA075710
C 38	314	50.2	412	9	AA084249
C 39	312	49.9	312	12	BF726644
C 40	307	49.1	349	9	AA173739
C 41	307	49.1	408	12	BG057775
C 42	298	47.7	420	9	AI566797
C 43	294	47.0	475	9	AI363261
C 44	282	45.1	888	14	BQ689771
C 45	272	43.5	402	10	AM128849

ALIGNMENTS

RESULT 1
B0006545/c
LOCUS
DEFINITION
IMAGE:5846228 3', mRNA sequence.
ACCESSION
B0006545
VERSION
B0006545.1 GI:19731445
SOURCE
EST.
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Bases 1 to 702)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLA-yes.
FEATURES
Location/Qualifiers
I..702

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846228"
/clone_lib="NCI CGAP E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG_LIB="UI-H-E11"
TAG_TISSUE="Chondrosarcoma"
TAG_SEQ="ACACTTGCAC"
BASE COUNT      137 a      200 c      163 g      202 t
ORIGIN

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Query Match      88.8%; Score 555; DB 14; Length 702;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTTGACAGAGACCTGGGCGGAGCAAGCAAGCGGCGTCCAAAGCG 60
DB 625 AGTTCCTCTTGACAGAGACCTGGGCGGAGCAAGCAAGCGGCGTCCAAAGCG 566
QY 61 GGGCTGTGCTGGTGGAGTGGCCATGTACGCGAGCGCTTCTGCTTGGCGTCTG 120
DB 565 GGGCTGTGCTGGTGGAGTGGCCATGTACGCGAGCGCTTCTGCTTGGCGTCTG 506
QY 121 CAGCGACAGCGGCGACACACACACCTGACGAACACCGCGCAATCTGTCAGAGACAC 180
DB 505 CAGCGACAGCGGCGACACACACCTGACGAACACCGCGCAATCTGTCAGAGACAC 446
QY 181 CGGTACAGAGAGGGGTGTGTACCGAGCTGAGGTAGAAACGTCCTCCGAGAAAGGAG 240
DB 445 CGGTACAGAGAGGGGTGTGTACCGAGCTGAGGTAGAAACGTCCTCCGAGAAAGGAG 386
QY 241 GAGGATCATGTACGCCCGGAGTAGACCTGTCACAGTCTGCTTGGGTTGGCGCAGC 300
DB 385 GAGGATCATGTACGCCCGGAGTAGACCTGTCACAGTCTGCTTGGGTTGGCGCAGC 326
QY 301 CATGATCTCTCCGATCTGCTTGGGATCCAGCATACGCCCAATGTCAACAAATCAGCC 360
DB 325 CATGATCTCTCCGATCTGCTTGGGATCCAGCATACGCCCAATGTCAACAAATCAGCC 266
QY 361 TGGGACAGACAGAGAGAGAGAGAGAGAAAGAAACACACATGAGAAACAG 420
DB 265 TGGGACAGACAGAGAGAGAGAGAGAGAGAAAGAAACACACATGAGAAACAG 206
QY 421 TAAATGAATAAATTAATATTTAGCCCTCTGCTTGTGCTTACTGCGCAGAAAT 480
DB 205 TAAATGAATAAATTAATATTTAGCCCTCTGCTTGTGCTTACTGCGCAGAAAT 146
QY 481 GGTACCAATTTTTCAGTGTGGAGTGTACAGACTTTTGGCAACAGAGAGAAATTT 540
DB 145 GGTACCAATTTTTCAGTGTGGAGTGTACAGACTTTTGGCAACAGAGAGAAATTT 86
QY 541 AACACTGTTTCAACACCGGGGAGTGTGGCTGTGTTAAAGAAAGACCAATTAATCTTTAG 600
DB 85 AACACTGTTTCAACACCGGGGAGTGTGGCTGTGTTAAAGAAAGACCAATTAATCTTTAG 26
QY 601 ACAAGT 606
|||||

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DB 25 ACAAGT 20

RESULT 2
AI936826/c
LOCUS
DEFINITION
AI936826 678 bp mRNA linear EST 08-MAR-2000
wp69h10.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467075 3'
similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39. ; mRNA SEQUENCE.

ACCESSION
AI936826
VERSION
AI936826.1 GI:5675696
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 678)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke. Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 1143 Std Error: 0.00
Seq. primer: -400P from Gibco

High quality sequence stop: 454.
Location/Qualifiers
1. 678
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2467075"
/clone_lib="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTCACCAATCTGAAGTGGAGCGCGCATACGATTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

FEATURES
source

BASE COUNT 133 a 199 c 161 g 182 t 3 others
ORIGIN

```

Query Match      87.4%; Score 546; DB 9; Length 678;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 10 TGCAGAGACTGGCGCGGAGCGGAAGACACAGCGGCGCTGTC 69
DB 597 TGCAGAGACTGGCGCGGAGCGGAAGACACAGCGGCGCTGTC 538
QY 70 GGTGGTGGAGTGGCGCATGTACGCGAGCGCTTCTGCTTGGCGTCTCAGCAGAC 129
DB 537 GGTGGTGGAGTGGCGCATGTACGCGAGCGCTTCTGCTTGGCGTCTCAGCAGAC 478
QY 130 GCGCAGACAGACACTGACAGAACACCGCGCAAACTGTGCGAGACACCGTGTACAG 189
DB 477 GCGCAGACAGACACTGACAGAACACCGCGCAAACTGTGCGAGACACCGTGTACAG 418
QY 190 GAGCGGGTGTATGACCGAGTGTAGAGTGTGCAAGAAAGGAGAGAGATCAT 249

```


Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1M12722 row: h column: 07
 High quality sequence stop: 641.
 Location/Qualifiers

FEATURES

source

1. 696

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5727798"

/clone_lib="NIH_MGC_124"

/tissue_type="hippocampus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-Sport6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

BASE COUNT 188 a 160 c 197 g 134 t 17 others
 ORIGIN

Query Match 84.0%; Score 525; DB 13; Length 696;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTCAAGAGAGCTGGCGGACCGAAGACAGCGGCGCTGCACAAACG 60
 |||||||

DB 65 AGTTCCTCTTCAAGAGAGCTGGCGGACCGAAGACAGCGGCGCTGCACAAACG 124
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QY 61 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 |||||||

DB 125 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 184
 |||||||

QY 121 CAGGACAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
 |||||||

DB 185 CAGGACAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 244
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QY 181 CGTGTACAGGAGCGGTTGATGACCGAGCTGAGTGAAGAAACGTTCTCCGAGAGGAG 240
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DB 245 CGTGTACAGGAGCGGTTGATGACCGAGCTGAGTGAAGAAACGTTCTCCGAGAGGAG 304
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QY 241 GAGGATCATGACGCGCGAAGTAGACCTGCTCAGTCGTCGTTGGGTTGGCCGACG 300
 |||||||

DB 305 GAGGATCATGACGCGCGAAGTAGACCTGCTCAGTCGTCGTTGGGTTGGCCGACG 364
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QY 301 CATGATCTCCGAATCTGTTGGGCATCAGCATACGGCCAAATGTACAAACATCAGCC 360
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DB 365 CATGATCTCCGAATCTGTTGGGCATCAGCATACGGCCAAATGTACAAACATCAGCC 424
 |||||||

QY 361 TGGGACAGCAG 420
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DB 425 TGGGACAGCAG 484
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QY 421 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
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DB 485 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 544
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QY 481 GGTACCAATTTTTCAGTGTGAGCTTGAACGCTCTTTTGCACAAAGAGAGATTT 540
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DB 545 GGTACCAATTTTTCAGTGTGAGCTTGAACGCTCTTTTGCACAAAGAGAGATTT 604
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QY 541 AACACTGTTTCAACCCGGGGAGTTGGCTGTGTTA 576
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DB 605 AACACTGTTTCAACCCGGGGAGTTGGCTGTGTTA 640
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RESULT 8

AM590950/c
 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AM590950 649 bp mRNA linear EST 22-MAR-2000
 hg51e12.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2949166 3'

similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39.; mRNA sequence.

AM590950
 AM590950.1 GI:7278094

EST.
 human.

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

image.lnl.gov/image/html/lrsources.shtml

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from GIBCO

High quality sequence stop: 457.

FEATURES

source

1. 649

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2949166"

/clone_lib="NCI CGAP GC6"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
 from the normalized library NCI-CGAP.GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 1257096-1258631, 1469064-1470983, and 1475392-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 132 a 189 c 155 g 173 t
 ORIGIN

Query Match 82.6%; Score 516; DB 10; Length 649;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 566; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 CAAGGGGGCTGCACAAAGCGGGCGCTGCGGTGGAGAGTCCGATGACGACGCG 99
 |||||||

DB 568 CAAGGGGGCTGCACAAAGCGGGCGCTGCGGTGGAGAGTCCGATGACGACGCG 509
 |||||||

QY 100 CTTCTCGTGGTGGCGGTGCTGCAGCAGCGCGGACGACACACCTGACGACACCG 159
 |||||||

DB 508 CTTCTCGTGGTGGCGGTGCTGCAGCAGCGCGGACGACACACCTGACGACACCG 449
 |||||||

QY 160 CCGAAACTGCTCGAGAGACACCGTGTACAGAGCGGTTGATGACGAGCTAGGTAGA 219
 |||||||

DB 448 CCGAAACTGCTCGAGAGACACCGTGTACAGAGCGGTTGATGACGAGCTAGGTAGA 389
 |||||||

QY 220 AAAGCTTCGGAAGAGGGAGAGAGTATGATGACGCGGAGTGAAGACTGTCAGTGC 279
 |||||||

DB 388 AAAGCTTCGGAAGAGGGAGAGAGTATGATGACGCGGAGTGAAGACTGTCAGTGC 329
 |||||||

Qy	280	GTGCTTGGGTTTGGCCGAGCCATATCTCGAATTCGTGGTGGCATTCACACATACGC	339
Db	328	GTGCTTGGGTTTGGCCGAGCCATATCTCTCGAATTCGTGGTGGCATTCACACATACGC	269
Qy	340	CAATGTCAACCAATCAACCCCTGGCCAGACACAGCAGAGGAGAGACACAGAAAGA	399
Db	268	CAATGTCAACCAATCAACCCCTGGCCAGACACAGCAGAGGAGAGACACAGAAAGA	209
Qy	400	AAACACACATGAGAACACAGTAATGATATAAACCATATAATATTAGCCCTGTGTC	459
Db	208	AAACACACATGAGAACACAGTAATATAATAAACCATATAATATTAGCCCTGTGTC	149
Qy	460	TGTGCTTACTGGCCAGGAAATGTATCCAAATTTTGTAGTTTGGACTTTGACAGCTCTTT	519
Db	148	TGTGCTTACTGGCCAGGAAATGTATCCAAATTTTGTAGTTTGGACTTTGACAGCTCTTT	89
Qy	520	GCCACACAGCAGAGAGAAATTTAACACTGTTCACAAACCCGGGGAGTTGGCTGTAAAG	579
Db	88	GCCACACAGCAGAGAGAAATTTAACACTGTTCACAAACCCGGGGAGTTGGCTGTAAAG	29
Qy	580	AAAGACCAATTAATGCTTTAGACAGTG	606
Db	28	AAAGACCAATTAATGCTTTAGACAGTG	2

LOCUS	DEFINITION	551 bp	mRNA	linear	EST 29-SEP-2000
BE858216/c	BE858216	7919g07.x1	NCI_CGAP_Br123 Homo sapiens CDNA clone IMAGE:3306972 3'		

ACCESSION	BE858216
VERSION	BE858216.1
KEYWORDS	EST
	GT:10372861

ORGANISM	Homo sapiens
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2	2
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4	4
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99	99
100	100

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 551)
NCI/NINDS-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological

JOURNAL Unpublished (1998)

COMMENTS
Contact: Robert Sclausberg, Ph.D.
Email: rgsclaus@femaill.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

FEATURES

Location/Qualifiers

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3306972"
/clone_id="NCI_CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: p773D-Pec (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCCAATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.

```

Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldó."			
BASE COUNT	110 a	161 c	128 g
ORIGIN			152 t

Query Match:	79.8%	Score 499;	DB 12;	Length 551;
Best Local Similarity:	99.8%	Pred. No. 0;		
Matches 549;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	57	AGCGGCGCCTGTCGGTGTGGAGTGCAGATGACGCGCAGCGCTTCCTGCGTGGCGGT	116
Db	551	AGCGGCGCCTGTCGGTGTGGAGTGCAGATGACGCGCAGCGCTTCCTGCGTGGCGGT	492
OY	117	GCTGCAGCGACAGCGCGCAGCACAGCACCTGCAGCAACCCGCCGAAACTGCTCGAGG	176
Db	491	GCTGCAGCGACAGCGCGCGACACACACCTGCAGCAACCCGCCGAAACTGCTCGAGG	432
OY	177	ACACCGTGTACAGGAGCGGGGTGGATGACCGAGCTGAGTAAAGAAACGTCCTCCGAGAGG	236
Db	431	ACACCGTGTACAGGAGCGGGGTGGATGACCGAGCTGAGTAAAGAAACGTCCTCCGAGAGG	372
OY	237	GGAGAGGAGCATGATGACGCCCGGAAGTAGAGACTGTCAGTCGTCCTTGGGTTGGCCG	296
Db	371	GGAGAGGAGCATGATGACGCCCGGAAGTAGAGACTGTCAGTCGTCCTTGGGTTGGCCG	312
OY	297	CAGCCATGATCCCTCCGAATCTGCTGGTGGGCATCCAGCATACGGCCCAATGTACACAACTCA	356
Db	311	CAGCCATGATCCCTCCGAATCTGCTGGTGGGCATCCAGCATACGGCCCAATGTACACAACTCA	252
OY	357	GCCCTGGGCGACACACGACGAGGAGGAGACAGAGAAAAGAAAACACAGCATAGAAC	416
Db	251	GCCCTGGGCGACACACGACGAGGAGGAGACAGAGAAAAGAAAACACAGCATAGAAC	192
OY	417	ACAGTAATTAATTAACCAATTAATTAATTTTACGCCCTGCTGCTGGCTTACTGGCCAGG	476
Db	191	ACAGTAATTAATTAACCAATTAATTAATTTTACGCCCTGCTGCTGGCTTACTGGCCAGG	132
OY	477	AAATGTAACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCACAGCAGAGAGA	536
Db	131	AAATGTAACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCACAGCAGAGAGA	72
OY	537	ATTTAACACTGTTTAAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCT	596
Db	71	ATTTAACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCT	12
OY	597	TTAGACAGTG 606	
Db	11	TTAGACAGTG 2	

LOCUS	BF939693	540	mrna	linear	EST 22-JAN-2001
DEFINITION	nc800d12.x1 NCI-GAP_Brn23 Homo sapiens CDNA clone IMAGE:3440591 3'				

GPR39. ; mRNA sequence.

VERBOS	EST.
KEYWORDS	human.
SOURCE	human.
ORGANISM	human.

ORGANISM HOMO sapiens
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 540)		
NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .	
National Cancer Institute		National Institute of Neurological

JOURNAL COMMENT
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph. D.

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

gpr39.1, mRNA sequence.
ACCESSION AM075598
VERSION AM075598.1 GI:6030596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 500)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html

FEATURES
source
1..500
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2577252"
/clone_1lb="NCI CGAP Kid13"
/tissue_type="NCI pooled Wilms' tumors, one primary and one
metastatic to brain"
/lab_host="DH10B"
/note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

BASE COUNT
99 a 139 c 114 g 148 t

ORIGIN
Query Match 69.9%; Score 437; DB 10; Length 500;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 119 TGCAGCGACAGGGGGGCGACGACGACCTGCGAGAACCCCGCAACTGCTGCGAGGAC 178
|||||
DB 490 TGCAGCGACAGGGGGGCGACGACGACCTGCGAGAACCCCGCAACTGCTGCGAGGAC 431
|||||
OY 179 ACCGTGTACAGAGCGGGGTTGATGACGAGCTGAGGTGAGAAACGTCCTCGAGAAAGGG 238
|||||
DB 430 ACCGTGTACAGAGCGGGGTTGATGACGAGCTGAGGTGAGAAACGTCCTCGAGAAAGGG 371
|||||
OY 239 AGGAGATCATGTACGGCCGGAAGTAGACCTGCTCCAGTGTGCTGGTTGGCCGCA 298
|||||
DB 370 AGGAGATCATGTACGGCCGGAAGTAGACCTGCTCCAGTGTGCTGGTTGGCCGCA 311
|||||
OY 299 GCATGATCTCTCGCAATCTGTTGGGATCCAGCATACGGCAATGTCAACAATCAGC 358
|||||
DB 310 GCATGATCTCTCGCAATCTGTTGGGATCCAGCATACGGCAATGTCAACAATCAGC 251
|||||
OY 359 CCGTGGGACAG 418
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DB 250 CCGTGGGACAG 191
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OY 419 AGTAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAA 478
|||||
DB 190 AGTAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAA 131
|||||
OY 479 ATGTGATCAATTTTTCAGTGTGAGCTTGAGAGCTTCTTTGGCCACAGCAAGAAGAA 538
|||||
DB 130 ATGTGATCAATTTTTCAGTGTGAGCTTGAGAGCTTCTTTGGCCACAGCAAGAAGAA 71
|||||

OY 539 TTAACACTGTTTCAACCCGGGAGCTGGCTGTGTTAAAGAAAGACATTAAATGCTT 598
|||||
DB 70 TTAACACTGTTTCAACCCGGGAGCTGGCTGTGTTAAAGAAAGACATTAAATGCTT 11
|||||
OY 599 AGACAGTG 606
|||||
DB 10 AGACAGTG 3
|||||

RESULT 16
AI884686 591 bp mRNA linear EST 07-MAR-2000
LOCUS w183d07.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2431501 3'
DEFINITION similar to SW:GPR3_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.1, mRNA sequence.
ACCESSION AI884686
VERSION AI884686
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 591)
AUTHORS NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html
Insert Length: 1462 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers
1..591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2431501"
/clone_1lb="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTATCAATCTGAGCTGGGAGCGCGCATACGATGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT
109 a 179 c 147 g 155 t 1 others

ORIGIN
Query Match 68.0%; Score 425; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGTTTCCTTCAGAGACTGGCGCGGAGCGCAAGAGCAAGCGGCGTCACAAACG 60
|||||
DB 447 AGTTTCCTTCAGAGACTGGCGCGGAGCGCAAGAGCAAGCGGCGCTCACAAACG 388
|||||
OY 61 GGGCTGTGCGTGGTGGAGTGGCGCATGACGCGGCGCTTCTGTTGGGTGGCTGCT 120
|||||


```

Db      131 AGTGTGGACCTTGACAGCTTTTCCACAGCAAGACAGATTTACACTGTTTCAA 72
QY      555 CCGGGGGAGTTGGCTGTGTGTTAAGAGACCATTAATGCTTTAGACAGTG 606
      71 CCGGGGGAGTTGGCTGTGTGTTAAGAGACCATTAATGCTTTAGACAGTG 20

RESULT 20
LOCUS   A1018769/c 537 bp mRNA linear EST 27-AUG-1998
DEFINITION ov32e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639038
            3' similar to SW:NTFR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;
            mRNA sequence.
ACCESSION A1018769
VERSION   A1018769.1 GI:3232567
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 537)
            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL  Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgapbs-remail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1394 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 452.
            Location/Qualifiers
FEATURES
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                        /db_xref="taxon:9606"
                        /clone_image="1639038"
                        /clone_lib="Soares_testis_NHT"
                        /sex="male"
                        /lab_host="DH10B"
                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                        polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                        was prepared from mRNA obtained from Clontech Laboratories
                        , Inc., and primed with a Not I - oligo(dT) primer [5'
                        TGTTCACATCTGAGAGGAGGAGCGCGCCCAATTTTTTTTTTTT 3'].
                        Double-stranded cDNA was ligated to Eco RI adaptors
                        (Pharmacia), digested with Not I and cloned into the Not I
                        and Eco RI sites of the modified pT7T3 vector. Library
                        went through one round of normalization to Col5, and was
                        constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT  105 a 147 c 126 g 159 t
ORIGIN
Query Match      66.4%; Score 415; DB 9; Length 537;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      84 CATTGTACGGGAGGGGCTTCTGTTGGTGGCTGCAGCGACAGGGGCGACACAGCA 143
      537 CATTGTACGGGAGGGGCTTCTGTTGGTGGCTGCAGCGACAGGGGCGACACAGCA 478
Db      144 CCGTGCAGCAACCCCGCCAAACTGCTGCAGAGACACCGTGTACAGAGCGGGTGTATGA 203
      477 CCGTGCAGCAACCCCGCCAAACTGCTGCAGAGACACCGTGTACAGAGCGGGTGTATGA 418
QY      204 CCGAGCTGAGGTGAAAAAGCTCCGAGAGAGGAGAGAGATCATGTACCGCCGGAAGT 263
      417 CCGAGCTGAGGTGAAAAAGCTCCGAGAGAGGAGAGAGATCATGTACCGCCGGAAGT 358

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QY      264 AGGACCTCGTCCAGTGTGCTTGGGTTTGGCCGACACCCAGCAGTCCGAAATCGGTGG 323
      357 AGGACCTCGTCCAGTGTGCTTGGGTTTGGCCGACACCCAGCAGTCCGAAATCGGTGG 298
Db      324 GCATCCAGCATACGGCCCAATGTGCACAACATCAGCCCTGGGCGACAGCAGAGAGGGA 383
      297 GCATCCAGCATACGGCCCAATGTGCACAACATCAGCCCTGGGCGACAGCAGAGAGGGA 228
QY      384 GAGACAGAGAAAAAGAAAAACACAGCATGAGACACAGTAATGATTAATTAATTAATTA 443
      237 GAGACAGAGAAAAAGAAAAACCCAGCATGAGAACCCGTAATGTAATTAATTAATTAATTA 178
Db      444 TTTAGCCCTCTGTCTGTGCTTACTGAGCCAGGAATGTACCAATTTTTCAGTGTGGA 503
      177 TTTAGCCCTCTGTCTGTGCTTACTGAGCCAGGAATGTACCAATTTTTCAGTGTGGA 118
QY      504 CTTGACAGCTTTCTTTTGGCCACAAGAGAGATTTAACACTGTTCAAAACCCGGGGGA 563
      117 CTTGACAGCTTTCTTTTGGCCACAAGAGAGATTTAACACTGTTCAAAACCCGGGGGA 58
QY      564 GTTGGCTGTGTTAAGAGAGACCATTAATGCTTTAG 600
      57 GTTGGCTGTGTTAAGAGAGACCATTAATGCTTTAG 21

RESULT 21
A613995/c 396 bp mRNA linear EST 06-OCT-1997
DEFINITION no86c08.s1 NCI-CCAP A61 Homo sapiens cDNA clone IMAGE:113710 3'
            similar to SW:NTFR1_RAT P20789 NEUROTENSIN RECEPTOR ; mRNA sequence.
ACCESSION A613995
VERSION   A613995.1 GI:2466129
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396)
            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL  Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgapbs-remail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Stratagene, Inc., David B. Kitzman,
            Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 399.
            Location/Qualifiers
FEATURES
    source             1..396
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone_image="113710"
                        /clone_lib="NCI-CCAP_A61"
                        /tissue_type="adrenal adenoma"
                        /lab_host="SOLR (kanamycin resistant)"
                        /note="Organ: adrenal gland; Vector: Bluescript SK-;
                        Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
                        Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'
                        adaptor sequence: 5' GAATTCGACAGAG 3' 3' adaptor
                        sequence: 1.6 kb"
BASE COUNT  56 a 135 c 103 g 102 t
ORIGIN

```


cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbp/image/image.html
 Insert Length: 826 Std Error: 0.00
 Seg primer: -40up from Gibco
 High quality sequence stop: 395
 POLA-No.

FEATURES

Location/Qualifiers
 1..396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2177941"
 /clone_lib="NCI-CGAP_Ut2"
 /tissue_type="moderately-differentiated endometrial
 adenocarcinoma, 3 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
 Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.85 kb. Life Technologies catalog #:
 11339-012"
 BASE COUNT 62 a 124 c 96 g 114 t
 ORIGIN

Query Match 62.4%; Score 390; DB 9; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

58 GCGGGCGTGTGCTGTGAGTGCATGTACGCCAGCGCTTCTGTGTGCGTG 117
   |||||||
396 GCGGGCGTGTGCTGTGAGTGCATGTACGCCAGCGCTTCTGTGTGCGTG 337
   |||||||
118 CTGACGACGAGCGGCGACACGACCTGACGAAACACCGCGAACTGCTCCAGGA 177
   |||||||
336 CTGACGACGAGCGGCGACACGACCTGACGAAACACCGCGAACTGCTCCAGGA 277
   |||||||
178 CACCGGTACAGAGGCGGCTGTATGACGAGCTGAGTAAAGAGTCTCGAGAAGG 237
   |||||||
276 CACCGGTACAGAGGCGGCTGTATGACGAGCTGAGTAAAGAGTCTCGAGAAGG 217
   |||||||
238 GAGGAGGATCATGTATGACCCCGGAAGTAGACCTGTCACATGCTGTGGGTTGGCCGC 237
   |||||||
216 GAGGAGGATCATGTATGACCCCGGAAGTAGACCTGTCACATGCTGTGGGTTGGCCGC 157
   |||||||
298 AGCCATGATCCTCGAATCGTGTGGGCAATCCAGATAGCGCCAAATGTCAACAATCAG 357
   |||||||
156 AGCCATGATCCTCGAATCGTGTGGGCAATCCAGATAGCGCCAAATGTCAACAATCAG 97
   |||||||
358 CCCTGGGACAGACAGAGAGGAGAGACAGAGAAAACACAGCATGAGAAC 417
   |||||||
96 CCCTGGGACAGACAGAGAGGAGAGACAGAGAAAACACAGCATGAGAAC 37
   |||||||
418 CAGTAAATGAATAAACCATTAATTTTA 447
   |||||||
36 CAGTAAATGAATAAACCATTAATTTTA 7

```

RESULT 24
 BE350014/c 534 bp mRNA linear EST 18-JUL-2000
 LOCUS
 DEFINITION
 ht07g12.x1 NCI-CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146086 3'
 similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39. ; mRNA sequence.

ACCESSION BE350014
 VERSION BE350014
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 534)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE
 JOURNAL
 COMMENT
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue procurement: Chris Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seg primer: -40up from Gibco
 High quality sequence stop: 408.

FEATURES

Location/Qualifiers
 1..534
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3146086"
 /clone_lib="NCI-CGAP_Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one
 metastatic to brain"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Salt;
 Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies."
 BASE COUNT 98 a 172 c 143 g 121 t
 ORIGIN

Query Match 62.4%; Score 390; DB 10; Length 534;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 AGTTTCCTTTCAGAGAGACTGGCGCGCGGACCGGAAGAGCAAGCGCTGCACAAACG 60
   |||||||
390 AGTTTCCTTTCAGAGAGACTGGCGCGCGGACCGGAAGAGCAAGCGCTGCACAAACG 331
   |||||||
61 GCGGCTGTGCTGTGAGTGCATGTACGCCAGCGCTTCTGTGTGCGTGCTG 120
   |||||||
330 GCGGCTGTGCTGTGAGTGCATGTACGCCAGCGCTTCTGTGTGCGTGCTG 271
   |||||||
121 CAGCGACAGCGCGGACAGACGACCTGACGAAACACCGCGAACTGCTGCGAGAGCAC 180
   |||||||
270 CAGCGACAGCGCGGACAGACGACCTGACGAAACACCGCGAACTGCTGCGAGAGCAC 211
   |||||||
181 CGTGTACAGAGGCGGCTGTATGACCGAGCTGAGTAAAGAGTCTCCGAGAAGGGAG 240
   |||||||
210 CGTGTACAGAGGCGGCTGTATGACCGAGCTGAGTAAAGAGTCTCCGAGAAGGGAG 151
   |||||||
241 GAGGATCATGTATGACCCCGGAAGTAGACCTGTCACATGCTGTGGGTTGGCCGAGC 300
   |||||||
150 GAGGATCATGTATGACCCCGGAAGTAGACCTGTCACATGCTGTGGGTTGGCCGAGC 91
   |||||||
301 CATGATCCTCCGAATCGTGTGGGCAATCCAGATAGCGCCAAATGTCAACAATCAGCCC 360
   |||||||
90 CATGATCCTCCGAATCGTGTGGGCAATCCAGATAGCGCCAAATGTCAACAATCAGCCC 31
   |||||||
361 TGGGACAGACAGAGAGGAGAGAGAC 390
   |||||||
30 TGGGACAGACAGAGAGGAGAGAGAC 1

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RESULT 25
 A1765236/c 456 bp mRNA linear EST 21-DEC-1999
 LOCUS
 DEFINITION
 w172h08.x1 NCI-CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398911 3'
 similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39. ; mRNA sequence.

ACCESSION A1765236
 VERSION A1765236
 KEYWORDS
 SOURCE human

REFERENCE	ORGANISM	60.8%	Score 380;	DB 9;	Length 456;
1 (bases 1 to 456)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCI-GAP	http://www.ncbi.nlm.nih.gov/ncigap.				
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
Unpublished (1997)					
Contact: Robert Strausberg, Ph.D.					
Email: cgapb-remail.nih.gov					
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.					
CDNA Library Preparation: M. Bento Soares, Ph.D.					
CDNA Library Arrayed by: Greg Lennon, Ph.D.					
DNA Sequencing by: Washington University Genome Sequencing Center					
Clone Distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMUT at: www-bio.illn.gov/bbrp/Image/Image.html					
Insert Length: 961					
Seq Primer: -40UP from Glbco					
High quality sequence stop: 453.					
Location/Qualifiers					
1. 456					
/organism="Homo sapiens"					
/db_xref="taxon:9606"					
/clone IMAGE:2398911"					
/clone_1db="NCI-GAP_Kid12"					
/tissue_type="2 pooled tumors (clear cell type)"					
/lab_host="DH10B"					
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-GAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 132912-1325831, 1471366-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."					
BASE COUNT	93 a 122 c 99 g 142 t				
ORIGIN					
Query Match	60.8%; Score 380; DB 9; Length 456;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 430; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
157	CCGCCGAACGCTCGAGGACACCGCTGACGAGCGGTTGATCAGCCAGCTAGGTA 216				
456	CCGCGGAACGCTGCTCGAGGACACCGCTGACGAGCGGTTGATCAGCCAGCTAGGTA 397				
217	GAAGAACGCTCTCCGAGAGGGAGGAGGATCATGTACGCCGAGTGAAGACTGTGCA 276				
396	GAAGAACGCTCTCCGAGAGGGAGGAGGATCATGTACGCCGAGTGAAGACTGTGCA 337				
277	GTCGTGCTTGGGTTGGCCGACCCATGATCCTCGAATCTGGTTGGCATCCAGCATAC 336				
336	GTCGTGCTTGGGTTGGCCGACCCATGATCCTCGAATCTGGTTGGCATCCAGCATAC 277				
337	GGCCAAATGTCACAAATCAGCCCTGGGCGACACAGCAGAGGAGGAGACAGAGAAA 396				
216	GGCCAAATGTCACAAATCAGCCCTGGGCGACACAGCAGAGGAGGAGACAGAGAAA 217				
397	GAAGAACGCTCTCCGAGAGGGAGGAGGATCATGTACGCCGAGTGAAGACTGTGCA 456				
456	GAAGAACGCTCTCCGAGAGGGAGGAGGATCATGTACGCCGAGTGAAGACTGTGCA 157				
156	TTCGTGCTTACTGCGCAGGAATGTCACAAATTTTCAGTGTGACCTGACACTTCT 97				
517	TTTGCCACAGCAGAGAGAAATTTTAACACTGTTTAAACCCGGGGAGTGGCTGTGTA 576				
96	TTTGCCACAGCAGAGAGAAATTTTAACACTGTTTAAACCCGGGGAGTGGCTGTGTA 37				

OY		577	AAGAAACCA 587 	
Dd		36	AAGAAGACA 26	
RESULT 26		BFO54837	381 bp mRNA linear EST 16-OCT-2000	
LOCUS		BFO54837	7411h01.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340177.5'	
DEFINITION			similar to SW:G939_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR	
ACCESSION		GPR39., / mRNA sequence.		
VERSION		BFO54837		
KEYWORDS		BFO54837.1 GI:10808733		
SOURCE		EST.		
ORGANISM		human.		
REFERENCE		Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		1 (bases 1 to 381) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL		National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project		
COMMENT		(CGAP/BTCAP), Tumor Gene Index Unpublished (1998)		
		Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim Jacobson, Ph.D.		
		CNA Library Preparation: David B. Krizman, Ph.D. CNA library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN, send email to: info@image.llnl.gov Putative full length read The vector to vector length is 382 Seq primer: -40R from Glbpco.		
FEATURES		Location/Qualifiers		
source		1..381		
		/organism="Homo saplens"		
		/db_xref="taxon:9606"		
		/clone="IMAGE:3340177"		
		/clone_lib="NCI CGAP Brn20"		
		/tissue_type="Oligodendrogloma"		
		/dex_stage="adult"		
		/lab_host="DH10B"		
		/note-"Organ: brain; Vector: PAMPI; mRNA made from oligodendroglioma tissue, CDNA made by oligo-dr priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."		
BASE COUNT		123 a 81 c 94 g 83 t		
ORIGIN				
Query Match		59.0%; Score 369; DB 12; Length 381; Best Local Similarity 100.0%; Pred. No. 0;		
Matches 369:		Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	237	GGAGAGCATGTATGCACC GGGAATGAGACTTGTCACACTGCTGTGGTTGGCCG	296	
Dd	1	GGAGAGCATGTATGCACC CCGAAGTAGGACCTCGTCCATCGTGTGGATTGGCG	60	
OY	297	CAGCATATCTCTCGAATCGTGGTGGCACCCAGCAATGCCCAATGTCACAACAATCA	356	
Dd	61	CAGCATATCTCTCGAATCTGGTTGGCATCCAGCATATGCCCAATGTCACAACAATCA	120	
OY	357	GCCCTGGGCACACAGACAGAGGAGAGACAGAAAATAAAAAACACACATGAGAAC	416	
Dd	121	GCCCTGGGCACACAGACAGAGGAGAGACAGAAAATAAAAAACACACATGAGAAC	180	
OY	417	ACATTAATGATATAAACCATAAATATTATTAGCCCCCTGTCTGTGCTTACTGCGCAGG	476	

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Db 181 ACAGTAATGAAATAACCATAAATATTAGCCCTCGTCTGTGCTTACTGCGCAGC 240
Oy 477 AATGATACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACACAGACAGAGA 536
Db 241 AATGATACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACACAGACAGAGA 300
Oy 537 AATTAACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCT 596
Db 301 AATTAACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCT 360
Oy 597 TTAGACAGT 605
Db 361 TTAGACAGT 369

RESULT 27
BF054680 371 bp mRNA linear EST 16-OCT-2000
LOCUS 7169f08.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:333975 5'
DEFINITION similar to SW:GPR39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.;, mRNA sequence.
ACCESSION BF054680
VERSION BF054680.1 GI:10808576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 371)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Other ESTs: 7169f08.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
cDNA Library Preparation: David B. Kriman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40R from Gibco
High quality sequence stop: 361.
FEATURES
Source Location/Qualifiers
1..371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="333975"
/clone_lib="NCI_CGAP_Brn20"
/tissue_type="Oligodendrogloma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: brain; Vector: PAMPI; mRNA made from
oligodendrogloma tissue; cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 114 a 81 c 93 g 83 t
ORIGIN
Query Match 58.9%; Score 368; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 238 GAGGAGATCATGTACGCCGAGTAGACCTGCTGCTGCTGGTTGGCCGC 297
Db 1 GAGGAGATCATGTACGCCGAGTAGACCTGCTGCTGCTGGTTGGCCGC 60

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Oy 298 ACCCATGATCTCCGATGCTGGTGGCATCCAGCATAGCCCAATGTCAACAATCAG 357
Db 61 ACCCATGATCTCCGATGCTGGTGGCATCCAGCATAGCCCAATGTCAACAATCAG 120
Oy 358 CCGTGGGACAGACGACGAGAGGAGAGACAGAGAAAAAACAACATGAGACAGA 417
Db 121 CCGTGGGACAGACGACGAGAGGAGAGAGAGAAAAAACAACATGAGACAGA 180
Oy 418 CAGTAATTAATAAACCATAAATATTAGCCCTCGTCTGTGCTTACTGCGCAGGA 477
Db 181 CAGTAATTAATAAACCATAAATATTAGCCCTCGTCTGTGCTTACTGCGCAGGA 240
Oy 478 AATGATACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACACAGACAGAGA 537
Db 241 AATGATACCAATTTTTCAGTGTGACCTTGACAGCTTTTTCACACAGACAGAGA 300
Oy 538 TTTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 597
Db 301 TTTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 360
Oy 598 TTAGACAGT 605
Db 361 TTAGACAGT 368

RESULT 28
A1742092/c 578 bp mRNA linear EST 19-DEC-1999
LOCUS A1742092/c
DEFINITION wg38h03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2367413.3 similar to SW:GPR39_HUMAN O43194 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR39.;, mRNA sequence.
ACCESSION A1742092
VERSION A1742092.1 GI:5110380
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 578)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 806 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
FEATURES
Source Location/Qualifiers
1..578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2367413"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker. Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326653 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

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BASE COUNT 102 a 176 c 142 g 158 t
ORIGIN

Query Match 58.4%; Score 365; DB 9; Length 578;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGACTGGCCGGGAGCGAAGACAGCGGCGCTGCACAAAGC 60
DB 455 AGTTCTCTTGCAGAGACTGGCCGGGAGCGAAGACAGCGGCGCTGCACAAAGC 396
QY 61 GCGCCTCTCGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTGTGGTGGCGTCTG 120
DB 395 GCGCCTCTCGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTGTGGTGGCGTCTG 336
QY 121 CAGGACAGCGCGGAGCAGCAGCAGCTGCAGACAGCAGCGCGAATGCTGGAGAGACAC 180
DB 335 CAGGACAGCGCGGAGCAGCAGCAGCTGCAGACAGCAGCGCGAATGCTGGAGAGACAC 276
QY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240
DB 275 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 216
QY 241 GAGGATCATGTACCGCCGGAAGTAGAGACTGCTGCTGCTCTTGGTGGCGGACG 300
DB 215 GAGGATCATGTACCGCCGGAAGTAGAGACTGCTGCTGCTCTTGGTGGCGGACG 156
QY 301 CATGATCTCCGATCTGTGTGGGATCGAGATACGGGCAATGTACAAACATCAGCCG 360
DB 155 CATGATCTCCGATCTGTGTGGGATCGAGATACGGGCAATGTACAAACATCAGCCG 96
QY 361 TGGGACAGACAGAGAGAGAGAGAGACAGAAAAACACAGCATGAGAAC 416
DB 95 TGGGACAGACAGAGAGAGAGAGAGACAGAAAAACACAGCATGAGAAC 40

RESULT 29
AM087372/c 432 bp mRNA linear EST 15-OCT-1999
LOCUS xbl19602.x1 NCI-CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576786.3,
DEFINITION similar to SW:GP39, HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39, mRNA sequence.
ACCESSION AM087372
VERSION AM087372.1 GI:6043177
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html

FEATURES
source
Possible reversed clone: similarity on wrong strand
Seq primer: -40up from gibco
High quality sequence stop: 306.
Location/Qualifiers
1..432

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2576786"

/clone_lib="NCI-CGAP Kid13"
/tissue_type="2 pooled WILMs' tumors, one primary and one
metastatic to brain"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

BASE COUNT 92 a 116 c 89 g 134 t 1 others
Query Match 55.5%; Score 347; DB 10; Length 432;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AAGTAGAGCCCTCCGTCAGTGTGCTGGTGGTGGCCGAGCCATGATCTCGAATCTGG 319
DB 353 AAGTAGAGCCCTCCGTCAGTGTGCTGGTGGTGGCCGAGCCATGATCTCGAATCTGG 294
QY 320 TTGGGCAATCCAGCATGAGCCCAATGTACACAAATCAGCCCTGGGACAGACAGAGA 379
DB 293 TTGGGCAATCCAGCATGAGCCCAATGTACACAAATCAGCCCTGGGACAGACAGAGA 234
QY 380 GGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAATAAACCATTA 439
DB 233 GGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAATAAACCATTA 174
QY 440 AATATTTAGCCCTCTGTGCTGTCTTACTGTGCGGAGAAATGTACCAATTTTACGT 499
DB 173 AATATTTAGCCCTCTGTGCTGTCTTACTGTGCGGAGAAATGTACCAATTTTACGT 114
QY 500 TGGACTTGACAGCTTCTTTGGCCAAAGCAGAGAGAAATTAACACTTTTCAACCCG 559
DB 113 TGGACTTGACAGCTTCTTTGGCCAAAGCAGAGAGAAATTAACACTTTTCAACCCG 54
QY 560 GGGAGTTGGCTGTGTAAAGAACCAATTAATGCTTTAGACAGTG 606
DB 53 GGGAGTTGGCTGTGTAAAGAACCAATTAATGCTTTAGACAGTG 7

RESULT 30
BF126050 759 bp mRNA linear EST 24-OCT-2000
LOCUS 601762888F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026092.5,
DEFINITION mRNA sequence.
ACCESSION BF126050
VERSION BF126050.1 GI:10965090
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 759)
AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC/DCID/DMF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM855 row: 0 column: 21
High quality sequence stop: 723.
Location/Qualifiers
1..759

FEATURES
source
Possible reversed clone: similarity on wrong strand
Seq primer: -40up from gibco
High quality sequence stop: 723.
Location/Qualifiers
1..759

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4026092"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 192 c 221 g 155 t

ORIGIN

Query Match 54.2%; Score 339; DB 12; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACACGGCGCTGCACAAAGC 60
|||||
Db 161 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACACGGCGCTGCACAAAGC 220
|||||
QY 61 GGGCGTGTGGTGGAGTGGCGCATGTACGGCGGAGCGGCTTCTCGTGGTGGCGTGTG 120
|||||
Db 221 GGGCGTGTGGTGGAGTGGCGCATGTACGGCGGAGCGGCTTCTCGTGGTGGCGTGTG 280
|||||
QY 121 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCGCGGAACCTGCTGCAGAGACAC 180
|||||
Db 281 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCGCGGAACCTGCTGCAGAGACAC 340
|||||
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTTCCGAGAAAGGGAG 240
|||||
Db 341 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTTCCGAGAAAGGGAG 400
|||||
QY 241 GAGGATCATGTACGCCCGGAGAGTACCTGCTCGAGTGGTGGTGGCGCCAGC 300
|||||
Db 401 GAGGATCATGTACGCCCGGAGAGTACCTGCTCGAGTGGTGGTGGCGCCAGC 460
|||||
QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCGC 339
|||||
Db 461 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCGC 499
|||||

RESULT 31
BF125134 843 bp mRNA linear EST 24-OCT-2000
LOCUS 601162356F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4025340 5',
DEFINITION mRNA sequence.
BF125134
ACCESSION BF125134.1 GI:10964174
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 843)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1995)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LCM853 row: P column: 13
High quality sequence stop: 711.
Location/Qualifiers
1. 843

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4025340"
/clone_1ib="NIH_MGC_20"
/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 225 a 192 c 255 g 171 t

ORIGIN

Query Match 54.2%; Score 339; DB 12; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACACGGCGCTGCACAAAGC 60
|||||
Db 161 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACACGGCGCTGCACAAAGC 220
|||||
QY 61 GGGCGTGTGGTGGAGTGGCGCATGTACGGCGGAGCGGCTTCTCGTGGTGGCGTGTG 120
|||||
Db 221 GGGCGTGTGGTGGAGTGGCGCATGTACGGCGGAGCGGCTTCTCGTGGTGGCGTGTG 280
|||||
QY 121 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCGCGGAACCTGCTGCAGAGACAC 180
|||||
Db 281 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCGCGGAACCTGCTGCAGAGACAC 340
|||||
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTTCCGAGAAAGGGAG 240
|||||
Db 341 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGAGTGAAGAAAGCTTCCGAGAAAGGGAG 400
|||||
QY 241 GAGGATCATGTACGCCCGGAGAGTACCTGCTCGAGTGGTGGTGGCGCCAGC 300
|||||
Db 401 GAGGATCATGTACGCCCGGAGAGTACCTGCTCGAGTGGTGGTGGCGCCAGC 460
|||||
QY 301 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCGC 339
|||||
Db 461 CATGATCTCCGAATCTGGTTGGGATCCAGCATACGCGC 499
|||||

RESULT 32
A1272281 387 bp mRNA linear EST 18-NOV-1998
LOCUS ap23c03.x1 Schiller oligodendrogloma Homo sapiens CDNA clone
DEFINITION IMAGE:1956196 3' similar to SW-NTM1 RAT P20789 NEUROTENSIN RECEPTOR
TYPE 1; contains TAR1.t3 TAR1 repetitive element ; mRNA sequence.
A1272281
ACCESSION A1272281.1 GI:3894552
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 387)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Kritman, D., Kucab, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Stepec, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400p from 61bco
High quality sequence stop: 386.

TITLE
JOURNAL
COMMENT

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 480)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute / National Institute of Neurological
TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1073 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 372.
Location/Qualifiers
1. 480
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2097910"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="g1oblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGCCGCAATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 95 a 127 c 112 g 146 t
ORIGIN

Query Match 50.4%; Score 315; DB 9; Length 480;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 133 GCAGCAGACACTGCAGCAACACCGCGAATCTCTCGAGAGACCGGTGACAGAG 192
|||||
DB 480 GCAGCAGACACTGCAGCAACACCGCGAATCTCTCGAGAGACCGGTGACAGAG 421
OY 193 CGGGTTGATGACGAGCTGAGTAAAGAAAGCTCCGAGAGGAGGAGATCTGTA 252
|||||
DB 420 CGGGTTGATGACGAGCTGAGTAAAGAAAGCTCCGAGAGGAGGAGATCTGTA 361
OY 253 CGGCCGGAAGTAGACCTGCTCAGTCTGTGGTTGGCCGCGCATGATCCTCG 312
|||||
DB 360 CGGCCGGAAGTAGACCTGCTCAGTCTGTGGTTGGCCGCGCATGATCCTCG 301
OY 313 AATCTGTTGGGATCAGCATATGCGCAATGTACACATATGAGCCCTGGGACAG 372
|||||
DB 300 AATCTGTTGGGATCAGCATATGCGCAATGTACACATATGAGCCCTGGGACAG 241
OY 373 AGCAGAGGAGAGACAGAGAAAGAAACACAGATGAGAACAGTAATGATTA 432
DB 240 AGCAGAGGAGAGACAGAGAAAGAAACACAGATGAGAACAGTAATGATTA 181
OY 433 ACCATAAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGGAATGTTACCAATTT 492
|||||
DB 180 ACCATAAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGGAATGTTACCAATTT 121
OY 493 TCAGTGTGACTTGACAGCTCTTTTGCACAGCAAGAGAGAAATTTAACTGTTCA 552
|||||

DB 120 TCAGTGTGACTTGACAGCTCTTTTGCACAGCAAGAGAGAAATTAACACTGTTCA 61
OY 553 AACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTAG 600
|||||
DB 60 AACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTAG 13
RESULT 35
AA655640/c 337 bp mRNA linear EST 14-NOV-1997
LOCUS ag35d12.s1 Gessler Wilms tumor Homo sapiens cDNA clone
DEFINITION IMAGE:1126871 3', mRNA sequence.
ACCESSION AA655640
VERSION AA655640.1 GI:2620253
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 337)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellander, K., Stepien, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
JOURNAL Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 325.
Location/Qualifiers
1. 337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1126871"
/clone_lib="Gessler Wilms tumor"
/sex="pooled (6)"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dt selection. cDNA library preparation was with
the BRL/Life Tech. Superscript plasmid system. An
oligo-dt NotI primer for first strand synthesis generated
ggcgccccc(t)n at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcgaccagcgctcg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."

BASE COUNT 78 a 81 c 74 g 104 t
ORIGIN

Query Match 50.2%; Score 314; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 293 GCGCAGACCATGATCCCTCCGAATCTGTTGGGATCAGCATAGCGCAATGTCAACA 352
|||||
DB 314 GCGCAGACCATGATCCCTCCGAATCTGTTGGGATCAGCATAGCGCAATGTCAACA 255
OY 353 ATCAGCCCTGGGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGA 412
|||||
DB 254 ATCAGCCCTGGGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGATGA 195
OY 413 GAACACAGTAATGATTAATATTTAGCCCTCTGTCTGTCTTACTGGC 472
|||||
DB 194 GAACACAGTAATGATTAATATTTAGCCCTCTGTCTGTCTTACTGGC 135

QY 473 CAGAAATGGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAGCAGA 532
|||||
Db 134 CAGAAATGGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAGCAGA 75
QY 533 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAACCAATTAA 592
|||||
Db 74 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAACCAATTAA 15
QY 593 TGCTTTAGACAGTG 606
|||||
Db 14 TGCTTTAGACAGTG 1

RESULT 36
AA970361 354 bp mRNA linear EST 20-MAY-1998
LOCUS AA970361/c
DEFINITION OP52g06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1580506 3', mRNA sequence.
ACCESSION AA970361
VERSION AA970361.1 GI:3145874
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 354)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. RT from Amersham.
FEATURES
location/Qualifiers
source
1..354
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1580506"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687339,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 80 a 88 c 78 g 108 t
ORIGIN
Query Match 50.2%; Score 314; DB 9; Length 354;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GCCGAGCCATGATCTCCGATGTGTTGGGCAATCCAGCATACGCGCCCAATGTCAACA 352
|||||
Db 315 GCCGAGCCATGATCTCCGATGTGTTGGGCAATCCAGCATACGCGCCCAATGTCAACA 256
QY 353 ATCAGCCCTGGGAGACAGCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
|||||
Db 255 ATCAGCCCTGGGAGACAGCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 413 GAACACAGTAATGAATTAACATTAATATTTAGCCCTCTGTGTGTCTTACTGGC 472
|||||
Db 195 GAACACAGTAATGAATTAACATTAATATTTAGCCCTCTGTGTGTCTTACTGGC 136

QY 473 CAGAAATGGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAGCAGA 532
|||||
Db 135 CAGAAATGGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAGCAGA 76
QY 533 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAACCAATTAA 592
|||||
Db 75 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAACCAATTAA 16
QY 593 TGCTTTAGACAGTG 606
|||||
Db 15 TGCTTTAGACAGTG 2

RESULT 37
AA075710 373 bp mRNA linear EST 23-DEC-1997
LOCUS AA075710/c
DEFINITION zm89d04.s1 StrataGene ovarian cancer (#937219) Homo sapiens cDNA
clone IMAGE:545095 3', similar to contains Alu repetitive element;
mRNA sequence.
ACCESSION AA075710
VERSION AA075710.1 GI:1615580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 373)
Hillier, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins,
Chissoe, S., Linton, G., Becker, M., Bonaldo, M.F., Chlapell, B.,
Miller, S., Mullman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Treviski, E.,
Underwood, K., Wohlmann, P., Watson, R., Wilson, R. and Matre, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
JOURNAL 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 427 Std Error: 0.00
Seq primer: -40ml3 fwd. from Amersham
High quality sequence stop: 240.
FEATURES
location/Qualifiers
source
1..373
/organism="Homo sapiens"
/db_xref="GDB:3923283"
/db_xref="taxon:9606"
/clone="IMAGE:545095"
/clone_lib="StrataGene ovarian cancer (#937219)"
/sex="female"
/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Cloned unidirectionally. Primer: Oligo dT. Papillary
serous carcinoma, isolated from ascites, 64 year old
caucasian. Average insert size: 0.8 kb; uni-ZAP XR vector;
-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 83 a 96 c 80 g 114 t
ORIGIN
Query Match 50.2%; Score 314; DB 9; Length 373;

library synthesis. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor.

[5'-pGACTAGTTCTAGATCGGAGCGGCCGCTT)15-3']. Not I blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 100 a 76 c 89 g 47 t
ORIGIN

Query Match 49.9%; Score 312; DB 12; Length 312;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCACAGCACCCTGCGACGACACCCGCGAAGCTGCTGCGAGACACCGTGTACAGAGCGG 195
DB 1 GCACAGCACCCTGCGACGACACCCGCGAAGCTGCTGCGAGACACCGTGTACAGAGCGG 60
QY 196 GTTGATGACCGAGCTGAGAGAGAAACGCTCCGAGAGGGGAGGAGATCATGTACGC 255
DB 61 GTTGATGACCGAGCTGAGAGAGAAACGCTCCGAGAGGGGAGGAGATCATGTACGC 120
QY 256 CCGAAGTAGAGCCTGCTCCAGTCTGCTTGGGTTTGGCGGACGACCATGATCTCCGAT 315
DB 121 CCGAAGTAGAGCCTGCTCCAGTCTGCTTGGGTTTGGCGGACGACCATGATCTCCGAT 180
QY 316 CTGGTTGGGATCCAGCATACGCGCAATGTACACAAATCAGCCCTGGGCGACAGCAGC 375
DB 181 CTGGTTGGGATCCAGCATACGCGCAATGTACACAAATCAGCCCTGGGCGACAGCAGC 240
QY 376 AGGAGGAGAGCAG 435
DB 241 AGGAGGAGAGCAG 300
QY 436 ATTAATATTTTA 447
DB 301 ATTAATATTTTA 312

RESULT 40 349 bp mRNA linear EST 09-MAR-1998
AA173739
LOCUS zp04h05.r1 Striatogene ovarian cancer (#937219) Homo sapiens cDNA
DEFINITION clone IMAGE:595449 5', mRNA sequence.

ACCESSION AA173739
VERSION AA173739.1 GI:1753890
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 349)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kritman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Merra, M., Martin,
J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisling, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

JOURNAL This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
TITLE Insert Length: 792 Std Error: 0.00
COMMENT Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 236.

FEATURES
Source

Location/Qualifiers
1..349
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:595449"
/clone_lib="Striatogene ovarian cancer (#937219)"
/sex="female"
/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI
; Cloned unidirectionally. Primer: Oligo dT. Papillary
serous carcinoma, isolated from ascites, 64 year old
caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGCTTTTGTGTTTGTGTTT 3'."

BASE COUNT 79 a 84 c 78 g 108 t
ORIGIN

Query Match 49.1%; Score 307; DB 9; Length 349;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCATGATCTCCGGAATCTGTTGGGATCCAGATCCGCGCATATGCAACAATCAGCC 359
DB 310 CCATGATCTCCGGAATCTGTTGGGATCCAGATCCGCGCATATGCAACAATCAGCC 251
QY 360 CTGGGAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 419
DB 250 CTGGGAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 191
QY 420 GTTAATGAATTAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAGAA 479
DB 190 GTTAATGAATTAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGAGAA 131
QY 480 TGGTACCAATTTTTCAGTGTGACTTGAACGTTCTTTTCCACAGCAGAGAGATT 539
DB 130 TGGTACCAATTTTTCAGTGTGACTTGAACGTTCTTTTCCACAGCAGAGAGATT 71
QY 540 TACACTGTTTCAACCCGCGGAGTGGCTGTTTAAAGAGACCATTAATGCTTTTA 599
DB 70 TACACTGTTTCAACCCGCGGAGTGGCTGTTTAAAGAGACCATTAATGCTTTTA 11
QY 600 GACAGTG 606
DB 10 GACAGTG 4

RESULT 41 408 bp mRNA linear EST 25-JAN-2001
BG057775
LOCUS 7f75g10.x1 Lupski dorsal root ganglion Homo sapiens cDNA clone
DEFINITION IMAGE:3302971.3' similar to SM:GP39_HUMAN O43194 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.

ACCESSION BG057775
VERSION BG057775.1 GI:13523767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 408)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

JOURNAL Tissue Procurement: Dr. James Lupski
cDNA library Preparation: Lupski Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

info@image.llnl.gov
Seq primer: -40UP from GIBCO
High quality sequence stop: 376.
Location/Qualifiers

FEATURES

source

1. .408
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3302971"
/clone_lib="lupskl_dorsal_root_ganglion"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
directionally cloned using the following adaptors:
5'-TCGACCCAGCGGTCG-3' and
5'-GACTGATGTTAGATCGGAGGCGCCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 111 a 87 c 79 g 128 t 3 others

ORIGIN

Query Match 49.1%; Score 307; DB 12; Length 408;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCATGATCCTCCGATCTGTTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 359

Db 397 CCATGATCCTCCGATCTGTTGGGATCCAGCATACGGCCCAATGTCACAAATCAGCC 338

QY 360 CTGGGACAGACGAG 419

Db 337 CTGGGACAGACGAG 278

QY 420 GTAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 479

Db 277 GTAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 218

QY 480 TGTGACCAATTTTTCAGTGTGACCTTGACCTTCTTTTCCCAACAGAGAGAGATT 539

Db 217 TGTGACCAATTTTTCAGTGTGACCTTGACCTTCTTTTCCCAACAGAGAGAGATT 158

QY 540 TAAACATGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAACCATTAATGCTTTA 599

Db 157 TAAACATGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAACCATTAATGCTTTA 98

QY 600 GACAGTG 606

Db 97 GACAGTG 91

RESULT 42

AI566797/c 420 bp mRNA linear EST 12-MAY-1999

LOCUS t123908.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168510 3'

DEFINITION similar to SW:NTRI_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1; mRNA

sequence.

ACCESSION AI566797.1 GI:4525249

VERSION AI566797.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 420)

NCI/INNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

disorders and stroke, Brain Tumor Genome Anatomy Project

(CGAP/BRGAP), Tumor Gene Index

JOURNAL

Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapb-remail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 1148 Std Error: 0.00

Seq primer: -40UP from GIBCO

High quality sequence stop: 354

POLYA-NO.

FEATURES

source

Location/Qualifiers

1. .420

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2168510"

/clone_lib="NCI_CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCCGCAATGCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 89 a 114 c 88 g 128 t 1 others

ORIGIN

Query Match 47.7%; Score 298; DB 9; Length 420;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 258 GGAAGTAGACCTGCTCAGTCGTGCTTGGTTGGCCGACCATGATCTCCGAATCT 317

Db 349 GGAAGTAGACCTGCTCAGTCGTGCTTGGTTGGCCGACCATGATCTCCGAATCT 290

QY 318 GCTTGGCATCCAGCATACGGCCCAATGTCACAAATCAGCCCTGGGACAGAGAGAG 377

Db 289 GCTTGGCATCCAGCATACGGCCCAATGTCACAAATCAGCCCTGGGACAGAGAGAG 230

QY 378 GAGGAGAGACAG 437

Db 229 GAGGAGAGACAG 170

QY 438 AAAATATTAGCCCTCTGTTCTGTCTTACTGGCCAGGAATGGTACCAATTTTTCAGT 497

Db 169 AAAATATTAGCCCTCTGTTCTGTCTTACTGGCCAGGAATGGTACCAATTTTTCAGT 110

QY 498 GTTGGACTTGACAGCTTTTTCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAG 557

Db 109 GTTGGACTTGACAGCTTTTTCGCCACAGAGAGAGAGAGAGAGAGAGAGAGAG 50

QY 558 GGGGAGTGTGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTG 606

Db 49 GGGGAGTGTGCTGTGTTAAAGAACCATTAATGCTTTAGACAGTG 1

RESULT 43

AI363261/c 475 bp mRNA linear EST 16-FEB-1999

LOCUS q556102.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016027 3'

DEFINITION similar to SW:NTRI_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1; mRNA

sequence.

ACCESSION AI363261

VERSION AI363261

GI:4114882

DB 602 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAGAAAAAGCTCCGAGAGGGAG 661
 QY 241 GAGGATCATGTACGCCCGAAGTACCTCGTCCAGTGTG 282
 DB 662 GAGGATCATGTACGCCCGAAGTACCTCGTCCAGTGTG 703

RESULT 45

LOCUS AM128849 402 bp mRNA linear EST 25-OCT-1999
 DEFINITION x466112.x1 NCI-CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596847 3'
 similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
 GPR39. ; contains Aliu repetitive element; contains element MER4 MER37
 repetitive element ; mRNA sequence.

ACCESSION AM128849
 VERSION AM128849.1 GI:6116769
 KEYWORDS EST.

SOURCE

human.

ORGANISM

REFERENCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 402)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNT at:
www-bio.lnl.gov/dbcp/image/image.html

Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 303.
 Location/Qualifiers

FEATURES

source

1..402
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2596847"
 /clone_lib="NCI-CGAP_Ov23"
 /tissue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.35 kb. Tumor types include: mixed
 Mullerian tumor, papillary serous, clear cell, spindle
 cell. All are primary tumors, metastasis positive. Life
 Technologies catalog #: 11534-013"

BASE COUNT

86 a 97 c 80 g 139 t

Query Match 43.5%; Score 272; DB 10; Length 402;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 284 TTGGGTTTGGCCGACCATGATCTCCGAATCTGTTGGCATCCAGCATACGCCCAAT 343
 DB 344 TTGGGTTTGGCCGACCATGATCTCCGAATCTGTTGGCATCCAGCATACGCCCAAT 285
 QY 344 GTCAACAACATGACCCCTGGGCGACACGACGAGGAGGAGAGACAGAGAAAAAAC 403
 DB 284 GTCAACAACATGACCCCTGGGCGACACGACGAGGAGGAGAGACAGAGAAAAAAC 225
 QY 404 ACAGCATGAGACACAGTAATGAATAAACCATAAATATTAGCCCTCTGTCTGTG 463
 DB 224 ACAGCATGAGACACAGTAATGAATAAACCATAAATATTAGCCCTCTGTCTGTG 165

QY 464 CTTACTGGCCAGGAATGTTACCAATTTTCACTGTGGACTTGACAGCTTCTTTGCCA 523
 DB 164 CTTACTGGCCAGGAATGTTACCAATTTTCACTGTGGACTTGACAGCTTCTTTGCCA 105
 QY 524 CAAGCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAG 583
 DB 104 CAAGCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAG 45
 QY 584 ACCATTAAATGCTTTAGACAGTG 606
 DB 44 ACCATTAAATGCTTTAGACAGTG 22

Search completed: November 7, 2002, 23:07:37
 Job time : 846.445 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 13:45:13 ; Search time 27.1619 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agttctcttcgagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications - NA : *

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCF_US_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	99.8	625	US-09-825-294-210	Sequence 210, App
2	624	99.8	625	US-09-867-701-10876	Sequence 10876, A
3	624	99.8	1897	US-09-825-294-214	Sequence 214, App
4	613	98.1	1619	US-09-825-294-205	Sequence 205, App
5	613	98.1	1619	US-09-825-294-211	Sequence 211, App
6	433.2	69.3	558	US-09-867-701-2375	Sequence 2375, Ap
7	395.4	63.3	409	US-09-867-701-4240	Sequence 4240, Ap
8	361.6	57.9	1362	US-09-825-294-208	Sequence 208, App
9	361	57.8	1373	US-09-867-701-1516	Sequence 1516, Ap
10	353	56.5	390	US-09-867-701-1532	Sequence 1532, Ap
11	310.8	49.7	349	US-09-867-701-2409	Sequence 2409, Ap
12	207.8	33.2	381	US-09-867-701-7826	Sequence 7826, Ap
13	171.2	27.4	201	US-09-867-701-8894	Sequence 8894, Ap
14	56.4	9.0	1464	US-09-149-045-1	Sequence 1, Appl
15	47.8	7.6	2036	US-09-866-582-17	Sequence 17, Appl
16	43.8	7.0	894	US-09-815-242-4029	Sequence 4029, Ap
17	42.2	6.8	1137	US-10-037-616-3	Sequence 3, Appl
18	39	6.2	425	US-09-960-352-1711	Sequence 1711, Ap
19	38.6	6.2	1032	US-09-971-228-2	Sequence 2, Appl

C 20	38.6	6.2	1149	9	US-09-971-228-1	Sequence 1, Appl1
C 21	38.6	6.2	1376	9	US-09-971-228-4	Sequence 4, Appl1
C 22	38.6	6.2	2776	12	US-10-037-616-1	Sequence 1, Appl1
C 23	38.6	6.2	3381	10	US-09-764-847-1092	Sequence 1092, Ap
C 24	38.6	6.2	4063	10	US-09-764-847-1091	Sequence 1091, Ap
C 25	38.6	6.2	32177	10	US-09-764-877-3251	Sequence 3251, Ap
C 26	38.6	6.2	32207	10	US-09-764-877-3250	Sequence 3250, Ap
C 27	38.4	6.1	1089	10	US-09-939-844-14	Sequence 14, Appl
C 28	38.2	6.1	332	10	US-09-867-701-9973	Sequence 9973, Ap
C 29	37.2	6.0	1743	10	US-09-925-301-541	Sequence 541, App
C 30	37.2	6.0	3511	10	US-09-753-831-3	Sequence 3, Appl1
C 31	36.4	5.8	2314	10	US-09-962-832-105	Sequence 105, Appl
C 32	36	5.8	837	10	US-09-885-441-1	Sequence 1, Appl1
C 33	36	5.8	888	10	US-09-888-615-26	Sequence 26, Appl
C 34	35.8	5.7	2785	10	US-09-925-302-122	Sequence 122, App
C 35	35.8	5.7	3977	10	US-09-764-869-1999	Sequence 1999, Ap
C 36	35.8	5.7	3977	10	US-09-764-869-2001	Sequence 2001, Ap
C 37	35.8	5.7	21860	10	US-09-764-877-3803	Sequence 3803, Ap
C 38	35.4	5.7	2462	10	US-09-964-824A-289	Sequence 289, App
C 39	35.4	5.7	2462	10	US-09-880-107-2251	Sequence 2251, Ap
C 40	34.8	5.6	624	10	US-09-804-551B-41	Sequence 41, Appl
C 41	34.8	5.6	1788	10	US-09-148-012-1	Sequence 1, Appl1
C 42	34.6	5.5	371	10	US-09-969-347-117	Sequence 117, App
C 43	34.6	5.5	457	10	US-09-960-352-12765	Sequence 12765, A
C 44	34.6	5.5	1200	10	US-09-815-242-4132	Sequence 4132, Ap
C 45	34.4	5.5	372	12	US-10-052-545-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-825-294-210
Sequence 210, Application US/09825294
Patent No. US20020004491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 210
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(625)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match 99.8%; Score 624; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 3.3e-159;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGTTCTCTTCGAGAGACTGGCGCGGAGCGGAAGCAAGCGGCGCTGCACAAACG	60
DB	1	AGTTCTCTTCGAGAGACTGGCGCGGAGCGGAGCGGAAGCAAGCGGCGCTGCACAAACG	60
QY	61	GCGCGTGTGCGTGTGAGTGGCGATGTACGCGGCGCTTCTGCTGCTGCTG	120
DB	61	GCGCGTGTGCGTGTGAGTGGCGATGTACGCGGCGCTTCTGCTGCTGCTG	120
QY	121	CACGCGACGGCGGAGACGACGACCGTCCGACGACACCGCGGAAACGCTCGAGGACAC	180
DB	121	CACGCGACGGCGGAGACGACGACCGTCCGACGACACCGCGGAAACGCTCGAGGACAC	180


```
QY 181 CGTGTACAGAGGCGGTTGATGACCGAGCTAGTAGAAAAAGCTCTCCGAGAGGGGAG 240
    |||||||
Db 181 CGTGTACAGAGGCGGTTGATGACCGAGCTAGTAGAAAAAGCTCTCCGAGAGGGGAG 240
QY 241 GAGGATCATGTACGCCCGGAGTAGACCTCGTCCAGTCTGTGGGTTGGCCGAGC 300
    |||||||
Db 241 GAGGATCATGTACGCCCGGAGTAGAGACCTCGTCCAGTCTGTGGGTTGGCCGAGC 300
QY 301 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGCCAATGTCAACAATACAGCCC 360
    |||||||
Db 301 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGCCAATGTCAACAATACAGCCC 360
QY 361 TGGGACAGACGAGCAGAGGAGAGAGACAGAAAAAACAACATGAGAACAG 420
    |||||||
Db 361 TGGGACAGACGAGCAGAGGAGAGAGACAGAAAAAACAACATGAGAACAG 420
QY 421 TAAATGAATAAACCAATTAATTTAGCCCCCTGTCTGTCTTACTGCGCAGAAAT 480
    |||||||
Db 421 TAAATGAATAAACCAATTAATTTAGCCCCCTGTCTGTCTTACTGCGCAGAAAT 480
QY 481 GTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGCAGAGAAATT 540
    |||||||
Db 481 GTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGCAGAGAAATT 540
QY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
    |||||||
Db 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
QY 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
    |||||||
Db 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
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RESULT 2

```
US-09-867-701-10876
; Sequence 10876, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10876
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876
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Query Match 99.8%; Score 624; DB 10; Length 625;

Best Local Similarity 100.0%; Pred. No. 3.3e-159; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGG 60
    |||||||
Db 1 AGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGG 60
QY 61 GCGCTGTGCTGTGAGTGTGAGTGTACGTGCGCAGAGCGCTTCTGCTGTGGCTGTG 120
    |||||||
Db 61 GCGCTGTGCTGTGAGTGTGAGTGTACGTGCGCAGAGCGCTTCTGCTGTGGCTGTG 120
QY 121 CAGCGACAGGCGGAGCAGACAGCAGCAGAACAGCCGCCGAAGAACTGCTGAGAGAC 180
    |||||||
Db 121 CAGCGACAGGCGGAGCAGACAGCAGCAGAACAGCCGCCGAAGAACTGCTGAGAGAC 180
```

```
QY 181 CGTGTACAGAGGCGGTTGATGACCGAGCTAGTAGAAAAAGCTCTCCGAGAGGGGAG 240
    |||||||
Db 181 CGTGTACAGAGGCGGTTGATGACCGAGCTAGTAGAAAAAGCTCTCCGAGAGGGGAG 240
QY 241 GAGGATCATGTACGCCCGGAGTAGACCTCGTCCAGTCTGTGGGTTGGCCGAGC 300
    |||||||
Db 241 GAGGATCATGTACGCCCGGAGTAGAGACCTCGTCCAGTCTGTGGGTTGGCCGAGC 300
QY 301 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGCCAATGTCAACAATACAGCCC 360
    |||||||
Db 301 CATGATCTCTCCGAATCTGTGGGATCCAGCATACGCCAATGTCAACAATACAGCCC 360
QY 361 TGGGACAGACGAGCAGAGGAGAGAGACAGAAAAAACAACATGAGAACAG 420
    |||||||
Db 361 TGGGACAGACGAGCAGAGGAGAGAGACAGAAAAAACAACATGAGAACAG 420
QY 421 TAAATGAATAAACCAATTAATTTAGCCCCCTGTCTGTCTTACTGCGCAGAAAT 480
    |||||||
Db 421 TAAATGAATAAACCAATTAATTTAGCCCCCTGTCTGTCTTACTGCGCAGAAAT 480
QY 481 GTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGCAGAGAAATT 540
    |||||||
Db 481 GTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGCAGAGAAATT 540
QY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
    |||||||
Db 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600
QY 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
    |||||||
Db 601 ACAGTGNAAAAAAGAAAAAAGAAAAA 625
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RESULT 3

```
US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
```

Query Match 99.8%; Score 624; DB 10; Length 1897;

Best Local Similarity 99.8%; Pred. No. 5.9e-159; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGG 60
    |||||||
Db 1271 AGTTCTCTTGCAGAGAGTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGG 1330
QY 61 GCGCTGTGCTGTGAGTGTGAGTGTACGTGCGCAGAGCGCTTCTGCTGTGGCTGTG 120
    |||||||
Db 1331 GCGCTGTGCTGTGAGTGTGAGTGTACGTGCGCAGAGCGCTTCTGCTGTGGCTGTG 1390
QY 121 CAGCGACAGGCGGAGCAGACAGCAGCAGAACAGCCGCCGAAGAACTGCTGAGAGAC 180
    |||||||
```


Db	1391	CAGCGACAGCGCGCACACAGCACCCTGCACGAAACCCCGGAAACTGTCGCGAGAAC	1450
QY	181	CGTGTACAGAGACGGGTTGATGACCGAGCTGAGGTAGAAAAACGCTCTCCGAGAAAGGGAG	240
Db	1451	CCTGTACAGAGACCGGGTTGTATGCCGAGCTGAGGTAGAAAAACGCTCTCCGAGAAAGGGAG	1510
QY	241	GAGGATCATGTACGGCCGGGAAGAGACCTGTCGACATGGTGGCTTGGGTTTGGCCGAGC	300
Db	1511	GAGGATCATGTACGGCCGGGAAGAGACCTGTCGACATGGTGGCTTGGGTTTGGCCGAGC	1570
QY	301	CATGATCCTCCGAAATCTGGTTGGGCATCCAGCATACGAGCCATGTCAACAATCAGACC	360
Db	1571	CATGATCCTCCGAAATCTGGTTGGGCATCCAGCATACGAGCCAAATGTCAACAATCAGACC	1630
QY	361	TGGGCAGACACGACGACGAGGAGAGACAGAAAAAACAACAACAGCATGAGAACACAG	420
Db	1631	TGGGCAGACACGACGACGAGGAGAGAGAAAAAACAACAACAGCATGAGAACACAG	1690
QY	421	TAAATGAATAAAAACATAAATTTTAAAGCCCTGTCTGTGTTACTGTGCCAGGAAT	480
Db	1691	TAAATGAATAAAAACATAAATTTTAAAGCCCTGTCTGTGTTACTGTGCCAGGAAT	1750
QY	481	GGTACCAATTTTTCACGTGTGACCTGCACAGCTCTTTTGCCACAAGCAGAGAAATTT	540
Db	1751	GGTACCAATTTTTCACGTGTGTGACCTGCACAGCTCTTTTGCCACAAGCAGAGAAATTT	1810
QY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTTAAAGAAAGACATTAAATGCTTTAG	600
Db	1811	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTTAAAGAAAGACATTAAATGCTTTAG	
QY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAAA 625	
Db	1871	ACAGTGTAATAAAAAAAAAAAAAAAAAA 1895	

```

RESULT 4
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.48A05
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205

Query Match          98.1%; Score 613; DB 10; Length 1619;
Best Local Similarity 99.7%; Pred. No. 5e-156;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1.

QY      1 AGTTCCTGTCGAGAGGACTGGCGCGGAGCGGAGCAAGACACACGGGCGCTGCACAAAGCG 60
Db      992 AGTTCTCTCTGAGAGGACTGGCGCGGAGCGGAGCAAGACACACGGGCGCTGCACAAAGCG 1051

QY      61 GCGCGTGTGCGTGTGTGAGATGTACGGCGGAGGCGCTTCTGTGTGTGGCGTGTG 120
Db      1052 GCGCGTGTGCGTGTGTGAGATGTACGGCGGAGGCGCTTCTGTGTGTGGCGTGTG 1111

QY      121 CAGCCACAGGGCGGACACACAGCACC-TGCAGACAACCCGCCGAACACTGCTCGAGAGACA 179
Db      1112 CAGCCACAGGGCGGACACACAGCACCCTTGACACACACCAGCGGCAACACTGCTCGAGAGACA 1171

```

OY	180	CCGTGACAGAGAGCGGGTTGATACCGAGCTAGAGGTAGAAAAACGTCCGAGAAAGGGA	239
Db	1112	CCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGTGAAGAAAAAGCTCCGAGAAAGGGA	1231
OY	240	GGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTGTGCTGGGTTTGGCCGAC	299
Db	1232	GGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTGTGCTGGGTTTGGCCGAC	1291
OY	300	CCATGATCTCCGAATCTGGTTGGCATCCAGCATACGCCCAATGTACAACAATCAGCC	359
Db	1292	CCATGATCTCCGAATCTGGTTGGCATCCAGCATACGCCCAATGTACAACAATCAGCC	1351
OY	360	CTGGCGACAGACGAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA	419
Db	1352	CTGGCGACAGACGAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA	1411
OY	420	GTAATGAAATAAACCATAAATATTATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAA	479
Db	1412	GTAATGAAATAAACCATAAATATTATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAA	1471
OY	480	TGTAACCAATTTTTCGTGTGTGACCTTGACAGCTTCTTTGCCACAGCAAGAGAGATT	539
Db	1472	TGTAACCAATTTTTCGTGTGTGACCTTGACAGCTTCTTTGCCACAGCAAGAGAGATT	1531
OY	540	TAAACCTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA	599
Db	1532	TAAACCTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA	1591
OY	600	GACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1592	GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617	

Query Match	Best Local Similarity	Matches	624; Conservative	98.1%; 99.7%; 0;	Score 613; Pred. No. 5e-156;	DB 10;	Length 1619;	Indels 1;	Gaps 1;
OY 1	AGTTCTCCTTGACAGAGACTGGCGCGGAGCGGAAAGACAAACGGGCGCTGCACAAACGG	60							
Db 992	AGTTCTCCTTGACAGAGAGACTGGCGCGGAGCGGAAAGACAAACGGGCGCTGCACAAACGG	1051							
OY 61	GSGCGTGTGCGGTGGAGGTGGCATGTATGAGCGGAGCGGCGCTGTGCTGTGGCGGTGCTG	120							
Db 1052	GSGCGTGTGCGGTGGAGGTGGCATGTATGAGCGGAGCGGCGCTGTGCTGTGGCGGTGCTG	1111							
OY 121	CAGCAGCAGGCGGCGGACAGCAGCAGC -TGCACAGAACACCCCGCGAAACTGCTCGAGAGACA	179							
Db 1112	CAGCAGCAGGCGGCGGACAGCAGCAGCAGCCTTGCGACAGCAACCCCGCGAAACTGCTCGAGAGACA	1171							
OY 180	CCGTGTACAGCAGCGGCTGTATGATACCGAGACTGAGTATGAGAAAAACGCTTCCGAGAAAGGGA	239							

DB 1172 CCGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTAGAGAAAAACGTCCTCGAAGAGGGGA 1231
QY 240 GAGAGATCATGTAGCGCCGGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGACG 299
DB 1233 GGAGGATCATGTAGCGCCGGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGACG 1291
QY 300 CGATGATCCCTCGAATCTGTTGGGATCCAGCATACGGCCATGTCACAAACATACGCGC 359
DB 1292 CCATGATCCCTCGAATCTGTTGGGATCCAGCATACGGCCATGTCACAAACATACGCGC 1351
QY 360 CTGGGACAGACAG 419
DB 1352 CTGGGACAGACAG 1411
QY 420 GTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 479
DB 1412 GTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1471
QY 480 TGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAT 539
DB 1472 TGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAT 1531
QY 540 TTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 599
DB 1532 TTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 1591
QY 600 GACAGTGNAAAAAAGAAAAAAGAAAAA 625
DB 1592 GACAGTGNAAAAAAGAAAAAAGAAAAA 1617

RESULT 6

US-09-867-701-2375
; Sequence 2375, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2375
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n - A,T,C or G
US-09-867-701-2375

Query Match 69.3%; Score 433.2; DB 10; Length 558;

Best Local Similarity 95.6%; Pred. No. 1e-107; Indels 11; Gaps 9;

Matches 539; Conservative 0; Mismatches 14;

QY 1 AGTTTCCTTGGAGAGAGTGGCGCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1 ACTTTCCTTGGAGAGAGTGGCGCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 GGCCTGTGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 120
DB 61 GGCCTGTGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 118
QY 121 CAGGACAGAGCGGAG 180
DB 119 CAGGACAGAGCGGAG 176

QY 181 CGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTAGAGAAAAACGTCCTCGAAGAGGGAG 240
DB 177 CCGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTAGAGAAAAACGTCCTCGAAGAGGGAG 236
QY 241 GAGAGATCATGTAGC-CGGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGACG 299
DB 237 GAGAGATCATGTAGC-CGGAGAGTAGAGACCTGCTCCAGTCGTGCTTGGGTTGGCCGACG 296
QY 300 CCATGA-TGCTCGAATCTGTTGGGATCCAGCATACGGCCATGTCACAAACATACGCGC 358
DB 297 CATGATTCCTCGAATCTGTTGGGATCCAGCATACGGCCATGTCACAAACATACGCGC 356
QY 359 CCGGACAGACAG 417
DB 357 CCGGACAGACAG 416
QY 418 CAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 477
DB 417 CAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 474
QY 478 AATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAG 537
DB 475 AATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAG 532
QY 538 TTTAACACTGTTTCAAAACCCGGGG 561
DB 533 NTTAACAATTTGTTTCAANCCGGGG 556

RESULT 7

US-09-867-701-4240/C
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240

Query Match 63.3%; Score 395.4; DB 10; Length 409;

Best Local Similarity 99.5%; Pred. No. 1.4e-97; Indels 1; Gaps 1;

Matches 407; Conservative 0; Mismatches 1;

QY 198 TGATGACGAGCTGAGGTAGAGAAAAACGTCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 257
DB 409 TGATGACGAGCTGAGGTAGAGAAAAACGTCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 350
QY 258 GGAAGTAGAGACTGCTGCAAGTGTGCTTGGGTTGGCCGAGAGAGAGAGAGAGAGAGAG 317
DB 349 GGAAGTAGAGACTGCTGCAAGTGTGCTTGGGTTGGCCGAGAGAGAGAGAGAGAGAGAG 291
QY 318 GGTGGGATCCAGCATGATGAGGCGCAATGTCACAAACATACAGCCCTGGGACAGACGAGAG 377
DB 290 GGTGGGATCCAGCATGATGAGGCGCAATGTCACAAACATACAGCCCTGGGACAGACGAGAG 231
QY 378 GAGGAG 437
DB 230 GAGGAG 171
QY 438 AAAATATTTAGCCCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 497
DB 170 AAAATATTTAGCCCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 111

QY 498 GTTGACCTTGACAGCTTCTTTGGCCACAGAGAAATTTAACTGTTTCAAAACC 557
 |||||||
 Db 110 GTTGACCTTGACAGCTTCTTTGGCCACAGAGAAATTTAACTGTTTCAAAACC 51
 |||||||
 QY 558 GGGGAGCTTGGCTGTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTG 606
 |||||||
 Db 50 GGGGAGCTTGGCTGTGTGTTAAAGAAAGCAATTAATGCTTTAGACAGTG 2

RESULT 8

US-09-825-294-208/C
 ; Sequence 208, Application US/09825294
 ; Patent No. US2002004491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Fling, Steven P.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.484C5
 ; CURRENT APPLICATION NUMBER: US/09/825,294
 ; CURRENT FILING DATE: 2001-04-03
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 208
 ; LENGTH: 1362
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-825-294-208

Query Match 57.9%; Score 361.6; DB 10; Length 1362;
 Best Local Similarity 98.9%; Pred. No. 3,5e-88;
 Matches 364; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGTTCTCTTTCAGAGAGCTGCGCGCCGCGAGCGGAGAGCAAGCGCGCTGCACAAACG 60
 |||||||
 Db 1215 AGTTCTCTTTCAGAGAGCTGCGCGCCGCGAGCGGAGAGCAAGCGCGCTGCACAAACG 1156
 |||||||
 QY 61 GCGCGTGTGCGTGTGAGAGTGGCGATGTACGCGCGCGCTTCGTTGTTGGGCTGTG 120
 |||||||
 Db 1155 GCGCGTGTGCGTGTGAGAGTGGCGATGTACGCGCGCGCTTCGTTGTTGGGCTGTG 1096
 |||||||
 QY 121 CAGCGACAGGCGCGACACAGCACTGACAGAACCCCGCGAATCTGTCGAGAGAC 180
 |||||||
 Db 1095 CAGCGACAGGCGCGACACAGCACTGACAGAACCCCGCGAATCTGTCGAGAGAC 1036
 |||||||
 QY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAACGTTCCGAGAAAGGAG 240
 |||||||
 Db 1035 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAACGTTCCGAGAAAGGAG 976
 |||||||
 QY 241 GAGGATCATGTACGCGCGGAGTAGAGCTCGTCACTCGTGGTTGGCGCGAGC 300
 |||||||
 Db 975 GAGGATCATGTACGCGCGGAGTAGAGCTCGTCACTCGTGGTTGGCGCGAGC 916
 |||||||
 QY 301 CATGATCTTCCGAATCTGTTGGGATTCAGCATACGCGCAATGTCAACAATCAGCCC 360
 |||||||
 Db 915 CATGATCTTCCGAATCTGTTGGGATTCAGCATACGCGCAATGTCAACAATCAGCCT 856
 |||||||
 QY 361 TGGGCA 368
 || ||||
 Db 855 CAGGAAGA 848

RESULT 9

US-09-867-701-1516/C
 ; Sequence 1516, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1516
 ; LENGTH: 373
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-867-701-1516

Query Match 57.8%; Score 361; DB 10; Length 373;
 Best Local Similarity 99.7%; Pred. No. 2,6e-88;
 Matches 372; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 234 AGGGAGAGATCATGTACGCCCGGAGTAGAGACCTGTCAGTCTGTTGGTTGG 293
 |||||||
 Db 373 AGGGAGAGATCATGTACGCCCGGAGTAGAGACCTGTCAGTCTGTTGGTTGG-G 315
 |||||||
 QY 294 CCGGACCATGATCTCCGAAATCTGTTGGGATTCAGCATACGCGCAATGTCAACAA 353
 |||||||
 Db 314 CCGGACCATGATCTCCGAAATCTGTTGGGATTCAGCATACGCGCAATGTCAACAA 255
 |||||||
 QY 354 TCAGCCCTGGGACACAGCAGAGAGGAGAGACAGAGAAAGAAACACACATGAG 413
 |||||||
 Db 254 TCAGCCCTGGGACACAGCAGAGAGGAGAGACAGAGAAAGAAACACACATGAG 195
 |||||||
 QY 414 AACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 473
 |||||||
 Db 194 AACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 135
 |||||||
 QY 474 AGGAATGTATCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCACACAAAGAG 533
 |||||||
 Db 134 AGGAATGTATCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCACACAAAGAG 75
 |||||||
 QY 534 AGAATTAACACTGTTTCAACCCGCGGAGAGTGGCTGTGTTAAAGAAACATTAAT 593
 |||||||
 Db 74 AGAATTAACACTGTTTCAACCCGCGGAGAGTGGCTGTGTTAAAGAAACATTAAT 15
 |||||||
 QY 594 GCTTTAGACAGTG 606
 |||||||
 Db 14 GCTTTAGACAGTG 2

RESULT 10

US-09-867-701-1532
 ; Sequence 1532, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; CURRENT FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1532
 ; LENGTH: 390
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(390)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-867-701-1532

Query Match 56.5%; Score 353; DB 10; Length 390;
 Best Local Similarity 98.5%; Pred. No. 3,8e-86;

215

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 23.4202 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agttctctctgcagagact.....gnaaaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	56.4	9.0	1872	1	US-08-153-848-39
C 2	56.4	9.0	1872	3	US-08-289-843A-39
C 3	56.4	9.0	1872	4	US-08-088-337B-39
C 4	56.4	9.0	1872	5	PCT-US93-11153-39
C 5	50	8.0	6379	1	US-08-499-215-1
C 6	49.4	7.9	7218	1	US-08-232-463-14
C 7	46.6	7.5	1176	4	US-09-200-090-3
C 8	46	7.4	289	4	US-09-007-005-17
C 9	46	7.4	289	4	US-09-244-796-17
C 10	45.6	7.3	1342	3	US-08-832-399-1
C 11	45.6	7.3	1342	4	US-09-372-498-1
C 12	45.6	7.3	1575	3	US-08-858-876A-1
C 13	45.6	7.3	1575	4	US-09-472-880-1
C 14	44	7.0	1233	4	US-09-200-090-1
C 15	43	6.9	1335	4	US-09-668-680-12
C 16	42.2	6.8	1137	3	US-09-082-088-1
C 17	42.2	6.8	1137	4	US-09-546-117-1
C 18	40.8	6.5	1951	3	US-08-922-865-1
C 19	40.8	6.5	1951	4	US-09-510-949-1
C 20	40.2	6.4	30001	1	US-08-125-468-1
C 21	40.2	6.4	30001	2	US-08-474-933-1
C 22	39.4	6.3	1280	4	US-09-199-737-1
C 23	39.4	6.3	1280	4	US-08-900-230-1
C 24	39.4	6.3	1280	4	US-09-058-333A-1
C 25	39	6.2	1063	4	US-09-077-675A-1
C 26	39	6.2	1947	1	US-07-951-715A-3
C 27	39	6.2	1947	2	US-08-459-448A-3

C 28	39	6.2	1947	3	US-08-459-595A-3	Sequence 3, Appl1
C 29	39	6.2	1947	3	US-08-459-504B-3	Sequence 3, Appl1
C 30	39	6.2	1947	3	US-08-459-444-3	Sequence 3, Appl1
C 31	39	6.2	1947	4	US-09-547-422-3	Sequence 2, Appl1
C 32	39	6.2	3468	1	US-07-951-715A-2	Sequence 4, Appl1
C 33	39	6.2	3468	1	US-07-951-715A-4	Sequence 4, Appl1
C 34	39	6.2	3468	1	US-07-951-715A-8	Sequence 4, Appl1
C 35	39	6.2	3468	1	US-08-459-595A-2	Sequence 8, Appl1
C 36	39	6.2	3468	2	US-08-459-448A-2	Sequence 4, Appl1
C 37	39	6.2	3468	2	US-08-459-448A-4	Sequence 4, Appl1
C 38	39	6.2	3468	2	US-08-459-448A-8	Sequence 8, Appl1
C 39	39	6.2	3468	3	US-08-459-595A-2	Sequence 2, Appl1
C 40	39	6.2	3468	3	US-08-459-595A-4	Sequence 4, Appl1
C 41	39	6.2	3468	3	US-08-459-595A-8	Sequence 8, Appl1
C 42	39	6.2	3468	3	US-08-459-504B-2	Sequence 2, Appl1
C 43	39	6.2	3468	3	US-08-459-504B-4	Sequence 4, Appl1
C 44	39	6.2	3468	3	US-08-459-504B-8	Sequence 8, Appl1
C 45	39	6.2	3468	3	US-08-459-504B-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-153-848-39/c
Sequence 39, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-08-153-848-39

	Query Match	Similarity	9.0%	Score	56.4	DB	1	Length	1872
	Best Local	Similarity	52.6%	Pred	No. 5.3e-06				
	Matches	123	Conservative	0	Mismatches	111	Indels	0	Gaps
QY	127	CAGCGCAGCAGCAGCACCCTGCAGCAACACCCGCGAAACCTGCTGGAGAGACCGCTGTA	186	111	111	111	111	111	111
Db	1185	CTGGCCACACAGCAGACATGAGAGTGCAGGCCCTGGCGGAAGCGGGGTCGMAAAAGGCATA	1126	111	111	111	111	111	111
QY	187	CAGGAGCGGGTGTGATGACCGAGCTGAGGTGTAAGAAAACGTCCTCGGAAGAGGGAGAGGAT	246	111	111	111	111	111	111
Db	1125	GAGGAAGGGGTGGAAGCAGCTTTACCTGACCTGATGCAGGTGCAGTAAAGGGAAGATGTT	1066	111	111	111	111	111	111
QY	247	CATGTACGCCCGGGAAGTAGACCTTCGTCACGTCGTCCTTGGGCTTGGCCGACCCATGAT	306	111	111	111	111	111	111
Db	1065	CATGAGGAAGAGGTCAAAAGTCACAGGGGCCAGTGCAGCAGGCTGCCAGCATGTACAGCT	1006	111	111	111	111	111	111
QY	307	CTTCGAGATTCGTTGGGATTCACAGCATTCAGGCCCATGTCACAAACATCAGGCC	360	111	111	111	111	111	111
Db	1005	CTTCAACAGGTGTGAGGGCATTCACAGCAGGCAAAAGTCCACACACGACCAAC	952	111	111	111	111	111	111

RESULT 2
US-09-299-843A-39/c
; Sequence 39, Application US/09299843A
; Date of Invention 01/07/75

```

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schmelkart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 2/866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 202..1341
US-09-299-843A-39

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Query Match	9.0%	Score 56.4;	DB 3;	Length 1872;
Best Local Similarity	52.6%	Pred. No. 5.3e-06;		
Matches 123; Conservative	0;	Mismatches 111;	Indels 0;	Gaps 0;

QY	127	CAGGCGGACACACGACACCTTCGACAGAAACACCCGCGAAACCTCTCGAGAGACACCGCTA	186
	1127		1126
Db	1185	CTGGCCACACGACAGCATTTGAGAGTGTGACGAGCTCTGGCGGAACCGGGGCTGAAAAAGGCATA	1126
QY	187	CAGGAGCGGGGTTTGTATGCACCCAGCTGAGGTAGAAACGCTCTCCGAAAGGGGAGAGCAT	246
	1125		1125
Db	1125	GAGGAAGGGGTTGAGGACGCTGTTTGACGTATAGCATTCGAGTGTGACGTATGGGGAAGATCTT	1066
QY	247	CATGTACGCCCGGAGTAGGACCTCGTCCATGTCGTGTGGGTTTGGCCGACGCCATCAT	306
	1065		1066
Db	1065	CATGAGGAGAGGTCAAAGTCACACAGGGCCACGTGCAGCAGCGCTGCCACATGTACACGCT	1006
QY	307	CCTCCGAATCGGTTGGTGGGCATTCACGATTCAGGCGCATCATCAACATTCAGGCC	360
	1005		952
Db	1005	CTTACCAGGTGTGAGGCATCTCCAGCATCAGGGCAAAAGTCTACACACAGACACCAC	952

RESULT 3

US-09-088-337B-39/c
; Sequence 39, Application US/09088337B
; Patent No. 6348574

APPLICANT: Godiska, Ronald
 Gray, Patrick W.
 Schmehlart, Vicki L.
 TITLE OF INVENTION: NO. 6348574e1 Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/088,337B
 FILING DATE: 01-Jun-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 6348574and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO. 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1872 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

Db 1030 AGAGACGCGCTGTGTAGAGAGAGAGTACAGCTGAGCTGACGTAGAAAAGTGTGG 971
QY 231 AGAAGGAGAGAGATCATGTACGCCGGAAGTAGACCTGTCAGCTGCTGGTT 290
Db 970 TCACCATGTAGAACTAGTGTAGAAATGTACATGGTGTCCAGCCGTCATAGGTA 911
QY 291 TGGCCCGACCATGATCTCCGAAATCTGGTGGCATTCACATACGGCAATGTACAA 350
Db 910 CGTAGCATGATGAGCTCGCGCATGTATCGGCAGACAGATGACATACATAGACCA 851
QY 351 CATCAGCCTCG 363
Db 850 CGATGCTCCAG 838

RESULT 8

US-09-007-005-17
Sequence 17, Application US/09007005B
Patent No. 6238558
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007, 005B
EARLIER FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035, 963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064, 491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 7.4%; Score 46; DB 4; Length 289;

Best Local Similarity 9.3%; Pred. No. 0.0015; Matches 23; Conservative 103; Mismatches 120; Indels 0; Gaps 0;

QY 161 CGAACTGCTGCGAGACACCGGTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 220
Db 36 CRARARURARCARARURRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 95
QY 221 AACGTCTCCGAGAGAGAGAGATGATACGCCGGAAGTAGACCTGTCAGTCG 280
Db 96 NRSNR 155
QY 281 TGGTGGGTTGGCCGAGCATGATCTCCGATCTGTGGGATCCAGATACGGCC 340
Db 156 NRSNR 215
QY 341 AATGTCAACAATCAGCCCTGGCGAGACAGAGAGAGAGAGAGAGAGAGAGAA 400
Db 216 NRSRCRARGRCRURGRURARARCRURURGRRCRGRUAAAAAAAAAAAA 275
QY 401 AACACA 406
Db 276 AAAAAA 281

RESULT 9
US-09-244-796-17

Sequence 17, Application US/09244796
Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244, 796
EARLIER FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035, 963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064, 491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007, 005
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 7.4%; Score 46; DB 4; Length 289;

Best Local Similarity 9.3%; Pred. No. 0.0015; Matches 23; Conservative 103; Mismatches 120; Indels 0; Gaps 0;

QY 161 CGAACTGCTGCGAGACACCGGTGTACAGAGCGGTTGATGACCGAGCTGAGTAGAA 220
Db 36 CRARARURARCARARURRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 95
QY 221 AACGTCTCCGAGAGAGAGAGATGATACGCCGGAAGTAGACCTGTCAGTCG 280
Db 96 NRSNR 155
QY 281 TGGTGGGTTGGCCGAGCATGATCTCCGATCTGTGGGATCCAGATACGGCC 340
Db 156 NRSNR 215
QY 341 AATGTCAACAATCAGCCCTGGCGAGACAGAGAGAGAGAGAGAGAGAGAGAA 400
Db 216 NRSRCRARGRCRURGRURARARCRURURGRRCRGRUAAAAAAAAAAAA 275
QY 401 AACACA 406
Db 276 AAAAAA 281

RESULT 10

US-08-832-399-1/c
Sequence 1, Application US/08832399

PATENT NO. 6008050
GENERAL INFORMATION:
APPLICANT: Bergsma, Dierk
APPLICANT: Shabon, Uman
TITLE OF INVENTION: NOVEL HUMAN NEUTROPHIL RECEPTOR TYPE 2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: PA
ZIP: 19406

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832.399
FILING DATE: 02-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GH50020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5515
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-832-399-1

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Query Match 7.3% Score 45.6; DB 3; Length 1342;
Best Local Similarity 49.2%; Pred. No. 0.004;
Matches 120; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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```

QY 111 TGGCGTGTGACGACGACGAGCGGCGACACAGCAGCCTGCAGCAACCCGCCGAATCTCT 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 926 TGGGTGTGCTCTCCACACAGGAGCTGACGGCTTCCAGGAAGATTTCGAAGAGAG 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 GCGAGACACCGCTGTACAGAGCGGGTGTATGACCGAGCTGAGTAAAGTCTCCG 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 866 AGGACACGCGCTGTAGAGAGAGAGTACAGCTGAGCTGACGTGAGAAAGTGTGG 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 AGAAGGGAGAGATCATGATGACCGCGGAAGTAGACCTGCTCCAGTCGTCTGGGT 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 806 TCACCATGTAGAAGTAGTGTAAGAAATTGTACAGTGGCTCAGTCCAGCGTCATCAGTA 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 291 TGGCCGACGATGATCTCCGAATCTGTTGGCATCCAGCATCGGCCAATGTCAAA 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 746 CGTAGCAGTACATGAGCCTGCGGGCATGTAGCGCAGCAGATGATCATGACCA 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 351 CAAT 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 686 CGAT 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 11
US-09-372-498-1/C
Sequence 1, Application US/09372498
Patent No. 6166182
GENERAL INFORMATION:
APPLICANT: Dark J. Bergsma
ATTORNEY/AGENT INFORMATION:
NAME: Usman Shabon
TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
FILE REFERENCE: GH-50020-1
CURRENT APPLICATION NUMBER: US/09/372.498
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: 08/832.399
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1342
TYPE: DNA
ORGANISM: HOMO SAPIENS

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US-09-372-498-1

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Query Match 7.3% Score 45.6; DB 4; Length 1342;
Best Local Similarity 49.2%; Pred. No. 0.004;
Matches 120; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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QY 111 TGGCGTGTGACGACGACGAGCGGCGACACAGCAGCCTGCAGCAACCCGCCGAATCTCT 170
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DB 926 TGGGTGTGCTCTCCACACAGGAGCTGACGGCTTCCAGGAAGATTTCGAAGAGAG 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 GCGAGACACCGCTGTACAGAGCGGGTGTATGACCGAGCTGAGTAAAGTCTCCG 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 866 AGGACACGCGCTGTAGAGAGAGAGTACAGCTGAGCTGAGTAAAGTGTGG 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 AGAAGGGAGAGATCATGATGACCGCGGAAGTAGACCTGCTCCAGTCGTCTGGGT 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 806 TCACCATGTAGAAGTAGTGTAAGAAATTGTACAGTGGCTCAGTCCAGCGTCATCAGTA 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 291 TGGCCGACGATGATCTCCGAATCTGTTGGCATCCAGCATCGGCCAATGTCAAA 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 746 CGTAGCAGTACATGAGCCTGCGGGCATGTAGCGCAGCAGATGATCATGACCA 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 351 CAAT 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 686 CGAT 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12

```

US-08-858-876A-1/C
Sequence 1, Application US/0885876A
Patent No. 6022856
GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
APPLICANT: Pascal CHALON
APPLICANT: Pascual FERRARA
APPLICANT: VITA NATALIO
TITLE OF INVENTION: Type 2 Neurotensin Receptor
FILE REFERENCE: (HNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858.876A
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 37..1266

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 1598.8 Seconds

(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agtctcctgcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Geneml:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
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8: gb_ov:*
9: gb_ov:*
10: gb_ov:*
11: gb_ov:*
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19: gb_ov:*
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37: gb_ov:*
38: gb_ov:*
39: gb_ov:*
40: gb_ov:*
41: gb_ov:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.4	99.6	826	9 BC011449	BC011449 Homo sapi
2	607	97.1	129676	9 AC079773	AC079773 Homo sapi
3	604.4	96.7	1832	9 AK094501	AK094501 Homo sapi
4	598.4	95.7	1890	6 AX136281	AX136281 Sequence
5	479.4	76.7	587	6 AX136698	AX136698 Sequence
6	412.4	66.0	444	6 AX150120	AX150120 Sequence
7	393	62.9	1524	6 AX358762	AX358762 Sequence
8	393	62.9	1524	6 AX362255	AX362255 Sequence
9	361.6	57.9	1362	6 AX319942	AX319942 Sequence
10	361.6	57.9	1362	6 AF034633	AF034633 Homo sapi
11	361.6	57.9	1362	6 AX319944	AX319944 Sequence
12	302	48.3	209885	2 AC124493	AC124493 Mus muscu
13	300.8	48.1	92874	2 AC112072	AC112072 Rattus no
14	230.6	36.9	1797	10 AB041649	AB041649 Mus muscu
15	140	22.4	190503	2 AC128363	AC128363 Rattus no
16	59.8	9.6	3917	10 AB017027	AB017027 Mus muscu
17	58.2	9.3	1254	6 E11480	E11480 CDNA encodl
18	58.2	9.3	1257	6 AX280911	AX280911 Sequence
19	58.2	9.3	4131	9 HSNURA	X70070 H. sapiens m
20	56.4	9.0	1140	6 E37240	E37240 Novel physl
21	56.4	9.0	1140	6 E63120	E63120 Peptide der
22	56.4	9.0	1148	9 AF100206	AF100206 Macaca mu
23	56.4	9.0	1583	9 HSU03642	U03642 Human G pro
24	56.4	9.0	1754	9 BC032688	BC032688 Homo sapi
25	56.4	9.0	1801	9 HSHG110RP	X89271 H. sapiens m
26	56.4	9.0	1872	6 AR107256	AR107256 Sequence
27	56.4	9.0	1872	6 AR194356	AR194356 Sequence
28	56.4	9.0	169216	2 AC090238	AC090238 Homo sapi
29	56.4	9.0	171744	9 AP001786	AP001786 Homo sapi
30	54.8	8.8	3248	9 AK097232	AK097232 Homo sapi
31	50	8.0	6379	1 RERAMO	D37875 Nocardia co
32	50	8.0	6379	6 E08269	E08269 gDNA of alk
33	50	8.0	6379	6 E10607	E10607 Alkenemoo
34	50	8.0	6379	6 E10980	E10980 Gene of alk
35	50	8.0	6379	6 I36963	I36963 Sequence 1
36	49.4	7.9	7218	6 I66494	I66494 Sequence 14
37	48.4	7.7	208050	1 AL646083	AL646083 Ralstonia
38	47.4	7.6	25362	1 SCF56	AL133424 Streptomy
39	47.4	7.6	99437	2 AC103419	AC103419 Rattus no
40	47.4	7.6	167929	2 AC128436	AC128436 Rattus no
41	47.2	7.6	1583	9 BC022501	BC022501 Homo sapi
42	47	7.5	35100	1 SC3A7	AL031155 Streptomy
43	47	7.5	115666	2 AC105744	AC105744 Oryza sat
44	46.2	7.4	125020	9 AF429315	AF429315 Homo sapi
45	46	7.4	289	6 AR162089	AR162089 Sequence

ALIGNMENTS

RESULT 1
BC011449
LOCUS BC011449 826 bp mRNA
DEFINITION Homo sapiens, clone IMAGE:4026092, mRNA.
ACCESSION BC011449
VERSION BC011449.1 GI:15277472
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 826)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadan@systemsbiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia Greene, Mark Ketterman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IMAGE Plate: 25 Row: n Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

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 /clone_id="NIH_MGC_20"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
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 Best Local Similarity 99.7% Pred. No. 1.3e-132
 Matches 623: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GCGCGTGTGCGGTGTGAGTGTGATGTACGCGGAGCGGCGCTGTCTGTGGTGGCGTGTG 120
DB 250 GCGCGTGTGCGGTGTGAGTGTGATGTACGCGGAGCGGCGCTGTCTGTGGTGGCGTGTG 309
QY 121 CAGGACAGGCGGCGAGCAGCACTGCAGCAGCAACCGCGCAACTGTGTGGAGAGCAGC 180
DB 310 CAGGACAGGCGGCGAGCAGCACTGCAGCAGCAACCGCGCAACTGTGTGGAGAGCAGC 369
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGGAGAG 240
DB 370 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAGGAGAG 429
QY 241 GAGGATCATGTACGCGCGGAGAGTACCTGCTCCAGTGTGCTTGGTGGCGGAGC 300
DB 430 GAGGATCATGTACGCGCGGAGAGTACCTGCTCCAGTGTGCTTGGTGGCGGAGC 489
QY 301 CATGATCTCTCGGAATCTGTGGTGGCATTCAGCATACGGCAATGTACAAACATAGCCC 360
DB 490 CATGATCTCTCGGAATCTGTGGTGGCATTCAGCATACGGCAATGTACAAACATAGCCC 549
QY 361 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 550 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
QY 421 TAAATGAATTAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCAGGAAT 480
DB 610 TAAATGAATTAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCAGGAAT 669
QY 481 GGTACCAATTTTTCAGTGTGAGTGTGAGCTTGTGACAGTCTTGTCCACAAAGAGAAATTT 540
DB 670 GGTACCAATTTTTCAGTGTGAGTGTGAGCTTGTGACAGTCTTGTCCACAAAGAGAAATTT 729

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QY 541 AACACTGTTTCAAAACCCGGGAGGAGTTGGCTGTGTAAAGAACCATTAATGCTTTAG 600
 DB 730 AACACTGTTTCAAAACCCGGGAGGAGTTGGCTGTGTAAAGAACCATTAATGCTTTAG 789
 QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
 DB 790 ACAGTGNAAAAAAAAAAAAAAAAAAAA 814

RESULT 2
 AC079773/c 129676 bp DNA linear PRI 09-JAN-2002
 LOCUS Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.
 DEFINITION AC079773
 ACCESSION AC079773.8 GI:15145561
 VERSION HTG.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074

REFERENCE
 AUTHORS Shah, N., Meyer, R., Boyer, E. and Dignan, G.
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17
 JOURNAL Unpublished (2001)
 REFERENCE
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 129676)
 Waterston, R.
 Direct Submission
 Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14488388.
 COMMENT
 Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 Summary Statistics
 Center project name: H_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis

MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanesse, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6**NEIGHBORING SEQUENCE INFORMATION:**

The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 6003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES**source**

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/chromosome="2"
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/clone_id="RP11-258B17"
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/note="match to EST BF804362 (NID:g12133351)"
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1387..3331
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repeat_region
2346..2370
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11961..11969
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19144..19250
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Query Match

97.1%: Score 607; DB 9; Length 129676;

Best Local Similarity 99.8%; Pred. No. 7, 5e-129; Indels 0; Gaps 0;

Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTGACAGAGACTGGCCGCGGACGCAAGAGCAACGGCGCTGCACAAACG 60
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Db 119919 AGTTCTCCTTGACAGAGACTGGCCGCGGACGCAAGAGCAACGGCGCTGCACAAACG 119960

[illegible]

Db	1770	AAATTTTCAGTGTGGACTTGAACAGTCTTTTGGCCACAGAACAGAAATTTAACT	1829
QY	547	GTTTCAACCCGGGGAGTGGCTGTGTTTAAAGAAAGACCATTAATGCTTTAGACAGTG	606
Db	1830	GTTTCAAAACCCGGGGAGTGGCTGTGTTTAAAGAAAGACCATTAATGCTTTAGACAGTG	1889
RESULT 5			
LOCUS	AX136698/c	587 bp	DNA
DEFINITION	Sequence 620 from Patent EP1067182.		linear
ACCESSION	AX136698		
VERSION	AX136698.1	GI:14273102	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Ota,T., Isoigai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: Ep 1067182-A 620 10-JAN-2001; Helix Research Institute (JP)		
FEATURES	Location/Qualifiers		
SOURCE	1..587		
BASE COUNT	117 a 162 c 140 g 162 t	6 others	
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Best Local Similarity	96.3%; Pred. No. 8.8e-100;		
Matches 498; Conservative	0; Mismatches 17; Indels 2; Gaps 1;		
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QY	150	CGAACACCCGCGGAACTGTCGAGAGACACCGTGTACAGAGCGGCTTGATGACCGAGC	209
Db	458	CGAACACCCGCGGAACTGTCGAGAGACACCGTGTACAGAGCGGCTTGATGACCGAGC	399
QY	210	TGAGGTACAAAACGCTTCCGAGAAAGGAGAGAGATCATGTACGCCCGGAAGTAGAGCC	269
Db	398	TGAGGTACAAAACGCTTCCGAGAAAGGAGAGAGATCATGTACGCCCGGAAGTAGAGCC	339
QY	270	TGTCACGTCGTCGTGGTGGTGGCGGAGCAGTATCCCGGAATCTGTTGGCATCC	329
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QY	330	AGCATACGGCCAAATGTCAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGACA	389
Db	278	AGCATACGGCCAAATGTCAACAATCAGCCCTGGGACAGACAGAGAGAGAGAGACA	219
QY	390	GAGAAAGAAAAACAGACGATGAGAACACAGTAATGATTAACCATTAATTTTAGC	449
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QY	450	CCCTCTGTTCTGTCTTACTGGCCAGGAAATGTACCAATTTTCAAGTGTGGACTTGAC	509
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QY	510	AGCTTTCTTTCCCAAGCAAGAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTTGGC	569
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QY	570	TGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG	606
Db	38	TGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG	2

AX150120/c
 LOCUS AX150120 444 bp DNA linear PAT 08-JUN-2001
 DEFINITION Sequence 95 from Patent WO0136685.
 ACCESSION AX150120
 VERSION AX150120.1 GI:14348148
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Kries, R.A., Moskal, J.R. and Yamamoto, H.
 TITLE Differential gene expression in cancer
 JOURNAL Patent: WO 0136685-A 95 25-MAY-2001;
 Nixis Neurotherapies, Inc. (US)
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 Best Local Similarity 99.5%; Pred. No. 2.1e-84;
 Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 204 CCGAGCTAGGTAGTAAAGAAAGTCTCCGAGAGGAGGAGATGATGTCAGCCGGAAGT 263
 DB 431 CCGAGCTAGGTAGTAAAGAAAGTCTCCGAGAGGAGGAGATGATGTCAGCCGGAAGT 372
 QY 264 AGGACCTGCTCCAGTCTGCTGGGTTGGCCGAGCCATGATCTCCGATCTGGTTGG 323
 DB 371 AGGACCTGCTCCAGTCTGCTGGGTTGGCCGAGCCATGATCTCCGATCTGGTTGG 312
 QY 324 GCATCCAGCATTCGGCCATGTCACAAATCAGCCCTGGGAGACAGACAGAGAGGA 383
 DB 311 GCATCCAGCATTCGGCCATGTCACAAATCAGCCCTGGGAGACAGACAGAGAGGA 252
 QY 384 GAGACAG 443
 DB 251 GAGACAG 192
 QY 444 TTAGGCCCCCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGA 503
 DB 191 TTAGGCCCCCTGTTCTGCTTACTGCGCAGAAATGTTACCAATTTTTCAGTGTGA 132
 QY 504 CTTGACAGCTCTTTTGGCCACAAAGAGAGAGATTTACACTGTTTCAACCCGGGGGA 563
 DB 131 CTTGACAGCTCTTTTGGCCACAAAGAGAGAGATTTACACTGTTTCAACCCGGGGGA 72
 QY 564 GTTGGCTGTGTTAAAG 618
 DB 71 GTTGGCTGTGTTAAAG 17
 RESULT 7
 AX358762 1524 bp DNA linear PAT 13-FEB-2002
 LOCUS AX358762
 DEFINITION Sequence 15 from Patent WO0193983.
 ACCESSION AX358762
 VERSION AX358762.1 GI:18675282
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Baker, R.P., Desnoyers, L., Geritsen, M.E., Goddard, A.,
 1 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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 JOURNAL Patent: WO 0193983-A 15 13-DEC-2001;

Genentech Inc. (US)
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 /db_xref="taxon:9606"
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 Query Match 62.9%; Score 393; DB 6; Length 1524;
 Best Local Similarity 100.0%; Pred. No. 6.9e-80;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGTTCTCTTCAG 60
 DB 1132 AGTTCTCTTCAG 1191
 QY 61 GCGGCTGTCGTTGTTGAGTGTGATGTCGTCATGTCGTCGTCGTCGTCGTCGTCGTCG 120
 DB 1192 GCGGCTGTCGTTGTTGAGTGTGATGTCGTCATGTCGTCGTCGTCGTCGTCGTCGTCG 1251
 QY 121 CAGCGACAGCGCGGAG 180
 DB 1252 CAGCGACAGCGCGGAG 1311
 QY 181 CGTGTACAG 240
 DB 1312 CGTGTACAG 1371
 QY 241 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 1372 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
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 DB 1432 CATGATCTCTCCAAATCTGTTGGGATCCAGATACGGCCAAATGTCACAAATCAGCCC 1491
 QY 361 TGGGACAGACAG 333
 DB 1492 TGGGACAGACAG 1524
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 AX362255 1524 bp DNA linear PAT 15-FEB-2002
 LOCUS AX362255
 DEFINITION Sequence 15 from Patent WO0208288.
 ACCESSION AX362255
 VERSION AX362255.1 GI:18694585
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Baker, R.P., Desnoyers, L., Geritsen, M.E., Goddard, A.,
 1 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;
 Genentech, Inc. (US)
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 /db_xref="taxon:9606"
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 Query Match 62.9%; Score 393; DB 6; Length 1524;
 Best Local Similarity 100.0%; Pred. No. 6.9e-80;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGTTCTCTTCAG 60
 DB 1132 AGTTCTCTTCAG 1191

tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 92874)
Worley, K. C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 92874)
Worley, K. C.
Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:20303189.

Center: Baylor College of Medicine
Genome Center
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GRJD
Center clone name: CH230-286021

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 32512 bases at least Q40
Consensus quality: 34515 bases at least Q30
Consensus quality: 35930 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draat_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1058 1157: gap of unknown length
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Matches 445; Conservative	0; Mismatches 138; Indels 12; Gaps 5;	
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DB	75494	TGAAGTAGGACAGCTGCTGTCTTCTCTCTGTGGTGGCATGTGTCGAGAGTCAGACGGCGACAGCA 75553
OY	141	GCACCTGCACGAAACCCGCGAACTGCTGCGAGACACCGTGTACAGACGGGGTTGA 200
DB	75554	GAACTGCGCAAAACCTTCGGAACCTGCTGAGAAAGACACGTTGTAGAGAGAGAGGTTGA 75613
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DB	75674	AGTAGGACTGTGTCAGATCATTTTGGGTTTGTGCGGCCATGATCCCTCGATCTGAT 75733
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DB	75794	AGAAAGAGGA-CGGGAGAAAGAAAGCATGGAACAAATAAATAAATAAACCCAT 75852
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DB	75853	AAATATTCAGCCCTTGTGTTCTGTGCTTACTGGCTGGGAAACGTTACCATCTTTTCAG 75912
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DEFINITION	AB041649	Mus musculus brain cDNA, clone MNcb-0671.
ACCESSION	AB041649.1	GI:7670499
VERSION		1
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SOURCE		Mus musculus
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE		1 (sites)
AUTHORS		Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and Hashimoto,K.
TITLE		Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method
JOURNAL		unpublished
REFERENCE		2. (bases 1 to 1797)
AUTHORS		Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.

TITLE Direct Submission
JOURNAL Submitted (13-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 (E-mail: khashi@nih.go.jp, URL: <http://www.nih.go.jp/yoken/genebank/>, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)
 URL: <http://www.nih.go.jp/yoken/genebank/>
COMMENT Lab Name: Sugano mouse brain mcb
 Lab host: TOP10
 Vector: pME185-FL3
 1st strand cDNA was primed with an oligo(dN) primer [ATGTCGCCCTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME185-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCCTCTTAAAGCTGCG]; 3' end primer [CGACCTGACCTCGAGACAA]).
 A part of this sequence is reported in A0035640.
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***, 69 unordered pieces.
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VERSION
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1 (bases 1 to 190503)
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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Galisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulik, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S.,
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Locado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
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Orgunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
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Scheerer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
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Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
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Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 190503)
Worley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GZCA
Center clone name: CH230-22808
Summary Statistics

Sequencing vector: Plasmid.
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 13119 bases at least Q40
Consensus quality: 13608 bases at least Q30
Consensus quality: 141839 bases at least Q20
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 69 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1001: contig of 1001 bp in length
1101: gap of unknown length
1102: contig of 1178 bp in length
2279: gap of unknown length
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3707: contig of 1247 bp in length
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* 113667 117113: contig of 3447 bp in length
* 117114 117214: gap of unknown length
* 117215 120342: contig of 3129 bp in length
* 120343 120442: gap of unknown length
```

Query Match 22.4%: Score 140; DB 2; Length 190503;
Best Local Similarity 71.0%: Pred. No. 1.5e-21;
Matches 233; Conservative 0; Mismatches 80; Indels 15; Gaps 3;

```
OY 34 GAAGAGCAAGCGGCGTGCACAAAGCGGCGTGTGCGTGTGAGTGCAGTGTACGGC 93
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169311 GAAGATGAGGGGCGTGTGTGCTGAGCTAGTGTCTTGTGAGACTGAAGTGTGAACG 169370

OY 94 CAGCGGCTTCTGTGTGTGCGGTGCTGCAGGACAGCGGCGACACAGCCTGCACGAA 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169371 CTGGTGTCTTCTGTGTGCTGCAGTGTGCAGAGTACGCCGACAGAGTACTGAGAGAA 169430

OY 154 CACCGCGGCAATGCTGCAGAGACACCGTGTACAGAGCGGTTGATGACCGAGCTGAG 213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 169431 CAGTCTCCCAACTGTTGATACATTTGTAGAGAGAGGGTTGACACCGAGCTGAG 169490
OY 214 GTAGAAAAAGCTCTCCGAGAGGGAGAGAGATCATGTAGCCCGGAAGTAGACTTCGT 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169491 GTAGAGAAAGATGTCAAGAGAGAGGGAGAGAGATCATATATATGC-----CTTGCT 169538

OY 274 CCAGTGTGCTGTGGGTTGGCCCGAGCCATGATCTCCGAATCTGTGGGATCCA--G 331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169539 CCAGTGTGTTGGGTTT-TCTTCAGCCGATGATCTGTGATCTGATTTGGCATCCAAACA 169597

OY 332 CAAACGGCCAATGTCACAAACATCAGCC 359
Db 169598 CACACAGCCAGTATCACCAATCAGAC 169625
```

Search completed: November 7, 2002, 13:31:03
Job time : 1917.05 secs

XX	10	606.6	97.1	1608	24	AAE524231	Human ovarian anti
XX	11	606.5	97.1	1953	21	AAE524200	Human secreted prot
XX	12	606.6	97.1	1956	22	AAE64188	Human secreted prot
XX	13	598.4	97.7	1890	22	AAE93845	Human cDNA encoding
XX	14	479.4	76.7	587	22	AAE94186	Primer specific fdd
XX	15	433.2	69.3	558	24	ABL79397	Human ovarian cancer
XX	16	412.4	66.0	444	22	AAH50766	Human tumour assoc
XX	17	395.4	63.3	409	24	ABL81262	Human ovarian cancer
XX	18	393	62.9	1524	24	ABL33543	CDNA encoding huma
XX	19	361.6	57.9	1362	24	ABT03279	Human ovarian carcinoma
XX	20	361.6	57.9	1362	24	ABL40347	Ovarian carcinoma
XX	21	361.6	57.9	2528	22	AAAD18690	Human G protein cou
XX	22	361	57.8	373	24	ABL78854	Human ovarian cancer
XX	23	353	56.5	390	24	ABL78854	Human ovarian cancer
XX	24	310.8	43.7	349	24	ABL79431	Human ovarian cancer
XX	25	207.8	33.2	381	24	ABL84848	Human ovarian cancer
XX	26	174.4	27.9	468	22	AAK54063	Human ovarian cancer
XX	27	171.2	27.4	201	24	ABL85916	Murine transport a
XX	28	58.2	9.3	1254	17	AAAT31127	Human ovarian cancer
XX	29	58.2	9.3	1257	23	ABT198007	Human neurotensin
XX	30	58.2	9.3	4149	23	AAST6503	Non-endothelial hum
XX	31	58	9.3	3609	22	AAK94581	DNA encoding novel
XX	32	56.4	9.0	1140	20	AAK83839	Human full-length
XX	33	56.4	9.0	1140	21	AAAI3593	G protein coupled
XX	34	56.4	9.0	1140	22	ABA02182	Human APJ G protei
XX	35	56.4	9.0	1143	21	AAA30623	Human G protein-cou
XX	36	56.4	9.0	1143	21	AAA30726	DNA encoding human
XX	37	56.4	9.0	1370	22	AAK94107	Human full-length
XX	38	56.4	9.0	1464	21	AAAI0298	DNA encoding human
XX	39	56.4	9.0	1583	24	AAK84189	Human cDNA differ
XX	40	56.4	9.0	1872	15	AAO66176	Seven transmembran
XX	41	56.4	9.0	1872	19	AAV18354	Human R20 seven tr
XX	42	56.4	9.0	1872	21	AAV91723	Human 7TM receptor
XX	43	56.4	9.0	1872	24	AAK54252	Human 7 transmembr
XX	44	56.4	9.0	10210	24	AAK518100	Human angiotensin
XX	45	56	9.0	3249	23	AAST6504	DNA encoding novel

PT detecting the presence of ovarian cancer in a patient, and in
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Claim 2, page 194, 197pp: English.

XX The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.

XX Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 99.8%; Score 624; DB 24; Length 625;

Best Local Similarity 100.0%; Pred. No. 4.6e-154; Mismatches 0; Indels 0; Gaps 0;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60
 DB 1 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60

QY 61 GGGCGTGTGGGTGGAGTGGCATGTACGGCGGAGCGGCTTCTCGTGGTTGGCGTCTG 120
 DB 61 GGGCGTGTGGGTGGAGTGGCATGTACGGCGGAGCGGCTTCTCGTGGTTGGCGTCTG 120

QY 121 CAGCGACAGCGCGGACAGACAGCTGACAGAACACCGCGGAACCTGCTGCAGAGACAC 180
 DB 121 CAGCGACAGCGCGGACAGACAGCTGACAGAACACCGCGGAACCTGCTGCAGAGACAC 180

QY 181 CGTGTACAGAGAGCGGGTGTGACCGAGCTGAGGTAGAAAAACGTCCTCGAGAGAGGAG 240
 DB 181 CGTGTACAGAGAGCGGGTGTGACCGAGCTGAGGTAGAAAAACGTCCTCGAGAGAGGAG 240

QY 241 GAGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTGGTGGTTGGCGGAGC 300
 DB 241 GAGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTGGTGGTTGGCGGAGC 300

QY 301 CATGATCTCTCCGAATCTGTTGGGACATCCAGCATACGCGCCAAATGTCAACAATCAAGCC 360
 DB 301 CATGATCTCTCCGAATCTGTTGGGACATCCAGCATACGCGCCAAATGTCAACAATCAAGCC 360

QY 361 TGGGACAGACAGCGAGAGGAGAGACAGAGAAAAAACAACAGATGAGACAGAC 420
 DB 361 TGGGACAGACAGCGAGAGGAGAGACAGAGAAAAAACAACAGATGAGACAGAC 420

QY 421 TAATGAATTAACCATTAATATTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 480
 DB 421 TAATGAATTAACCATTAATATTAGCCCTCTGTTCTGCTTACTGCGCAGGAAT 480

QY 481 GGATCAATTTTTCACTGTTGACCTTGACAGCTCTTTTGGCACAGCAAGAGAGAAATT 540
 DB 481 GGATCAATTTTTCACTGTTGACCTTGACAGCTCTTTTGGCACAGCAAGAGAAATT 540

QY 541 AACACGTTTCAACACCGGAGAGTGGCTGTAAAGAAAAACCATTAATAGCTTTAG 600
 DB 541 AACACGTTTCAACACCGGAGAGTGGCTGTAAAGAAAAACCATTAATAGCTTTAG 600

QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
 DB 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625

RESULT 2
 ABL40348
 ID ABL40348 standard; cDNA; 625 BP.
 XX ABL40348;
 AC
 XX 28-JUN-2002 (first entry)
 DT
 XX Ovarian carcinoma O1034C EST clone nucleotide sequence.
 DE
 XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW

KW expressed sequence tag; EST; ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOL/) STOLK J A.

XX (ALGA/) ALGATE P A.

XX (FLIN/) FLING S P.

XX XU J, Stolk JA, Algate PA, Fling SP;

XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

XX prevention and/or treatment of cancer, especially ovarian cancer

XX Claim 1a; page 125; 131pp: English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides

XX that may be utilised in cancer therapy, for example in a vaccine or

XX gene therapy. Polypeptides and polynucleotides of the invention are

XX useful for detecting a cancer in a patient, for stimulating and/or

XX expanding T-cells specific for a tumour protein, and for inhibiting the

XX development of a cancer in a patient. They are also useful for

XX stimulating an immune response in a patient, and for treating a cancer in

XX a patient and for determining the presence of a cancer in a patient.

XX The isolated polynucleotides of the invention are useful for their

XX ability to selectively form duplex molecules with complementary stretches

XX of the entire desired gene or gene fragments, and for designing and

XX preparing ribozyme molecules for inhibiting expression of tumour

XX polypeptides in tumour cells. Polypeptides and polynucleotides of the

XX invention are also useful in recombinant DNA molecules to direct

XX expression of a polypeptide in appropriate host cells. The current

XX sequence represents the ovarian carcinoma O1034C EST clone nucleotide

XX sequence.

XX Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

XX Query Match 99.8%; Score 624; DB 24; Length 625;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-154;

XX Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60

DB 1 AGTTCCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60

QY 61 GGGCGTGTGGGTGGAGTGGCATGTACGGCGGAGCGGCTTCTCGTGGTTGGCGTCTG 120

DB 61 GGGCGTGTGGGTGGAGTGGCATGTACGGCGGAGCGGCTTCTCGTGGTTGGCGTCTG 120

QY 121 CAGCGACAGCGCGGACAGACAGCTGACAGAACACCGCGGAACCTGCTGCAGAGACAC 180

DB 121 CAGCGACAGCGCGGACAGACAGCTGACAGAACACCGCGGAACCTGCTGCAGAGACAC 180

QY 181 CGTGTACAGAGAGCGGGTGTGACCGAGCTGAGGTAGAAAAACGTCCTCGAGAGAGGAG 240

DB 181 CGTGTACAGAGAGCGGGTGTGACCGAGCTGAGGTAGAAAAACGTCCTCGAGAGAGGAG 240

QY 241 GAGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTGGTGGTTGGCGGAGC 300

DB 241 GAGATCATGTACGCCCGGAAGTAGACCTGTCAGTGTGCTGGTGGTTGGCGGAGC 300

OY	301	CATGATCCCTCCGAAATGTGTTGGGCAATCCAGCATACGCGCAATGTCACAACAATCAGCC	360		
OY	301	CATGATCCCTCCGAAATGTGTTGGGCAATCCAGCATACGCGCAATGTCACAACAATCAGCC	360		
Db	301	CATGATCCCTCCGAAATGTGTTGGGCAATCCAGCATACGCGCAATGTCACAACAATCAGCC	360		
OY	361	TGGGCGAGACACGACGAGGAGAGACAGAGAAAACACAGCATGAGAACACAG	420		
Db	361	TGGGCGAGACACGACGAGGAGAGAGACAGAGAAAACACAGCATGAGAACACAG	420		
OY	421	TAAATGAATAAACCATTAATATTGCCCCCTGTCTGTCTGCTACTGGCCAGAAAT	480		
Db	421	TAAATGAATAAACCATTAATATTGCCCCCTGTCTGTCTGCTACTGGCCAGAAAT	480		
OY	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAGACAGAGAAATTT	540		
Db	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGGCACAGACAGAGAAATTT	540		
OY	541	AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAGACCATTAATGCTTTAG	600		
Db	541	AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAGACCATTAATGCTTTAG	600		
OY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625			
Db	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625			
RESULT 3					
ABL87898	ABL87898 standard; DNA; 625 BP.				
AC	ABL87898;				
DT	17-MAY-2002 (first entry)				
DE	Human ovarian cancer related DNA clone SEQ ID NO:10876.				
XX	Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.				
OS	Homo sapiens.				
PN	WO200192581-A2.				
XX	06-DEC-2001.				
PF	29-MAY-2001; 2001WO-US17756.				
PR	26-MAY-2000; 2000US-207484P.				
PA	(CORI-) CORIXA CORP.				
PI	Algate PA, Harlocker SL, Jones R;				
DR	WPI; 2002-122075/16.				
XX	Composition for therapy and diagnosis of ovarian cancer comprising				
PT	polypeptide of a ovarian tumor polypeptide, polynucleotide encoding				
PT	polypeptide, antibody specific to polypeptide or T cell expressing				
PI	polypeptide				
PS	Claim 1; SEQ ID 10876; 489pp; English.				
XX					
CC	The present invention describes a composition (I) comprising: carriers				
CC	and immunostimulants; and a polypeptide (II) of a ovarian tumour				
CC	polypeptide encoded by a polynucleotide (III) having a cDNA sequence				
CC	(SI) from the 10912 nucleotide sequences as given in ABL77023 to				
CC	AB67934, (III) encoding (II) having a sequence (S2), a T cell				
CC	population of (II), or antigen presenting cells that express (II).				
CC	(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to				
CC	(SI) can be used for detecting ovarian cancer in a patient's biological				
CC	sample preferably serum or ovarian tissue. The method comprises				
CC	contacting a biological sample from a patient with (IV), detecting the				
CC	amount of polynucleotide hybridising to (IV) and comparing the amount to				
CC	a predetermined cutoff value and thereby detecting ovarian cancer in the				

	CC	patient, where the amount of polynucleotide hybridizing to (IV) is
	CC	detected preferably by polymerase chain reaction (PCR). (II) comprising
	CC	(III) and/or (II) is useful for stimulating and/or expanding T cells
	CC	specific for an ovarian tumour protein comprising contacting T cells
	CC	with (III) or (II). (III) is useful in design and preparation of
	CC	ribozyme molecules for inhibiting expression of the tumour polypeptides
	CC	and proteins in tumour cells; and to isolate a full length gene from a
	CC	suitable library e.g., a tumour cDNA library using well known
	XX	techniques.
SQ	Sequence	625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;
Query Match	99.8%; Score 624; DB 24; Length 625;	
Best Local Similarity	100.0%; Pred. NO. 4.6e-154;	
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 AGTTCTCCTTGCAGAGACTGGCGCCGGGACGCGAAGAAGACAAGCGCGCTGCACAAACG 60	
Db	1 AGTTCTCCTTGAGAGACTGGCGCCGGGACCGGAAGAGCAACGGGCCCTGCACAAACG 60	
OY	61 GGCGCTGTGGGTGTGAGAGTCGATGTACGGCAGCGCTTCTGTGGTGGCGTGTG 120	
Db	61 GGCGCTGTGGGTGTGAGAGTCGATGTACGGCAGCGCTTCTGTGGTGGCGTGTG 120	
OY	121 CAGGACAGGGGGGACAGACACCTGACGAAACACC CGGCGAACTCTGTGSAGACAC 180	
Db	121 CAGCACAGGGGGGACAGACACCTGACGAAACACC CGGCGAACTCTGTGSAGACAC 180	
OY	181 CGTGACAGAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCCTCGAAGAGGGAG 240	
Db	181 CGTGACAGAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCCTCGAAGAGGGAG 240	
OY	241 GAGGATCATGTACGCCCGGAAGTAGACCTCGTCCAGTCGTGCTTGGTTTGGCCGACG 300	
Db	241 GAGGATCATGTACGCCCGGAAGTAGACCTCGTCCAGTCGTGCTTGGTTTGGCCGACG 300	
OY	301 CATGATCCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTACAAACAATGACGCC 360	
Db	301 CATGATCCTCCGAATCTGGTGGGATCCAGATACGCGCAATGTACAAACAATGACGCC 360	
OY	361 TGGGAGACAGACAGCAGAGGAGAGACAGAAAAGAAAACACAGCATGGAACACAG 420	
Db	361 TGGGAGACAGACAGCAGAGGAGAGACAGAAAAGAAAACACAGCATGGAACACAG 420	
OY	421 TAAATGAATAAACCATTAATATTATTAGCCCCCTGTCTGTGCTTACTGCGCAGAAAT 480	
Db	421 TAAATGAATAAACCATTAATATTATTAGCCCCCTGTCTGTGCTTACTGCGCAGAAAT 480	
OY	481 GSTACCAATTTTTCAGTGTGGACTTGACAGCTTTTGGCCACAAGCAGAGAAATT 540	
Db	481 GSTACCAATTTTTCAGTGTGGACTTGACAGCTTTTGGCCACAAGCAGAGAAATT 540	
OY	541 AACACTGTTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATAGCTTAG 600	
Db	541 AACACTGTTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATAGCTTAG 600	
OY	601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
RESULT 4		
ABT03284		
ID	ABT03284 standard; CDNA; 1897 BP.	
XX	ABT03284;	
AC		
XX		
DT	05-SEP-2002 (first entry)	
XX		
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.	
XX		
KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy; cytostatic; gene; ss.	

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XX OS Homo sapiens.
XX PN MO200239885-A2.
XX PD 23-MAY-2002.
XX PF 13-NOV-2001; 2001WO-US45395.
XX PR 14-NOV-2000; 2000US-0713550.
XX PR 03-APR-2001; 2001US-0825294.
XX PR 02-OCT-2001; 2001US-0970966.
XX PA (CORI-) CORIYA CORP.
XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX DR WPI; 2002-500186/53.
XX PT Novel ovarian cancer polypeptide and polynucleotide, useful for
XX PT detecting the presence of ovarian cancer in a patient, and in
XX PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX PT
XX PS Claim 2; Page 196; 197pp; English.
XX CC The present invention provides human ovarian cancer associated proteins
XX CC and coding sequences. The sequences can be used in the diagnosis and
XX CC treatment of ovarian cancers. The present sequence is a coding sequence
XX CC of the invention.
XX SO Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

Query Match          99.8%; Score 624; DB 24; Length 1897;
Best Local Similarity 99.8%; Pred. No. 7.4e-154;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGTCTCTCTTGAGAGAGAGCTGGCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 60
DB 1271 AGTTCTCCTTGAGAGAGAGCTGGCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 1330
OY 61 GGCGGCTGCGGTGGTGGAGTGGCGATGTACGCGGAGCGGCTTCTGTGGTGGCTGCTG 120
DB 1331 GGCGGCTGCGGTGGTGGAGTGGCGATGTACGCGGAGCGGCTTCTGTGGTGGCTGCTG 1390
OY 121 CAGCGACAGCGCGGAGCGAGCAGCAGCAGCAACCGCGCAAACTGCTGGAGAGACAC 180
DB 1391 CAGCGACAGCGCGGAGCGAGCAGCAGCAGCAACCGCGCAAACTGCTGGAGAGACAC 1450
OY 181 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAGCGTCTCGAGAGGGGAG 240
DB 1451 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAGCGTCTCGAGAGGGGAG 1510
OY 241 GAGGATCATGTACGCGCGGAGTAGGAGCTGCTCCAGTGTCTCTGGTGGTGGCGGACG 300
DB 1511 GAGGATCATGTACGCGCGGAGTAGGAGCTGCTCCAGTGTCTCTGGTGGTGGCGGACG 1570
OY 301 CATGATCTCTCGGAATCTGTTGGGATCCAGATACGGCAATGTACAAACATCAGGCC 360
DB 1571 CATGATCTCTCGGAATCTGTTGGGATCCAGATACGGCAATGTACAAACATCAGGCC 1630
OY 361 TGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1631 TGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
OY 421 TAAATGATTAATAAACCATTAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT 480
DB 1691 TAAATGATTAATAAACCATTAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT 1750
OY 481 GGATACCAATTTTTCAGTGTGGAGTGTGACAGCTTCTTTGGCACAAGCAAGAGAGAAATT 540
DB 1751 GGATACCAATTTTTCAGTGTGGAGTGTGACAGCTTCTTTGGCACAAGCAAGAGAGAAATT 1810

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OY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTAG 600
DB 1811 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGCATTAAATGCTTAG 1870
OY 601 ACAGTCNAAAAAAAAAAAAAAAAAAAA 625
DB 1871 ACAGTCNAAAAAAAAAAAAAAAAAAAA 1895

RESULT 5
ABL40352
ID ABL40352 standard; cDNA; 1897 BP.
AC ABL40352;
XX 28-JUN-2002 (first entry)
XX DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX KW ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 260..685
XX FT /*tag= a
XX FT /product= "Ovarian carcinoma protein O1034C/O591S"
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX DR P-PSDB; ABB09417.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX PT prevention and/or treatment of cancer, especially ovarian cancer.
XX PS Claim 1a; Page 127-128; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or
XX CC gene therapy. Polypeptides and polynucleotides of the invention are
XX CC useful for detecting a cancer in a patient, for stimulating and/or
XX CC expanding T-cells specific for a tumour protein, and for inhibiting the
XX CC development of a cancer in a patient. They are also useful for
XX CC stimulating an immune response in a patient, and for treating a cancer in
XX CC a patient and for determining the presence of a cancer in a patient.
XX CC The isolated polynucleotides of the invention are useful for their
XX CC ability to selectively form duplex molecules with complementary stretches
XX CC of the entire desired gene or gene fragments, and for designing and
XX CC preparing ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX CC invention are also useful in recombinant DNA molecules to direct
XX CC expression of a polypeptide in appropriate host cells. The current
XX CC sequence represents the ovarian carcinoma O1034C/O591S consensus
XX CC nucleotide sequence.

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ID	ABT03281	standard; CDNA; 1619 BP.
XX	AC	ABT03281;
XX	DT	05-SEP-2002 (first entry)
XX	DE	Human ovarian carcinoma associated coding sequence SPO ID NO: 211.
XX	KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX	OS	cytostatic; gene; ss.
XX	PN	Homo sapiens.
XX	PD	WO200239885-A2.
XX	PR	23-MAY-2002.
XX	PR	13-NOV-2001; 2001WO-US45395.
XX	PR	14-NOV-2000; 2000US-0713550.
XX	PR	03-APR-2001; 2001US-0825294.
XX	PA	02-OCT-2001; 2001US-0970966.
XX	PS	(CORI-) CORIXA CORP.
XX	PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX	DR	WPI; 2002-500186/53.
XX	PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
XX	PT	detecting the presence of ovarian cancer in a patient, and in
XX	PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX	PS	Claim 2; Page 195; 197pp; English.
XX	CC	The present invention provides human ovarian cancer associated proteins
XX	CC	and coding sequences. The sequences can be used in the diagnosis and
XX	CC	treatment of ovarian cancers. The present sequence is a coding sequence
XX	CC	of the invention.
XX	CC	Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
XX	CC	Query Match
XX	CC	Best Local Similarity 99.7%; Score 613; DB 24; Length 1619;
XX	CC	Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1.
QY	1	AGTTCCTTCGAGAGGAGCTGGCGCGGAGCGAGCAAGAGCAAGCGGCGCTGCACAAAGCG 60
DB	992	AGTTCTCCTTCGAGAGGAGCTGGCGCGGAGCGGAGCGAGCAAGAGCAAGCGGCGCTGCACAAAGCG 1051
OY	61	GGCGCTGTGGGTGTGAGAGTGGCATGTACGGCGAGCGCGCTTCTGTGGTGTGGCTGCTG 120
DB	1052	GGCGCTGTGGGTGTGAGAGTGGCATGTACGGCGAGCGCGCTTCTGTGGTGTGGCTGCTG 1111
OY	121	CAGGACAGAGGGCGGAGCAGCAGACC-TGCAGACACACCCCGGAAACCTCTCGAGGAGCA 179
DB	1112	CAGGACAGAGGGCGGAGCAGCAGACCCTTGCAGCAACACCCCGGAAACCTCTCGAGGAGCA 1171
OY	180	CGGTGTACAGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGCTCTCGAGAGAGGGA 239
DB	1172	CGGTGTACAGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGCTCTCGAGAGAGGGA 1231
OY	240	GGAGGATCATGTAGACCCCGGAAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 299
DB	1232	GGAGGATCATGTAGACCCCGGAAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 1291
OY	300	CCATGATCCTCCGAAATCTGGTTGGGATTCACACATACGGCCAAATGCAACAATACAGCC 359
DB	1292	CCATGATCCTCCGAAATCTGGTTGGGATTCACACATACGGCCAAATGCAACAATACAGCC 1351

Oy	360	CTGGCACAACACGACAGGAGAGACAGACAGAAAAACAGCATGAGAACACA	419
Db	1352	CTGGGCAACACGACAGAGAGAGACAGAGAAAAACACAGCATGAGAACACA	1411
Oy	420	GTAATGATAAATAAACCATAAATATTTAGCCCCCTGTGTTCTGTCTTACTGGCCAGGAAA	479
Db	1412	GTAATGATAAATAAACCATAAATATTTAGCCCCCTGTGTTCTGTCTTACTGGCCAGGAAA	1471
Oy	480	TGGTACCAATTTTTCAGTGTGGACTTGACACTTCTTTTGGCACAGCAAGAGAAAT	539
Db	1472	TGGTACCAATTTTTCAGTGTGGACTTGACACTTCTTTTGGCACAGCAAGAGAAAT	1531
Oy	540	TAACTCTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA	599
Db	1532	TAACTCTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA	1591
Oy	600	GACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1592	GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617	
RESULT 8			
ABL40345			
ID	ABL40345 standard; cDNA, 1619 BP.		
XX	ABL40345;		
XX	28-JUN-2002 (first entry)		
DE	Ovarian carcinoma sequence isolate 57887 extended cDNA.		
XX	Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;		
KW	ss.		
XX	Homo sapiens.		
XX	US2002004491-A1.		
FN	10-JAN-2002.		
PD	03-APR-2001; 2001US-0825294.		
XX	10-SEP-1999; 99US-0394374.		
PR	01-MAY-2000; 2000US-0561778.		
PR	15-AUG-2000; 2000US-0640173.		
PR	07-SEP-2000; 2000US-0656668.		
PR	14-NOV-2000; 2000US-0713550.		
XX	(XUJ/) XU J.		
PA	(SNOL/) STOLK J A.		
PA	(ALGA/) ALGATE P A.		
PA	(FLIN/) FLING S P.		
XX	XU J, Stolk JA, Algate PA, Fling SP;		
PI	WPI: 2002-171027/22.		
XX	Ovarian tumour polypeptide and polynucleotide useful in diagnosis, -		
PT	prevention and/or treatment of cancer, especially ovarian cancer		
XX	Claim 1a; Page 119-120; 131pp; English.		
PS	The invention relates to ovarian tumour polynucleotides and polypeptides		
XX	that may be utilised in cancer therapy, for example in a vaccine or		
CC	gene therapy. Polypeptides and polynucleotides of the invention are		
CC	useful for detecting a cancer in a patient, for stimulating and/or		
CC	expanding T-cells specific for a tumour protein, and for inhibiting the		
CC	development of a cancer in a patient. They are also useful for		
CC	stimulating an immune response in a patient, and for treating a cancer in		
CC	a patient and for determining the presence of a cancer in a patient.		
CC	The isolated polynucleotides of the invention are useful for their		
CC	ability to selectively form duplex molecules with complementary stretches		
CC	of the entire desired gene or gene fragments, and for designing and		

CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the extended cDNA sequence of ovarian carcinoma
 CC isolate 57887 given in record ABL48956.

XX Sequence 1619 BP: 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 98.1%; Score 613; DB 24; Length 1619;
 Best Local Similarity 99.7%; Pred. No. 5.4e-151;

Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGTTCTCTTCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGCGTGCACAAAGCG 60
 DB 992 AGTTCTCTTCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGCGTGCACAAAGCG 1051
 QY 61 GCGCGTGTGCGGTGGAGTGGCATGTAGCGGAGCGCGTCTCTGTTGGCTGCTG 120
 DB 1052 GCGCGTGTGCGGTGGAGTGGCATGTAGCGGAGCGCGTCTCTGTTGGCTGCTG 1111
 QY 121 CAGGACAGAGGCGGACAGCAGCACC-TGCACAGACACCGCGAACTGCTGGAGAGACA 179
 DB 1112 CAGGACAGAGGCGGACAGCAGCACC-TGCACAGACACCGCGAACTGCTGGAGAGACA 1171
 QY 180 CCGTGTACAGAGCGCGTGTATGACCGAGCTGAGTAGAAGAAACGTCTCCGAGAGGGGA 239
 DB 1172 CCGTGTACAGAGCGCGTGTATGACCGAGCTGAGTAGAAGAAACGTCTCCGAGAGGGGA 1231
 QY 240 GAGAGATCATGTAGCGCGCGGAGTAGAGACCTGTCACAGTGTGCTGGTGGCGCCGAG 299
 DB 1232 GAGAGATCATGTAGCGCGCGGAGTAGAGACCTGTCACAGTGTGCTGGTGGCGCCGAG 1291
 QY 300 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATAGCGCAATGTACAAACATCAGCC 359
 DB 1292 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATAGCGCAATGTACAAACATCAGCC 1351
 QY 360 CTGGGACAGACAGCAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAGACA 419
 DB 1352 CTGGGACAGACAGCAGAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAGACA 1411
 QY 420 GTAATGATTAACCAATTAATATTATTTAGCCCTCTGTCGTGGTCTACTGGCCAGAGAA 479
 DB 1412 GTAATGATTAACCAATTAATATTATTTAGCCCTCTGTCGTGGTCTACTGGCCAGAGAA 1471
 QY 480 TGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGCAGAGAGAAAT 539
 DB 1472 TGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGCAGAGAGAAAT 1531
 QY 540 TAAACAGTGTTCAAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 599
 DB 1532 TAAACAGTGTTCAAACCCGGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 1591
 QY 600 GACAGTGNAAAAAAGAAAAA 625
 DB 1592 GACAGTGNAAAAAAGAAAAA 1617

RESULT 9

ABLA0349

ID ABLA0349 standard; cDNA; 1619 BP.

XX ABLA0349;

DT 28-JUN-2002 (first entry)

XX Ovarian carcinoma O591s nucleotide sequence.

XX Ovarian cancer: cancer therapy; vaccine; gene therapy; tumour; cancer;

SS.

XX Homo sapiens.

XX

PN US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP;

DR WPI; 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PS prevention and/or treatment of cancer, especially ovarian cancer.

XX Claim 1a; Page 125-126; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The current
 CC sequence represents the ovarian carcinoma O591s nucleotide sequence.

XX Sequence 1619 BP: 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 98.1%; Score 613; DB 24; Length 1619;
 Best Local Similarity 99.7%; Pred. No. 5.4e-151;

Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGTTCTCTTCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGCGTGCACAAAGCG 60
 DB 992 AGTTCTCTTCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGCGTGCACAAAGCG 1051
 QY 61 GCGCGTGTGCGGTGGAGTGGCATGTAGCGGAGCGCTTCTGTTGGCTGCTG 120
 DB 1052 GCGCGTGTGCGGTGGAGTGGCATGTAGCGGAGCGCTTCTGTTGGCTGCTG 1111
 QY 121 CAGGACAGAGGCGGACAGCAGCACC-TGCACAGACACCGCGAACTGCTGCAGAGACA 179
 DB 1112 CAGGACAGAGGCGGACAGCAGCACC-TGCACAGACACCGCGAACTGCTGCAGAGACA 1171
 QY 180 CCGTGTACAGAGCGGTTATGACAGCTGAGTAGAAGAAAGCTCCGAGAGGGGA 239
 DB 1172 CCGTGTACAGAGCGGTTATGACAGCTGAGTAGAAGAAAGCTCCGAGAGGGGA 1231
 QY 240 GAGAGATCATGTAGCGCGCGGAGTAGAGACCTGTCAGTGTGCTGGTGGCGCCAG 299
 DB 1232 GAGAGATCATGTAGCGCGCGGAGTAGAGACCTGTCAGTGTGCTGGTGGCGCCAG 1291
 QY 300 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATAGCGCAATGTACAAACATCAGCC 359
 DB 1292 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATAGCGCAATGTACAAACATCAGCC 1351

PD 21-DEC-2000.
 XX 01-JUN-2000; 2000WO-US14973.
 XX 11-JUN-1999; 99US-0138630.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 DR WPI: 2001-071258/08.
 DR P-PSDB; AAB75518.
 XX
 PT Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 XX
 PS Claim 1; Page 443-444; 542pp; English.
 CC Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide
 CC sequences AAF64176 - AAF64224. The specification includes amino acid
 CC sequences AAB75555 - AAB75606 which represent fragments of the human
 CC secreted proteins, and protein sequences with which they share homology.
 CC The proteins and polynucleotides, their agonists and antagonists have
 CC activities dependent on the tissues and cells in which they are
 CC expressed, examples of these activities include, immunosuppressive;
 CC antirheumatic; antiproliferative; cytostatic; cardiant;
 CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
 CC virucide; fungicide; ophthalmological; and vulnerary. The proteins,
 CC polynucleotides, agonists and antagonists can be used to treat or detect
 CC or diagnose various diseases and disorders including, autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
 CC e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angioneurosis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin ageing due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities. Included in the invention are
 CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which
 CC are used in the isolation, identification and characterisation of the
 CC proteins of the invention.
 CC
 XX
 SO Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other:
 Query Match 97.1%; Score 606.6; DB 22; Length 1956;
 Best Local Similarity 99.7%; Pred. No. 2.8e149;
 Matches 606; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 301 CATGATCTCCGAGATCTGGTGGGATCCAGCATACGGCCAAATGTGCACAATCAGCCC 360
 |||||||
 DB 384 CATGATCTCCGAGATCTGGTGGGATCCAGCATACGGCCAAATGTGCACAATCAGCCC 325
 QY 361 TGGGCGAGACAGCAGCAGGAGGAGAGACAGAGAAAAAAGAAAAACAGCATGAGAACAG 420
 |||||||
 DB 324 TGGGCGAGACAGCAGGAGGAGGAGAGACAGAGAAAAAAGAAAAACAGCATGAGAACAG 265
 QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGCAAT 480
 |||||||
 DB 264 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAGCAAT 205
 QY 481 GGATACCAATTTTTCAGTGTGGACTGACAGCTCTCTTCCACAAGCAGAGAAATT 540
 |||||||
 DB 204 GGATACCAATTTTTCAGTGTGGACTGACAGCTCTCTTCCACAAGCAGAGAAATT 145
 QY 541 AACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
 |||||||
 DB 144 AACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 85
 QY 601 ACAAGTGA 608
 |||||||
 DB 84 ACAAGTGA 77
 RESULT 13
 AAF93845
 ID AAF93845 standard; CDNA; 1890 BP.
 XX
 XX AAF93845;
 AC 23-MAY-2001 (first entry)
 DT
 XX
 XX Human CDNA encoding a membrane or secretory protein clone PSEC0181.
 DE
 XX Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes; ss.
 RN
 XX Homo sapiens.
 OS
 XX
 PN EP1067182-A2.
 XX
 PD 10-JAN-2001.
 XX
 PE 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR WPI: 2001-093989/11.
 DR P-PSDB; AAB88418.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX
 PS Claim 1; SEQ ID 203; 609pp + CD ROM; English.
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary

Db 278 AGCATACGGCCATGTCACACATCAGCCCTGGCCAGACAGCAGAGAGAGACA 219
 QY 390 GAGAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATAAACCATTAATTTAGC 449
 CC |||||||
 Db 218 GAGAAAGAAAAACACAGCATGAGAAACACAGTAAATGAATAAACCATTAATTTAGC 159
 QY 450 CCCCTGTTCTGCTGCTTACTGGCCAGAAATGTGTACCAATTTTTCAGTGTGGACTTGC 509
 CC |||||||
 Db 158 CCCCTGTTCTGCTGCTTACTGGCCAGAAATGTGTACCAATTTTTCAGTGTGGACTTGC 99
 QY 510 ACCTCTTTTGGCCAGAGAGAGAAATTTTAACTGTTTCAAAACCCGGGAGTTGGC 569
 CC |||||||
 Db 98 ACCTCTTTTGGCCAGAGAGAGAAATTTTAACTGTTTCAAAACCCGGGAGTTGGC 39
 QY 570 TGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG 606
 CC |||||||
 Db 38 TGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG 2

RESULT 15

ABL79397
 ID ABL79397 standard; cDNA; 558 BP.

AC ABL79397;

XX 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:2375.

KM Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX Homo sapiens.

PN WO200192581-A2.

PD 06-DEC-2001.

PF 29-MAY-2001; 2001WO-US17756.

PR 26-MAY-2000; 2000US-207484P.

XX (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

DR WPI: 2002-122075/16.

XX Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

XX polypeptide

PS Claim 1; SEQ ID 2375; 489bp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
 CC (SI) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.

XX Sequence 558 BP; 147 A; 133 C; 166 G; 106 T; 6 other;

XX Query Match 69.3%; Score 433.2; DB 24; Length 558;

XX Best Local Similarity 95.6%; Pred. No. 5.9e-104;

Matches 539; Conservative 0; Mismatches 14; Indels 11; Gaps 9;

QY 1 AGTTCTCTTGCAGAGAGACTGGCCGGGACGCGGAAGAGACAGCGGCTGCACAAAGC 60
 CC |||||||
 Db 1 AGTTCTCTTGCAGAGAGACTGGCCGGGACGCGGAAGAGACAGCGGCTGCACAAAGC 60
 QY 61 GGGCTGTGGTGGTGGAGTGGCCATGTACGCCCAAGCGGCTGTGGTGGCGTGTG 120
 CC |||||||
 Db 61 GGGCTGTGGTGGTGGAGTGGCCATGTACGCC--AGCCTTCTGTGTGTGGTGGCTGTG 118
 QY 121 CAGCGACAGCGCGCAGCAGACAGCACTGCAAGAACACCCGCGAAGCTGTGCGAGAGAC 180
 CC |||||||
 Db 119 CAGCGACAGCGCGCA--ACAGCACTGCAAGAACACCCGCGAAGCTGTGCGAGAGAC 176
 QY 181 CGTGTACAGAGCGGGGTGTGATGACCGAGCTGAGGTGAGAAACGTCCTCGAAGAGGAG 240
 CC |||||||
 Db 177 CGTGTACAGAGCGGGGTGTGATGACCGAGCTGAGGTGAGAAACGTCCTCGAAGAGGAG 236
 QY 241 GAGGATCATGTAGC--CCCGAAGTAGGACCTGCTCAAGTGTGGTGGTGGCGGAG 299
 CC |||||||
 Db 237 GAGGATCATGTAGCCGCCGGAAGTAGGACCTGCTCAAGTGTGGTGGTGGCGGAG 296
 QY 300 CCATGA--TCCTCCGAATCTGTTGGGCAATCCAGCATACGCCAATGTACACAAATCAGC 358
 CC |||||||
 Db 297 CATTGATTCCTCGAATCTGTTGGGCAATCCAGCATACGCCAATGTACACAAATCAGC 356
 QY 359 CCTGGGACAGCAGCAGCAGC--AGGAGAGACACAGAAAGAAACACACAGCATGAGAC 417
 CC |||||||
 Db 357 CCTGGGACAGCAGCAGCAGCAGAGAGAGAGACAGAGAAAGAAACACACAGCATGAGAC 416
 QY 418 CAGTAAATGAATTAACCAATTAATATTTAGCCCTGTGCTGTGCTGTGCTGAGCAG 477
 CC |||||||
 Db 417 CAGTAAATGAAT--AAACCAATTAATATTTAG--CCCTGTGCTGTGCTGTGCTGAGCAG 474
 QY 478 AATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAGCAGAGAGAA 537
 CC |||||||
 Db 475 AATGTAC--ATTTTTCAGTGTGAGCTTTCAGCTTTCACCAAGCAGAGAG--A 532
 QY 538 TTTAACAAGTGTTCACCAACCGGGG 561
 CC |||||||
 Db 533 NTTAACAATGTTCACCAACCGGGG 556

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Job time : 135.06 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 ; Search time 1400.5 Seconds
(without alignments)
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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
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2	624	99.8	625	31 US-09-825-294-210	Sequence 210, App
3	624	99.8	625	33 US-09-867-701-10876	Sequence 10876, A
4	624	99.8	625	36 US-09-970-966-210	Sequence 210, App
5	624	99.8	625	42 US-10-212-677-210	Sequence 210, App
6	624	99.8	1897	1 PCT-US01-45395-214	Sequence 214, App
7	624	99.8	1897	31 US-09-825-294-214	Sequence 214, App
8	624	99.8	1897	36 US-09-970-966-214	Sequence 214, App
9	624	99.8	1897	42 US-10-212-677-214	Sequence 214, App
10	616.4	98.6	1867	1 PCT-US02-29964-16	Sequence 16, App1
11	613	98.1	1619	1 PCT-US01-45395-205	Sequence 205, App
12	613	98.1	1619	28 US-09-713-550-205	Sequence 205, App
13	613	98.1	1619	31 US-09-825-294-211	Sequence 205, App
14	613	98.1	1619	31 US-09-825-294-205	Sequence 205, App
15	613	98.1	1619	36 US-09-970-966-205	Sequence 205, App
16	613	98.1	1619	36 US-09-970-966-205	Sequence 205, App
17	613	98.1	1619	36 US-09-970-966-211	Sequence 205, App
18	613	98.1	1619	42 US-10-212-677-205	Sequence 205, App
19	613	98.1	1619	42 US-10-212-677-211	Sequence 211, App
20	612.8	98.0	1918	17 US-09-397-022-4454	Sequence 4454, Ap
21	612.8	98.0	1918	31 US-09-808-385-4454	Sequence 4454, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```

c 22 608 97.3 1714 17 US-09-359-922-11555 Sequence 11555, A
c 23 608 97.3 1714 17 US-09-359-922-11555 Sequence 11555, A
c 24 608 97.3 1714 34 US-09-919-002-11555 Sequence 11555, A
c 25 607 97.1 43729 70 US-60-261-974-9 Sequence 9, App1
c 26 606.6 97.1 1608 1 PCT-US01-18569-111 Sequence 111, App
c 27 606.6 97.1 1608 43 US-10-264-049-111 Sequence 111, App
c 28 606.6 97.1 1925 25 US-09-652-121-7293 Sequence 7293, Ap
c 29 606.6 97.1 1925 25 US-09-652-128-3375 Sequence 9375, Ap
c 30 606.6 97.1 1925 25 US-09-652-917-3346 Sequence 3346, Ap
c 31 606.6 97.1 1925 28 US-09-659-997-11085 Sequence 11085, A
c 32 606.6 97.1 1925 28 US-09-710-281-4458 Sequence 4458, Ap
c 33 606.6 97.1 1925 29 US-09-726-805-1608 Sequence 1608, Ap
c 34 606.6 97.1 1953 36 PCT-US00-09066-38 Sequence 38, App1
c 35 606.6 97.1 1953 36 US-09-950-083-1914 Sequence 1914, Ap
c 36 606.6 97.1 1953 40 US-10-105-299-2414 Sequence 2414, Ap
c 37 606.6 97.1 1956 1 PCT-US00-14973-23 Sequence 23, App1
c 38 606.6 97.1 1956 36 US-09-950-083-1915 Sequence 1915, Ap
c 39 606.6 97.1 1956 40 US-10-105-299-2415 Sequence 2415, Ap
c 40 605.4 96.9 1866 42 US-10-208-408-26 Sequence 26, App1
c 41 605.4 96.9 1866 73 US-60-295-262-26 Sequence 26, App1
c 42 605.4 96.9 1866 74 US-60-308-868-26 Sequence 3346, Ap
c 43 605.4 96.9 1917 17 US-09-371-168-7188 Sequence 7188, Ap
c 44 605.4 96.9 1917 25 US-09-644-873-9077 Sequence 9077, Ap
c 45 605.4 96.9 1917 25 US-09-652-109-9370 Sequence 9370, Ap
```

ALIGNMENTS

```

RESULT 1
PCT-US01-45395-210
: Sequence 210, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-210
```

```

Query Match          99.8%; Score 624; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGAGCAAGCGCGCTGCACAAAGCG 60
DB 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGAGCAAGCGCGCTGCACAAAGCG 60
QY 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGTACGGCGGCGCTTCTGCTGTGGCTGTG 120
DB 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGTACGGCGGCGCTTCTGCTGTGGCTGTG 120
QY 121 CAGCGACAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
DB 121 CAGCGACAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
QY 181 CGTGTACAGAGCGGGGTGTGATGACCGAGCTGAGTGAAGAAAAGTCTCGAGAGGGGAG 240
```

```

DB 181 CGTGTACAGAGCGGGGTGTGATGACCGAGCTGAGTGAAGAAAAGTCTCGAGAGGGGAG 240
QY 241 GAGGATCATGTACGCCCGGAGAGTAGAGCTGCTGCTGTGGTGGTGGCGGAGC 300
DB 241 GAGGATCATGTACGCCCGGAGAGTAGAGCTGCTGCTGTGGTGGTGGCGGAGC 300
QY 301 CATGATCCTCCGAAATGCTGTGGGATCCAGCATACGGCCATGTACAAATCAGGCC 360
DB 301 CATGATCCTCCGAAATGCTGTGGGATCCAGCATACGGCCATGTACAAATCAGGCC 360
QY 361 TGGGACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
DB 361 TGGGACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
QY 421 TAAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
DB 421 TAAATGATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 481 GGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
DB 481 GGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
QY 541 AACACTGTTTCAACCCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600
DB 541 AACACTGTTTCAACCCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600
QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
```

```

RESULT 2
US-09-825-294-210
: Sequence 210, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Filing, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.4845
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(625)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210
```

```

Query Match          99.8%; Score 624; DB 31; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGAGCAAGCGCGCTGCACAAAGCG 60
DB 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGAGCAAGCGCGCTGCACAAAGCG 60
QY 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGTACGGCGGCGCTTCTGCTGTGGCTGTG 120
DB 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGTACGGCGGCGCTTCTGCTGTGGCTGTG 120
QY 121 CAGCGACAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
DB 121 CAGCGACAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
```

OY	181	CGTGCACGAGCGGGTTGATGACCCAGCTGAGGTAGAAAAAGCTCCGAGAAAGGGAG	240
Db	181	CGTGCACGAGCGGGTTGATGACCCAGCTGAGGTAGAAAAAGCTCTCGAGAAAGGGAG	240
OY	241	GAGGATCATGTAGCCCGCGGAAGTAGACCTGTCAGCTGTGGTTTGGCCGAGC	300
Db	241	GAGGATCATGTAGCCCGCGGAAGTAGACCTGTCAGCTGTGGTTTGGCCGAGC	300
OY	301	CATGATCCTCCGAACTGTGGGCAATCCAGCATACGCCCAATGTCAACATCAAGCC	360
Db	301	CATGATCCTCCGAACTGTGGGCAATCCAGCATACGCCCAATGTCAACATCAAGCC	360
OY	361	TGGGCAGACAGCAGCAGGAGGGAGAGACAGAGAAAAAACAACAGCATAGAACACAG	420
Db	361	TGGGCAGACAGCAGCAGGAGGGAGAGACAGAGAAAAAACAACAGCATAGAACACAG	420
OY	421	TAAATGAAATAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTAATCTGCGCAGAAAT	480
Db	421	TAAATGAAATAAACCATTAATATTTAGCCCTCTGTTCTGTGCTTAATCTGCGCAGAAAT	480
OY	481	GGTACCAATTTTTCAGTGTGGACTTACAGCTCTTTTCCCAACAGCAGACAGAAATT	540
Db	481	GGTACCAATTTTTCAGTGTGGACTTACAGCTCTTTTCCCAACAGCAGACAGAAATT	540
OY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
OY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	

```

RESULT 3
US-09-867-701-10876
: Sequence 10876, Application US/09867701
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ For Windows Version 4.0
SEQ ID NO 10876
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 607
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

```

Query Match:	99.8%	Score 624	DB 33	Length 625
Best Local Similarity	100.0%	Pred. NC	5e-116	
Matches 625	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	AGTTCTCCTTTCACAAGGAGCTGCGCCGGAGCGCAGAACGCGCGTGCACAAGAAGCG	60
Db	1	AGTTCTCCTTTCACAAGGAGCTGCGCCGGAGCGCAGAACGCGCGTGCACAAGAAGCG <td>60</td>	60
QY	61	GGCCTGCGGTGTGGAGTGCATGACGCGGAGCGCTTCGTAAGTGTGGCGTCTG	120
Db	61	GGCCTGCGGTGTGGAGTGCATGACGCGGAGCGCTTCGTAAGTGTGGCGTCTG	120
QY	121	CAGGACAGGCGGACACACACACTTGCACGACACCCCGCGGAATCTGCTGCAGGACAC	180
Db	121	CAGGACAGGCGGACACACACACTTGCACGACACCCCGCGGAATCTGCTGCAGGACAC	180

OY	181	CGTGCACAGGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGTCGCGAAGGGGAG	240
Db	181	CGTGCACAGGAGCGGGTGTGATGACCGAGCTAGGTAGAAAAACGTCGCGAAGGGGAG	240
OY	241	GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTTGGGTTTGGCCGAGC	300
Db	241	GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTTGGGTTTGGCCGAGC	300
OY	301	CATGATCTCCGAATCTGTTGGGCAATCCAGCATACGGCCCAATGTCAACAAATCAACC	360
Db	301	CATGATCTCCGAATCTGTTGGGCAATCCAGCATACGGCCCAATGTCAACAAATCAACC	360
OY	361	TGGGCAGACAGCAGCAGGAGGAGAGACAGACAGAAAAAAGAAAAACACACATAGAACACAG	420
Db	361	TGGGCAGACAGCAGGAGGAGGAGAGACAGACAGAAAAAAGAAAAACACACATAGAACACAG	420
OY	421	TAAATGATTAATAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCCACGAAAT	480
Db	421	TAAATGATTAATAACCATTAATATTTAGCCCTCTGTTCTGTGCTTACTGCCACGAAAT	480
OY	481	GGTACCAATTTTTCAGTGTGACCTTGACACACTCTTTTGGCCACACAGACAGGAAAT	540
Db	481	GGTACCAATTTTTCAGTGTGACCTTGACACACTCTTTTGGCCACACAGACAGGAAAT	540
OY	541	AACACTGTTCAAAACCCGGGGAGCTTGCTGTGTTAAAGAAAGCACTTAATAGCTTTAG	600
Db	541	AACACTGTTCAAAACCCGGGGAGCTTGCTGTGTTAAAGAAAGCACTTAATAGCTTTAG	600
OY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	

```

RESULT 4
US-09-970-966-210
: Sequence 210, Application US/099709366
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesh, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C6
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
US-09-970-966-210

```

Query Match	99.8%	Score 624	DB 36	Length 625
Best Local Similarity	100.0%	Pred. NO.	5e-116	
Matches 625	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	AGTTCTCCTTTCAGAGGACCTGGCCCGGAGCCGCAAGGAGGGGCTGCACAAAGC	60
QY	1	AGTTCTCCTTTCAGAGGACCTGGCCCGGAGCCGCAAGGAGGGGCTGCACAAAGC <td>60</td>	60
Db	1	AGTTCTCCTTTCAGAGGACCTGGCCCGGAGCCGCAAGGAGGGGCTGCACAAAGC	60
QY	61	GGCCGTGTCGGTGGTGGAGTGGCATGTAGCGCGAGGCGCTCTCTGTTGGTGGCTCTG	120
Db	61	GGCCGTGTCGGTGGTGGAGTGGCATGTAGCGCGAGGCGCTCTCTGTTGGTGGCTCTG	120
QY	121	CAGCGACAGGCGGACGACACACCTGACAAACACCGCGGAAACTGCTGGAGGACAC	180
Db	121	CAGCGACAGGCGGAGGACGACACACCTGACAAACACCGCGGAAACTGCTGGAGGACAC	180

```
OY 181 CGGTACAGAGACGGGTTGATGACCGAGCTAGAGTAAAGAAAGCTCTCCGAGAGGGAG 240
DB 181 CCGTACAGAGACGGGTTGATGACCGAGCTAGAGTAAAGAAAGCTCTCCGAGAGGGAG 240
OY 241 GAGGATCATGTACGCGCGGAGTAGAGCTGCTCAGTGTGCTGGTGGTGGCCGACG 300
DB 241 GAGGATCATGTACGCGCGGAGTAGAGCTGCTCAGTGTGCTGGTGGTGGCCGACG 300
OY 301 CATGATCTCCGAATCTGCTGGGATCCAGATACGGCAATGTCCACAATCAGCCC 360
DB 301 CATGATCTCCGAATCTGCTGGGATCCAGATACGGCAATGTCCACAATCAGCCC 360
OY 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 421 TAAATGAATAAACATTAATATTAGCCCTCTGCTGTGCTTACTGCGCAGGAAT 480
DB 421 TAAATGAATAAACATTAATATTAGCCCTCTGCTGTGCTTACTGCGCAGGAAT 480
OY 481 GGTACCAATTTTTCAGTGTGAGCTTGTGACAGCTTCTTTTGCACAGAGAGAGATTT 540
DB 481 GGTACCAATTTTTCAGTGTGAGCTTGTGACAGCTTCTTTTGCACAGAGAGATTT 540
OY 541 AACACGTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
DB 541 AACACGTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
OY 601 ACAGTGNMAAAAAAAAAAAAAA 625
DB 601 ACAGTGNMAAAAAAAAAAAAAA 625
```

RESULT 5

```
US-10-212-677-210
; Sequence 210, Application us/10212677
; GENERAL INFORMATION:
; APPLICANT: Chemault, Ruth A.
; APPLICANT: Xu, Jlangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-210
```

```
Query Match 99.8%; Score 624; DB 42; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGTTCTCTTTCAGAGAGATGCGCGCGGAGCGGAAGAGACAGCGGCGCTGCACAAAGG 60
DB 1 AGTTCTCTTTCAGAGAGATGCGCGCGGAGCGGAAGAGACAGCGGCGCTGCACAAAGG 60
OY 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
OY 121 CAGGACAGAGCGGACAGACAGCAGCAGTGCAGCAACCCGCGAATCTGCTGCGAGGACAC 180
```

```
DB 121 CAGGACAGAGCGGACAGACAGCAGCAGTGCAGCAACCCGCGAATCTGCTGCGAGGACAC 180
OY 181 CCGTACAGAGACGGGTTGATGACCGAGCTAGAGTAAAGAAAGCTCTCCGAGAGGGAG 240
DB 181 CCGTACAGAGACGGGTTGATGACCGAGCTAGAGTAAAGAAAGCTCTCCGAGAGGGAG 240
OY 241 GAGGATCATGTACGCGCGGAGTAGAGCTGCTCAGTGTGCTGGTGGTGGCCGACG 300
DB 241 GAGGATCATGTACGCGCGGAGTAGAGCTGCTCAGTGTGCTGGTGGTGGCCGACG 300
OY 301 CATGATCTCCGAATCTGCTGGGATCCAGATACGGCAATGTCCACAATCAGCCC 360
DB 301 CATGATCTCCGAATCTGCTGGGATCCAGATACGGCAATGTCCACAATCAGCCC 360
OY 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 421 TAAATGAATAAACATTAATATTAGCCCTCTGCTGTGCTTACTGCGCAGGAAT 480
DB 421 TAAATGAATAAACATTAATATTAGCCCTCTGCTGTGCTTACTGCGCAGGAAT 480
OY 481 GGTACCAATTTTTCAGTGTGAGCTTGTGACAGCTTCTTTTGCACAGAGAGAGATTT 540
DB 481 GGTACCAATTTTTCAGTGTGAGCTTGTGACAGCTTCTTTTGCACAGAGAGATTT 540
OY 541 AACACGTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
DB 541 AACACGTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
OY 601 ACAGTGNMAAAAAAAAAAAAAA 625
DB 601 ACAGTGNMAAAAAAAAAAAAAA 625
```

RESULT 6

```
PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214
```

```
Query Match 99.8%; Score 624; DB 1; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 AGTTCTCTTTCAGAGAGATGCGCGCGGAGCGGAAGAGACAGCGGCGCTGCACAAAGG 60
DB 1271 AGTTCTCTTTCAGAGAGATGCGCGCGGAGCGGAAGAGACAGCGGCGCTGCACAAAGG 1330
OY 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1331 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1390
OY 121 CAGGACAGAGCGGACAGACAGCAGCAGTGCAGCAACCCGCGAATCTGCTGCGAGGACAC 180
```

```
Db 1391 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTCTGCGAGAGACAC 1450
Qy 181 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 240
Db 1451 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 1510
Qy 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACATGCTGTGGTTGGCCGAGC 300
Db 1511 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACATGCTGTGGTTGGCCGAGC 1570
Qy 301 CATGATCTCCGAAATCTGTTGGGATTCACAGCATACGCGCAATGTCACAAATCAGCC 360
Db 1571 CATGATCTCCGAAATCTGTTGGGATTCACAGCATACGCGCAATGTCACAAATCAGCC 1630
Qy 361 TGGGACAGACAGAGCAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
Db 1631 TGGGACAGACAGAGCAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 1690
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTTGCTTCTACTGCGCAGAAAT 480
Db 1691 TAAATGAATAAACATTAATATTTAGCCCTCTGTTGCTTCTACTGCGCAGAAAT 1750
Qy 481 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATTT 540
Db 1751 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATTT 1810
Qy 541 AACACTGTTTCAAAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
Db 1811 AACACTGTTTCAAAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 1870
Qy 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
Db 1871 ACAGTGNAAAAAAAAAAAAAAAAAAAA 1895
```

```
RESULT 7
US-09-825-294-214
; Sequence 214, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
```

```
Query Match 99.8%; Score 624; DB 31; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGTTTCCTTGCAGAGACTGGCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 60
Db 1271 AGTTTCCTTGCAGAGACTGGCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 1330
Qy 61 GCGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCTGTGCTG 120
Db 1331 GCGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCTGTGCTG 1390
Qy 121 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTGCTGCGAGGACAC 180
```

```
Db 1391 CACGACAGGCGGCGACAGACCTGACGAACACCCGCCGAAACTCTGCGAGAGACAC 1450
Qy 181 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 240
Db 1451 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAG 1510
Qy 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACATGCTGTGGTTGGCCGAGC 300
Db 1511 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACATGCTGTGGTTGGCCGAGC 1570
Qy 301 CATGATCTCCGAAATCTGTTGGGATTCACAGCATACGCGCAATGTCACAAATCAGCC 360
Db 1571 CATGATCTCCGAAATCTGTTGGGATTCACAGCATACGCGCAATGTCACAAATCAGCC 1630
Qy 361 TGGGACAGACAGAGCAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 420
Db 1631 TGGGACAGACAGAGCAGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACAG 1690
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTTGCTTCTACTGCGCAGAAAT 480
Db 1691 TAAATGAATAAACATTAATATTTAGCCCTCTGTTGCTTCTACTGCGCAGAAAT 1750
Qy 481 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATTT 540
Db 1751 GGTACCAATTTTCAAGTGTGAGCTTGACAGCTTCTTTGGCACAAGCAGAGAAATTT 1810
Qy 541 AACACTGTTTCAAAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
Db 1811 AACACTGTTTCAAAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 1870
Qy 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
Db 1871 ACAGTGNAAAAAAAAAAAAAAAAAAAA 1895
```

```
RESULT 8
US-09-970-966-214
; Sequence 214, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stoik, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970.966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-214
```

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Query Match 99.8%; Score 624; DB 36; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGTTTCCTTGCAGAGACTGGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGCG 60
Db 1271 AGTTTCCTTGCAGAGACTGGCGCGGAGCGGAGAGCAAGCGGCGCTGCACAAAGCG 1330
Qy 61 GCGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCTGTGCTG 120
Db 1331 GCGCGTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCTGTGCTG 1390
Qy 121 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTGCTGCGAGGACAC 180
Db 1391 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTGCTGCGAGGACAC 1450
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OY	181	CGTTCACGAGCGGGTTGATGTGACCCAGCTGAGGTGAAGAAAAGCTCCGAGAAAGGGAG	240
Db	1451	CGTGTACAGGAGCGGGTTGATGTGACCCAGCTGAGGTGAAGAAAAGCTCCGAGAAAGGGAG	1510
OY	241	GAGGATCATGTACGCCCGGGAAGTAGGACCTCGTCAGTCTGGTCTTGGGTTTGGCCGAGC	300
Db	1511	GAGGATCATGTACGCCCGGGAAGTAGGACCTCGTCAGTCTGGTCTTGGGTTTGGCCGAGC	1570
OY	301	CATGATCCTCCGAATCTGTTGGGCAATCCAGCATTCGGCCAAATGTGCACAAATATCAGCC	360
Db	1571	CATGATCCTCCGAATCTGTTGGGCAATCCAGCATTCAGGCGCAATGTGCACAAATATCAGCC	1630
OY	361	TGGGCGACACGAGCAGAGGAGGAGACACAGAAAAAGAAAACACAGCATGAGAACACAG	420
Db	1631	TGGGCGACACGAGCAGAGGAGGAGAGACAGAAAAAGAAAACACAGCATGAGAACACAG	1690
OY	421	TAAATGAATTAACCATTAATTTTAGCCCTCTGTCTGTGCTTACTGGCCAGAGAAAT	480
Db	1691	TAAATGAATTAACCATTAATTTTAGCCCTCTGTCTGTGCTTACTGGCCAGAGAAAT	1750
OY	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTCTTTGGCCACAAGCAAGAGACATTT	540
Db	1751	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTCTTTGGCCACAAGCAAGAGACATTT	1810
OY	541	AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG	600
Db	1811	AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG	1870
OY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1871	ACAGTGNAAAAAAAAAAAAAAAAAAAA 1895	

```

RESULT 9
US-10-212-677-214
: Sequence 214, Application US/10121677
: GENERAL INFORMATION:
: APPLICANT: Chenaull, Ruth A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C7
: CURRENT APPLICATION NUMBER: US/10/212,677
: CURRENT FILING DATE: 2002-08-02
: NUMBER OF SEQ ID NOS: 288
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
:
US-10-212-677-214

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	Query Match	Similarity	99.8%	Score 624	DB 42	Length 1897
	Best Local	Similarity	99.8%	Pred. No. 6	3-116	
	Matches	624	Conservative	0	Mismatches	1
					Indels	0
					Gaps	0
QY	1	AGTTCTCCTTGGAGAGGACTGGCGCCGGGACGCCAAGACAAACGGCGCTGCAACAAAGC	60			
Db	1271	AGTTCTCCTTGGAGAGGACTGGCGCCGGGACGCCAAGACAAACGGCGCTGCAACAAAGC	1330			
QY	61	GGCGCTGTGCGTGTGGAGTGGCGCATGTACGGCGGACGGCGCTTCTGTGGTGGCTGTGG	120			
Db	1331	GGCGCTGTGCGTGTGGAGTGGCGCATGTACGGCGGACGGCGCTTCTGTGGTGGCTGTGG	1390			
QY	121	CAGCAGACAGGGGGGACAGCAGCAGCTGGACAGCAACCCGGCGCAAACTGGTGGAGGACAC	180			
Db	1391	CAGCAGACAGGGGGGACAGCAGCAGCTGGACAGCAACCCGGCGCAAACTGGTGGAGGACAC	1450			
QY	181	CCTGTACAGGAGCGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTTCTCCGAGAGGGGAG	240			

Db	1451	CGTGACAGGAGCGGGTTGATGACCGAGCTGAGAGTAGAAAAAGTCTCGAGAAAGGGAG	1511
QY	241	GAGGATCATGTGAGCCCGGGAAAGTAGAGACCTCTGTCACAGTGTGCTTGCGTTGGCTTGCCGCGACG	300
Db	1511	GAGATCATGTAGCCCGGGAAAGTAGAGACCTCTGTCACAGTGTGCTTGCGTTGGCTTGCCGCGACG	1570
QY	301	CATGATCCTCCGAATCTGTTTGGGCATCCAGCATACGGCCATGTCACAAACATCAGCC	360
Db	1571	CATGATCCTCCGAATCTGTTTGGGCATCCAGCATACGGCCATGTCACAAACATCAGCC	1630
QY	361	TGGGCACAGACAGCAGAGGAGGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAG	420
Db	1631	TGGGCACAGACAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAG	1690
QY	421	TAAATGAAATAAACCATAAATATTAAGCCCCCTCTGTGCTTACGTGGCAGGAAT	480
Db	1691	TAAATGAAATAAACCATAAATATTAAGCCCCCTCTGTGCTTACGTGGCAGGAAT	1750
QY	481	GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTCTCTTTGGCACAAGCAGAGAAATTT	540
Db	1751	GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTCTCTTTGGCACAAGCAGAGAAATTT	1810
QY	541	AACACTGTTTCAAAACCCGGGGAGATTGGCTGTCTTAACAAAGACCATTAAATGCTTTAG	600
Db	1811	AACACTGTTTCAAAACCCGGGGAGATTGGCTGTCTTAACAAAGACCATTAAATGCTTTAG	1870
QY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1871	ACAGTGNAAAAAAAAAAAAAAAAAAAA 1895	

```

10 RESULT 10
11 PCT-US02-29964-16
12 Sequence 16, Application PC/TUS0229964
13 GENERAL INFORMATION:
14 APPLICANT: Tang, Y. Tom
15 APPLICANT: Ren, Felyan
16 APPLICANT: Zhang, Jie
17 APPLICANT: Zhao, Qing A.
18 APPLICANT: Wang, Jian-Rui
19 APPLICANT: Xue, Aidong J.
20 APPLICANT: Wang, Dunrui
21 APPLICANT: Ghosh, Malabika
22 APPLICANT: Asundi, Vinod
23 APPLICANT: Wehrman, Tom
24 APPLICANT: Zhou, Ping
25 APPLICANT: Goodrich, Ryle W.
26 APPLICANT: Wang, Gezhi
27 APPLICANT: Haley-Vicente, Dana
28 APPLICANT: Drmanac, Radoje T
29 TITLE OF INVENTION: Novel Nucleic Acids and
30 TITLE OF INVENTION: Polypeptides
31 FILE REFERENCE: 809ACIP PCT
32 CURRENT APPLICATION NUMBER: PCT/US02/29964
33 CURRENT FILING DATE: 2002-09-19
34 PRIOR APPLICATION NUMBER: US 60/323,739
35 PRIOR FILING DATE: 2001-09-19
36 PRIOR APPLICATION NUMBER: US 09/488,725
37 PRIOR FILING DATE: 2000-01-21
38 PRIOR APPLICATION NUMBER: US 09/552,317
39 PRIOR FILING DATE: 2000-04-25
40 PRIOR APPLICATION NUMBER: PCT/US00/35017
41 PRIOR FILING DATE: 2000-12-22
42 PRIOR APPLICATION NUMBER: US 09/491,404
43 PRIOR FILING DATE: 2000-01-25
44 PRIOR APPLICATION NUMBER: PCT/US01/02623
45 PRIOR FILING DATE: 2001-01-25
46 PRIOR APPLICATION NUMBER: US 09/496,914
47 PRIOR FILING DATE: 2000-02-03
48 PRIOR APPLICATION NUMBER: US 09/560,875
49 PRIOR FILING DATE: 2000-04-27
50 PRIOR APPLICATION NUMBER: PCT/US01/03800
51 PRIOR FILING DATE: 2001-02-05

```



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; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-211

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Query Match          98.1%; Score 613; DB 1; Length 1619;
Best Local Similarity 99.7%; Pred. No. 1e-113;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1 AGTTCTCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60
DB 992 AGTTCTCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 1051
QY 61 GCGCTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1052 GCGCTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGCGCGGACAGCAGCACC-TGCACGAAACACCCCGGAAACTCTGCGAGAGACA 179
DB 1112 CAGCGACAGCGCGGACAGCAGCACC-TGCACGAAACACCCCGGAAACTCTGCGAGAGACA 1171
QY 180 CCGTGTACAGAGCGGGGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 239
DB 1172 CCGTGTACAGAGCGGGGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1231
QY 240 GGAGGATCATGTACGCGCCGGAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 299
DB 1232 GGAGGATCATGTACGCGCCGGAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTCCAGCAATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTCCAGCAATCAGCC 1351
QY 360 CTGGGACAGACAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 1352 CTGGGACAGACAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGT 479
DB 1412 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGT 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 539
DB 1472 TGGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
QY 600 GACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 1592 GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617

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RESULT 13
US-09-713-550-205
; Sequence 205, Application US/09713550
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09-713, 550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205

```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-713-550-205

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```

Query Match          98.1%; Score 613; DB 28; Length 1619;
Best Local Similarity 99.7%; Pred. No. 1e-113;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

QY 1 AGTTCTCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60
DB 992 AGTTCTCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 1051
QY 61 GCGCTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1052 GCGCTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGCGCGGACAGCAGCACC-TGCACGAAACACCCCGGAAACTCTGCGAGAGACA 179
DB 1112 CAGCGACAGCGCGGACAGCAGCACC-TGCACGAAACACCCCGGAAACTCTGCGAGAGACA 1171
QY 180 CCGTGTACAGAGCGGGGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 239
DB 1172 CCGTGTACAGAGCGGGGTGATGACCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1231
QY 240 GGAGGATCATGTACGCGCCGGAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 299
DB 1232 GGAGGATCATGTACGCGCCGGAAGTAGAGACTGTCCAGTGTGCTTGGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTCCAGCAATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTGGGATCCAGCATACGGCCCAATGTCCAGCAATCAGCC 1351
QY 360 CTGGGACAGACAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 1352 CTGGGACAGACAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 479
DB 1412 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 539
DB 1472 TGGTACCAATTTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
QY 600 GACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 1592 GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617

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RESULT 14
US-09-825-294-205
; Sequence 205, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619

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272

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 17.4612 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agtctctctgcagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 193892 segs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_MA_New:*
1: /cgn2_6/pdata1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/pdata1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/pdata1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/pdata1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/pdata1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/pdata1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/pdata1/pna/US10_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #	Match	Length	DB	ID	Description
1	393	62.9	1524	6	US-10-230-437-15		Sequence 15, Appl
2	46	7.4	2196	6	US-10-270-333-38		Sequence 38, Appl
3	46	7.4	6472	6	US-10-270-333-37		Sequence 37, Appl
4	45	7.2	667	7	US-60-416-172-67		Sequence 67, Appl
5	38.6	6.2	1032	1	PCT-US02-12342-1		Sequence 2, Appl
6	38.6	6.2	1149	1	PCT-US02-12342-2		Sequence 1, Appl
7	38.6	6.2	1376	1	PCT-US02-12342-4		Sequence 4, Appl
8	38	6.1	1251	6	US-10-270-333-98		Sequence 98, Appl
9	38	6.1	9268	6	US-10-270-333-97		Sequence 97, Appl
10	37.4	6.0	5927	6	US-10-270-333-115		Sequence 115, Appl
11	36.4	5.8	990	6	US-10-270-333-116		Sequence 116, Appl
12	36.2	5.8	852	6	US-10-267-255-36		Sequence 36, Appl
13	36.2	5.8	53500	6	US-10-267-255-76		Sequence 76, Appl
14	35.8	5.7	1285	1	PCT-US02-32094-2		Sequence 2, Appl
15	35.8	5.7	1285	6	US-10-265-872-2		Sequence 11, Appl
16	34.4	5.5	1248	6	US-10-272-983-11		Sequence 11, Appl
17	33.8	5.4	3829	6	US-10-240-425-1329		Sequence 35, Appl
18	33.6	5.4	828	6	US-10-267-255-35		Sequence 11576, A
19	33.4	5.3	515	5	US-09-513-999C-11576		Sequence 97, Appl
20	33.4	5.3	1696	6	US-10-240-965-97		Sequence 193, Appl
21	33.2	5.3	15825	6	US-10-270-333-193		Sequence 111, Appl
22	33.2	5.3	135259	6	US-10-240-485-111		Sequence 1585, Appl
23	33.2	5.3	23889	6	US-10-240-425-1585		Sequence 255, Appl
24	33	5.3	23683	6	US-10-240-965-256		Sequence 176, Appl
25	32.8	5.2	246	5	US-09-513-999C-14062		Sequence 14062, A
26	32.8	5.2	246	5	US-09-513-999C-14062		Sequence 14062, A

27	32.8	5.2	473	5	US-09-513-999C-14061	Sequence 14061, A
28	32.8	5.2	1024	6	US-10-270-377-1	Sequence 1, Appl
29	32.8	5.2	1201	6	US-10-240-425-334	Sequence 334, Appl
30	32.8	5.2	1242	7	US-60-417-298-5	Sequence 5, Appl
31	32.8	5.2	1772	5	US-09-674-988A-3	Sequence 3, Appl
32	32.6	5.2	1926	6	US-10-194-046-3	Sequence 3, Appl
33	32.4	5.2	3096	1	PCT-US02-06147-9	Sequence 9, Appl
34	32.4	5.2	3949	1	PCT-US02-06147-7	Sequence 7, Appl
35	32.2	5.2	415	5	US-09-513-999C-1158	Sequence 1158, Appl
36	32	5.1	1335	6	US-10-282-958-3	Sequence 3, Appl
37	32	5.1	2689	6	US-10-282-958-1	Sequence 18015, A
38	31.8	5.1	308	5	US-09-513-999C-18015	Sequence 553, Appl
39	31.8	5.1	831	6	US-10-272-490-3	Sequence 30, Appl
40	31.8	5.1	2739	6	US-10-264-237-553	Sequence 1277, Appl
41	31.6	5.1	2080	6	US-10-257-022-30	Sequence 207, Appl
42	31.6	5.1	2158	6	US-10-264-237-1227	Sequence 207, Appl
43	31.6	5.1	2845	6	US-10-131-813A-207	Sequence 207, Appl
44	31.6	5.1	2845	6	US-10-131-819A-207	Sequence 207, Appl
45	31.6	5.1	2845	6	US-10-131-823A-207	Sequence 207, Appl

ALIGNMENTS

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William T.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C94
CURRENT FILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 62.9%; Score 393; DB 6; Length 1524;

Best Local Similarity 100.0%; Pred. No. 4.3e-96;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 AGTTTCCTTGGAGAGACTGGCCGGGACCGAAGACAGACGGCCCTGCACAAAGCG 60
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Db 1132 AGTTTCCTTGGAGAGACTGGCCGGGACCGAAGACAGACGGCCCTGCACAAAGCG 1191
OY 61 GGCCTGTGCTGTGAGTGGCATGTATGCGGACGCGCTTCTGCTGTGGCTGCTG 120
    |||
Db 1192 GGCCTGTGCTGTGAGTGGCATGTATGCGGACGCGCTTCTGCTGTGGCTGCTG 1251
OY 121 GAGCGACAGCGGCGACACAGCACTGACGAAACCCCGGAAATGCTGCGAGAGAC 180
    |||
Db 1252 GAGCGACAGCGGCGACACAGCACTGACGAAACCCCGGAAATGCTGCGAGAGAC 1311
OY 181 CGTGTACAGAGCGGGTTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAG 240
    |||
Db 1312 CGTGTACAGAGCGGGTTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAG 1371
OY 241 GAGGATCATGTATGCGCGGAGTAGGACCTGCTCCAGTGTGCTGCTGCTGCGCCAGC 300
    |||
Db 1372 GAGGATCATGTATGCGCGGAGTAGGACCTGCTCCAGTGTGCTGCTGCTGCGCCAGC 1431
OY 301 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360
    |||
Db 1432 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 1491
OY 361 TGGGACAGACGAGGAGGAGAGACAGACA 393
    |||
Db 1492 TGGGACAGACGAGGAGGAGAGAGACAGACA 1524

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RESULT 2 US-10-270-333-38/c

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; Sequence 38, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: THEREOF AS INSECTICIDAL TARGETS
; CURRENT APPLICATION NUMBER: US/10/270,333
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-38

```

Query Match 7.4%; Score 46; DB 6; Length 2196;
Best Local Similarity 52.6%; Pred. No. 0.0025;
Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```

OY 63 CGCTGTGCTGTGAGTGGCATATGACGCGGCTTCTGCTGTGCTGCTGCTGCA 122
    |||
Db 1888 CGCTGTGCTGTGAGTGGCATATGACGCGGCTTCTGCTGTGCTGCTGCTGCT 1829
OY 123 GCGACAGCGGCGACACAGCACTGACGAAACCCCGGAAATGCTGCGAGACCG 182
    |||
Db 1828 GCGCGACAGCACTGACGAAACCCCGGAAATGCTGCGAGACATCAGCT 1769
OY 183 TGTACAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAGGA 242
    |||
Db 1768 TGTACAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAGGA 1709

```

```

OY 243 GGATCATGTA 252
    |||
Db 1708 GGTTGTAGTA 1699

```

RESULT 3 US-10-270-333-37/c

```

; Sequence 37, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: THEREOF AS INSECTICIDAL TARGETS
; CURRENT APPLICATION NUMBER: US/10/270,333
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 37
; LENGTH: 6472
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-37

```

Query Match 7.4%; Score 46; DB 6; Length 6472;
Best Local Similarity 52.6%; Pred. No. 0.0041;
Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```

OY 63 CGCTGTGCTGTGAGTGGCATATGACGCGGCTTCTGCTGTGCTGCTGCTGCA 122
    |||
Db 5164 CGCTGTGCTGTGAGTGGCATATGACGCGGCTTCTGCTGTGCTGCTGCTGCT 5105
OY 123 GCGACAGCGGCGACACAGCACTGACGAAACCCCGGAAATGCTGCGAGACCG 182
    |||
Db 5104 GCGCGACAGCACTGACGAAACCCCGGAAATGCTGCGAGACATCAGCT 5045
OY 183 TGTACAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAGGA 242
    |||
Db 5044 TGTACAGAGCGGCTGTGATGACGAGCTGAGTGAAGAAAACGTTCCGAGAGGGAGGA 4985
OY 243 GGATCATGTA 252
    |||
Db 4984 GGTTGTAGTA 4975

```

RESULT 4 US-60-416-172-67

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; Sequence 67, Application US/60416172
; GENERAL INFORMATION:
; APPLICANT: Chang, Hwai Wen
; APPLICANT: Felts, Katherine A.
; APPLICANT: Warren, Amy J.
; APPLICANT: Cooper, Judith R.
; TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors
; FILE REFERENCE: 216019-153
; CURRENT APPLICATION NUMBER: US/60/416,172
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Gallus gallus
; NAME/KEY: misc_feature
; FEATURE:
; OTHER INFORMATION: Human extended sequence for VOG3_71
US-60-416-172-67

```

```
Query Match 7.2%; Score 45; DB 7; Length 667;
Best Local Similarity 46.8%; Pred. No. 0.0026;
Matches 141; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 46 GGGCTCCACAAAGCGGGCGCTGTGGGTGGAGTGGCATGTACGGCAGAGCGCTTCTC 105
DB 187 GCGGACAGACACGACGACGACGCTTACGGGGTGGCCGGGCGCTTCCAGCGGGA 246
QY 106 GTGGTGGCGTGTGTCAGACAGCGCGGACAGACACCTGACAGAACCCCGCGAAA 165
DB 247 GTGGGTGGAGTGGCGGCGGCGCTTGGCGCAGACCCGCGCGCGGTGACAGCCGGA 306
QY 166 CTCTCTCGAGAGACCTGTACAGAGAGCGGGTATATGACCGATGGAGTGAAGAAACGT 225
DB 307 GTACGAGGACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
QY 226 CTCCGAGAAAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 285
DB 367 CTGTGAGACAGAGACAGACAGATGATGATGATGATGATGATGATGATGATGATGAT 426
QY 286 GGGTTTGGCCGACCATGATCTCCGATCTGTTGGGATCCAGCATAGCCCAATGT 345
DB 427 GGGTGAAGAGACACCGCGCCCTGAGGACCTGACAGGAGCCGACAGCGCTGCT 486
QY 346 C 346
DB 487 C 487

RESULT 5
PCT-US02-12342-2/C
; Sequence 2, Application PC/TUS0212342
; GENERAL INFORMATION:
; APPLICANT: Chu, Peter
; APPLICANT: Jlang, Yingping
; APPLICANT: Li, Congfen
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Pardo, Jorge
; APPLICANT: Spencer, Colin
; APPLICANT: Zhao, Haoran
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310PC
; CURRENT APPLICATION NUMBER: PCT/US02/12342
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/284,763
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 09/971,228
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mutant #1, C-terminally truncated variant of
; OTHER INFORMATION: human endothelial differentiation G-protein
; OTHER INFORMATION: coupled receptor (GPCR) 1 (EDG1)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1031)
; OTHER INFORMATION: mutant #1 human EDG1
PCT-US02-12342-2

Query Match 6.2%; Score 38.6; DB 1; Length 1032;
Best Local Similarity 63.4%; Pred. No. 0.17;
Matches 59; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 121 CAGCGACAGCGCGGACGACGACCTGACGACAGCCCGGAAACTGCTGCGAGACAC 180
DB 996 CCGGCACTTGCAGACGACGATGATCCGATGAGAGCCCGGACGATCTCTTGTGTGAC 937
QY 181 CGTGTACAGAGCGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 213
DB 936 AGTGTAAATGATGGGTGTGTCGCGGAGTGTGAG 904

RESULT 6
PCT-US02-12342-1/C
; Sequence 1, Application PC/TUS0212342
; GENERAL INFORMATION:
; APPLICANT: Chu, Peter
; APPLICANT: Jlang, Yingping
; APPLICANT: Li, Congfen
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Pardo, Jorge
; APPLICANT: Spencer, Colin
; APPLICANT: Zhao, Haoran
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310PC
; CURRENT APPLICATION NUMBER: PCT/US02/12342
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/284,763
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 09/971,228
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: wild-type human endothelial differentiation
; OTHER INFORMATION: G-protein coupled receptor (GPCR) 1 (EDG1)
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION: wild type human EDG1
PCT-US02-12342-1

Query Match 6.2%; Score 38.6; DB 1; Length 1149;
Best Local Similarity 63.4%; Pred. No. 0.17;
Matches 59; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 121 CAGCGACAGCGCGGACGACGACCTGACGACAGCCCGGAAACTGCTGCGAGACAC 180
DB 996 CCGGCACTTGCAGACGACGATGATCCGATGAGAGCCCGGACGATCTCTTGTGTGAC 937
QY 181 CGTGTACAGAGCGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 213
DB 936 AGTGTAAATGATGGGTGTGTCGCGGAGTGTGAG 904

RESULT 7
PCT-US02-12342-4/C
; Sequence 4, Application PC/TUS0212342
; GENERAL INFORMATION:
; APPLICANT: Chu, Peter
; APPLICANT: Jlang, Yingping
; APPLICANT: Li, Congfen
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Esteban
; APPLICANT: Pardo, Jorge
; APPLICANT: Spencer, Colin
; APPLICANT: Zhao, Haoran
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310PC
; CURRENT APPLICATION NUMBER: PCT/US02/12342
; CURRENT FILING DATE: 2002-08-26
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;; PRIOR APPLICATION NUMBER: US 60/284,763
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: US 09/971,228
;; PRIOR FILING DATE: 2001-10-03
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 1376
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: mutant #3, C-terminally truncated variant of
;; OTHER INFORMATION: human endothelial differentiation G-protein
;; OTHER INFORMATION: coupled receptor (GPCR) 1 (EDG1)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (338)..(1375)
;; OTHER INFORMATION: mutant #3 human EDG1
PCT-US02-12342-4

Query Match
Best Local Similarity 6.2%; Score 38.6; DB 1; Length 1376;
Matches 59; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 121 CAGGACAGGCGGCGACACACCTGACAGAACCCCGGAAACTGCTGCGAGACAC 180
Db 1333 CGGCGACTTCCACAGACATGATCCGATGAAGCCCGGACGATCTGTTGTCAG 1274
QY 181 CGTGTACAGGAGCGGCTGTGACCCGAGCTGAG 213
Db 1273 AGTGTAAATGATGGGGTGGTGGTCCGAGATTGAG 1241

RESULT 8
US-10-270-333-98/c
; Sequence 98, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-98

Query Match
Best Local Similarity 6.1%; Score 38; DB 6; Length 1251;
Matches 59; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 124 CGACGAGGCGGCGACACCTGACAGAACCCCGGAAACTGCTGCGAGACACCGT 183
Db 1221 CGAATAGCGGCGACAGACACCTTCTTGAAGCGCTGCGGAAACACCTTGTGAATGAT 1162
QY 184 GTACAGAGCGGCTGTGATGACGAGACCTGAGTAG 217
Db 1161 GTAGAGATGGGCTTCCACCATGAGACGTAGCGTAG 1128

RESULT 9
US-10-270-333-97/c

;; Sequence 97, Application US/10270333
;; GENERAL INFORMATION:
;; APPLICANT: Cravchik, Anibal
;; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
;; FILE REFERENCE: CL000733CON
;; CURRENT APPLICATION NUMBER: US/10/270,333
;; CURRENT FILING DATE: 2002-10-15
;; PRIOR APPLICATION NUMBER: 60/168,677
;; PRIOR FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: 60/175,691
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/191,638
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 198
;; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 9268
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-97

Query Match
Best Local Similarity 6.1%; Score 38; DB 6; Length 9268;
Matches 59; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 124 CGACGAGGCGGCGACACACCTGACAGAACCCCGGAAACTGCTGCGAGACACCGT 183
Db 8238 CGAATAGCGGCGACAGACACCTTCTTGAAGCGCTGCGGAAACACCTTGTGAATGAT 8179
QY 184 GTACAGAGCGGCTGTGATGACCCGAGCTGAGTAG 217
Db 8178 GTAGAGATGGGCTTCCACCATGAGCTAGCGTAG 8145

RESULT 10
US-10-270-333-115
; Sequence 115, Application US/10270333
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 5927
; TYPE: DNA
; ORGANISM: Drosophila
US-10-270-333-115

Query Match
Best Local Similarity 6.0%; Score 37.4; DB 6; Length 5927;
Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 142 CACCTGCAGAACACCCCGGAAACTGCTGCGAGACACCTGTAAGAGCGGCTTGTAT 201
Db 1371 CACCTTGTGAAGGCGCTTCCGAAATCTCGGAGAGGAGCGCTAGACAGCGGATGAT 1430
QY 202 GACCGAGCTGAGGTAGAAAACGCTCCGAGAGGAGGAGAGATCAATGACCCGGA 261
Db 1431 ACAGAGCTGCTGTAGGCGAAGATCTGGGCGGTACCTGAGATCACTTGTGAGGAT 1490

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 ; Search time 837.306 Seconds
(without alignments)
12088.985 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625
Sequence: 1 agtctctcttcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_esta:
2: em_estnu:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_estc:
9: gb_estl:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vit:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	622.4	99.6	702	14	BQ006545	BQ006545 UI-H-E11-
C 2	621.4	99.4	627	13	BM669397	BM669397 UI-E-DW1-
C 3	610.4	97.7	696	13	BM547680	BM547680 AGENCOURT
C 4	603.4	96.5	678	9	AT936826	AT936826 wp69h10.x
C 5	601.2	96.2	616	9	AT990500	AT990500 ws40d07.x
C 6	601.2	96.2	649	10	AM590950	AM590950 hg51e12.x

Result No.	Score	Query Match	Length	DB	ID	Description
C 7	600.8	96.1	696	12	BF439382	BF439382 nab63q06.
C 8	599.4	95.9	690	10	AM149665	AM149665 xf40h05.x
C 9	583.8	93.4	645	12	BF432379	BF432379 nac53g11.
C 10	548.4	87.7	551	12	BE858216	BE858216 791907.x
C 11	538.4	86.1	540	12	BF939693	BF939693 nac80b12.
C 12	537	85.9	537	12	BF594242	BF594242 7n10d03.x
C 13	532.8	85.2	538	13	BM667957	BM667957 UI-E-DW0-
C 14	531.2	85.0	537	9	AT101876	AT101876 ov32e04.x
C 15	525.8	84.1	561	10	AM150789	AM150789 x939c02.x
C 16	524.4	83.9	527	10	AM338938	AM338938 hac8h04.x
C 17	523.8	83.8	359	9	AT859538	AT859538 wml3c03.x
C 18	512.4	82.0	515	9	AT133688	AT133688 qx86g11.x
C 19	495.6	79.3	676	10	BE385990	BE385990 601276636
C 20	494.2	79.1	500	10	AM075558	AM075558 w12h08.x
C 21	485.4	77.7	640	10	AM148557	AM148557 x888f11.x
C 22	472.6	75.6	480	9	AT423162	AT423162 t13c12.x
C 23	472	75.5	510	12	BF726459	BF726459 by06h03.y
C 24	466	74.6	475	9	AT1363261	AT1363261 qy56f02.x
C 25	451.8	72.3	456	9	AT1765236	AT1765236 w12h08.x
C 26	451.6	72.3	843	12	BF125134	BF125134 601762356
C 27	445.4	71.3	591	9	AT884666	AT884666 w183d07.x
C 28	444.4	71.1	463	9	AT1202043	AT1202043 q143d04.x
C 29	443	70.9	452	9	AT1391683	AT1391683 qy93f04.x
C 30	443	70.9	454	10	AM191974	AM191974 x178a02.x
C 31	443	70.9	814	9	AL567376	AL567376 AL567376
C 32	440.6	70.5	578	9	AT1742092	AT1742092 w938h03.x
C 33	439.4	70.3	759	12	BF126050	BF126050 601762888
C 34	433.2	69.3	558	9	AA173383	AA173383 zp04h05.s
C 35	427.4	68.4	432	10	AM087372	AM087372 x019d02.x
C 36	427.4	68.4	499	10	AM075549	AM075549 xb22e05.x
C 37	424	67.8	452	9	AA626797	AA626797 ad09h07.s
C 38	424	67.8	467	9	AT150931	AT150931 qb53c04.x
C 39	401.4	64.2	420	9	AT1566797	AT1566797 tn23g08.x
C 40	401	64.2	412	9	AA084249	AA084249 zn17f05.s
C 41	398.6	63.8	564	14	BM687629	BM687629 UI-E-CRO-
C 42	396	63.4	396	9	AA613995	AA613995 n086c08.s
C 43	395.4	63.3	409	9	AA419229	AA419229 zv35a11.s
C 44	390	62.4	396	9	AT499630	AT499630 t003b07.x
C 45	390	62.4	534	10	BE350014	BE350014 hc07g12.x

ALIGNMENTS

RESULT 1
LOCUS BQ006545/C 702 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-E11-aza-n-21-0-UI.s1 NCL_CGAP_E11 Homo sapiens cDNA clone
IMAGE:5846228 3', mRNA sequence.
ACCESSION BQ006545
VERSION BQ006545.1 GI:19731445
KEYWORDS EST.

ORGANISM human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 702)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercenude

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLA-yes.

FEATURES
source location/Qualifiers
1..702

```

/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone_id="NCL-GAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker. Site_1: EcoR I; Site_2: Not I; NCL-GAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGCGAC.
TAG_Lib=UI-H-E11
TAG_Tissue=chondrosarcoma
TAG_SEQ=ACACTTGAC"
BASE COUNT 137 a 200 c 163 g 202 t
ORIGIN

```

```

Query Match 99.6% Score 622.4; DB 14; Length 702;
Best Local Similarity 99.7%; Pred. No. 1.1e-102;
Matches 623; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCTGCACAAAGCG 60
DB 625 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCTGCACAAAGCG 566
OY 61 GCGCTGTGCTGTGAGAGTGGCATGTACGCGCAGCGCTTCTGCTGGTGGCTGCTG 120
DB 565 GCGCTGTGCTGTGAGAGTGGCATGTACGCGCAGCGCTTCTGCTGGTGGCTGCTG 506
OY 121 CAGGCACAGGGGGGAGCAGCAGCAGCAGCAACCCGCGCAACTGCTGGAGAGAC 180
DB 505 CAGGCACAGGGGGGAGCAGCAGCAGCAGCAACCCGCGCAACTGCTGGAGAGAC 446
OY 181 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCCGAGAGGGAG 240
DB 445 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCCGAGAGGGAG 386
OY 241 GAGGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGTGGCGGAGC 300
DB 385 GAGGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGTGGCGGAGC 326
OY 301 CATGATCCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCACAAATCAGCCC 360
DB 325 CATGATCCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCACAAATCAGCCC 266
OY 361 TGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
DB 265 TGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 206
OY 421 TAAATGAATAAACCATTAATATTAGCCCTCTGTCTGTGCTTACCTGGCCAGAGAA 480
DB 205 TAAATGAATAAACCATTAATATTAGCCCTCTGTCTGTGCTTACCTGGCCAGAGAA 146
OY 481 GGTACCAATTTTTCAGTGTGTGACCTGCTTTTGCACAAAGAGAGAGATTT 540
DB 145 GGTACCAATTTTTCAGTGTGTGACCTGCTTTTGCACAAAGAGAGAGATTT 86
OY 541 AACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
DB 85 AACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 26
OY 601 ACAGTGNAAAAAAAAAAAAAA 625
||||| ||||||| |||||||

```

```

DB 25 ACAGTGTAAAAAAAAAAAAAAA 1

RESULT 2
LOCUS BM669397/c 627 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-DWI-shd-c-11-0-UI-s1 UI-E-DWI Homo sapiens cDNA clone
ACCESSION BM669397
VERSION UI-E-DWI-shd-c-11-0-UI 3', mRNA sequence.
KEYWORDS BM669397.1 GI:18979294
SOURCE EST.
ORGANISM human.
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iuiiue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1..627
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone_id="UI-E-DWI-shd-c-11-0-UI"
/clone_lib="UI-E-DWI"
/tissue_type="lens"
/dev_stage="adult"
/notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker. Site_1: EcoR I; Site_2: Not I; UI-E-DWI is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATGACGCA. This library was created for the program. Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_Lib=UI-E-DWI
TAG_Tissue=human lens
TAG_SEQ=CGATTACGCA"
BASE COUNT 118 a 180 c 145 g 183 t 1 others
ORIGIN

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Query Match 99.4% Score 621.4; DB 13; Length 627;
Best Local Similarity 99.5%; Pred. No. 1.7e-102;
Matches 622; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCTGCACAAAGCG 60
DB 625 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCTGCACAAAGCG 566
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QY 61 GGGCTGTCGGTGGTGGAGTGCATGTACGCGAGCGGCTTCTGCTGGTGGCGTGC 120
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QY 121 CAGCGACAGCGCGGAGCAGACAGACCTTGCACAGAACCCCGGAAACCTCTGCGAGACAC 180
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Db 505 CAGCGACAGCGCGGAGCAGACAGACCTTGCACAGAACCCCGGAAACCTCTGCGAGACAC 446
QY 181 CGGTACAGAGGCGGTGTAGTACGCGAGCTGAGTAAAGAAACGCTCTCGAGAGAGGAG 240
    |||
Db 445 CGGTACAGAGGCGGTGTAGTACGCGAGCTGAGTAAAGAAACGCTCTCGAGAGAGGAG 386
QY 241 GAGGATCATGTACGCGCGGAGAGTACGAGCTGTCAGTCTGCTGGTGGTGGCGGAGC 300
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Db 385 GAGGATCATGTACGCGCGGAGAGTACGAGCTGTCAGTCTGCTGGTGGTGGCGGAGC 326
QY 301 CATGATCTCTCCGAATCTGTGGGCAATCCAGCAATAGGCGCAATGTACACAAATCAGCC 360
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Db 325 CATGATCTCTCCGAATCTGTGGGCAATCCAGCAATAGGCGCAATGTACACAAATCAGCC 266
QY 361 TGGGACAGACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||
Db 265 TGGGACAGACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAGAAAT 480
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Db 205 TAAATGAATAAACCATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAGAAAT 146
QY 481 GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTGCCACAGAGAGAGAAATTT 540
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Db 145 GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTGCCACAGAGAGAGAAATTT 86
QY 541 AATACGTCTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTAG 600
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Db 85 AATACGTCTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTAG 26
QY 601 ACACTGNAAAAAAAAAAAAAAAAAAAAA 625
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Db 25 ACACTGNAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3
BM547680 696 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798
DEFINITION 5', mRNA sequence.
ACCESSION BM547680
VERSION BM547680.1 GI:18781656
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cga@rs-remail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LMU at:
            http://lmage.lmu.edu
            Plate: LM12722 row: h column: 07
            High quality sequence stop: 641.
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FEATURES
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/tissue_type="hippocampus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site: 1: EcoRV
(deprecated); Site: 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (recovery site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 188 a 160 c 197 g 134 t 17 others
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QY 1 AGTTCTCCTTGCAGAGGAGTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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Db 65 AGTTCTCCTTGCAGAGGAGTGGCGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 124
QY 61 GGGCTGTCGGTGGTGGAGTGCATGTACGCGAGCGGCTTCTGCTGGTGGCGTGC 120
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Db 125 GGGCTGTCGGTGGTGGAGTGCATGTACGCGAGCGGCTTCTGCTGGTGGCGTGC 184
QY 121 CAGCGACAGCGCGGAGCAGACAGACCTTGCACAGAACCCCGGAAACCTCTGCGAGACAC 180
    |||
Db 185 CAGCGACAGCGCGGAGCAGACAGACCTTGCACAGAACCCCGGAAACCTCTGCGAGACAC 244
QY 181 CGGTACAGAGGCGGTGTAGTACGCGAGCTGAGTAAAGAAACGCTCTCGAGAGGAG 240
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Db 245 CGGTACAGAGGCGGTGTAGTACGCGAGCTGAGTAAAGAAACGCTCTCGAGAGGAG 304
QY 241 GAGGATCATGTACGCGCGGAGAGTACGAGCTGTCAGTCTGCTGGTGGTGGCGGAGC 300
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Db 305 GAGGATCATGTACGCGCGGAGAGTACGAGCTGTCAGTCTGCTGGTGGTGGCGGAGC 364
QY 301 CATGATCTCTCCGAATCTGTGGGCAATCCAGCAATAGGCGCAATGTACACAAATCAGCC 360
    |||
Db 365 CATGATCTCTCCGAATCTGTGGGCAATCCAGCAATAGGCGCAATGTACACAAATCAGCC 424
QY 361 TGGGACAGACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||
Db 425 TGGGACAGACGAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAGAAAT 480
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Db 485 TAAATGAATAAACCATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAGAAAT 544
QY 481 GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTGCCACAGAGAGAGAAATTT 540
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Db 545 GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTGCCACAGAGAGAGAAATTT 604
QY 541 AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTAG 600
    |||
Db 605 AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACATTAATGCTTAG 664
QY 601 ACACTGNAAAAAAAAAAAAAAAAAAAAA 621
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Db 665 ACACTGNAAAAAAAAAAAAAAAAAAAAA 685

RESULT 4
A1936826 678 bp mRNA linear EST 08-MAR-2000
LOCUS wp96h10.x1 NCI CGAP Brnz2 Homo sapiens cDNA clone IMAGE:2467075 3'
DEFINITION similar to SW:GP39 HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GP39 ; mRNA sequence.
ACCESSION A1936826
VERSION A1936826.1 GI:5675696
KEYWORDS EST.

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Source	Organism	Human
REFERENCE	1 (bases 1 to 678)	
AUTHORS	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGP), Tumor Gene Index	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapb-remail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.	
	CGNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	
	CDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:	
	www-bio.lnl.gov/bhrp/image/image.html	
	Insert length: 1143 Std Error: 0.00	
	Seq primer: ~400p from Gibco	
	High quality sequence stop: 454.	
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	/lab_host="DH10B"	
	/note="Organ: Brain; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACAACTGTAAGTGGAGGCGCGCATAGTGTGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT	133 a 199 c 161 g 182 t 3 others	
ORIGIN		
Query Match	96.5%; Score 603.4; DB 9; Length 678;	
Best local Similarity	99.7%; Pred. No. 2.9e-92;	
Matches 604; Conservative	0; Mismatches 9; Indels 0; Gaps 0;	
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606	AGTTCTCCNTGAGAGAGACTGGCGCGGAGCGCAAGAGACAGGGCGCTGCACAAAGC 547	
61	GGCGCTGTGCGTGTGAGAGTGGCATGTACGGCGAGCGCTTCTGAGTTGGCGTCTG 120	
546	GGCGCTGTGCGTGTGAGAGTGGCATGTACGGCGAGCGCTTCTGAGTTGGCGTCTG 487	
121	CAGGACAGGGCGGAGCAGACACTGTGACAGCAACCCGCGCAAACTGTGAGAGACAC 180	
486	CAGGACAGGGCGGAGCAGACACTGTGACAGCAACCCGCGCAAACTGTGAGAGACAC 427	
181	CCTGTACAGGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTCTCGAAGAGGGAG 240	
426	CCTGTACAGGAGCGGGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 367	
241	GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300	
366	GAGGATCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307	
301	CATGATCTCTCCAAATCTGTTGGGATCATCAGATTCAGGCGCAATGTCAACAATCAGCC 360	
306	CATGATCTCTCCAAATCTGTTGGGATCATCAGATTCAGGCGCAATGTCAACAATCAGCC 247	
361	TGGCGAGACAGCAGGAGGAGGAGACAGAGAAAAAGAAAAACACAGATGAGAACACAG 420	

D	b	246	TGGCGACAGCAGGAGGAGGAGACAGAAAAGAAAAAACACATGCATGAAACACAG	187
O	y	421	TAATTCGAATAAACCATTAAATATTACCCCTCTGTCTGTCTACTGCCCAAGAAAT	480
D	b	186	TAAATTAATTAACAACCATTAATATTACCCCCCTCTGTCTGTCTACTGCCCAAGAAAT	127
O	y	481	GGTACCAATTTTTCGTGTGTGACTTGTGACAGCTTCCTTTTGCCACAGAAGAAGAAATT	540
D	b	126	GGTACCAATTTTTCGTGTGTGACTTGTGACAGCTTCCTTTTGCCACAGAAGAAGAAATT	67
O	y	541	AACACTGTTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTAG	600
D	b	66	AACACTGTTTCAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTAG	7
O	y	601	ACAGTG 606	
D	b	6	ACAGTG 1	
R	E	S	RESULT 5	
L	O	C	AI990500/c	
D	E	F	AI990500	616 bp mRNA linear EST_08-MAR-2000
D	E	F	ws40d07.x1 NCI_CGAP_Gc6 Homo sapiens cDNA clone IMAGE:249661 3'	
D	E	F	similar to SW:Gg39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR	
D	E	F	GPR39.; , mRNA sequence.	
A	C	S	AI990500	
V	E	R	AI990500.1 GI:5837381	
K	E	Y	EST.	
S	O	U	human.	
O	R	G	Homo sapiens	
I	N	S	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
I	N	S	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
R	E	F	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
T	I	T	1 (bases 1 to 616)	
J	O	U	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
J	O	U	Tumor Gene Index	
J	O	U	Unpublished (1997)	
C	O	M	Contact: Robert Strausberg, Ph.D.	
C	O	M	Email: cgapbs-femail.nih.gov	
C	O	M	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael	
C	O	M	R. Emmert-Buck, M.D., Ph.D.	
C	O	M	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima	
C	O	M	Bonaldo, Ph.D.	
C	O	M	cDNA Library Arrayed by: Greg Lennon, Ph.D.	
C	O	M	DNA Sequencing by: Washington University Genome Sequencing Center	
C	O	M	Clone distribution: NCI-CGAP clone distribution information can be	
C	O	M	found through the I.M.A.G.E. Consortium/ILMIL at:	
C	O	M	www-bio.ln1l.gov/dbrr/image/image.html	
C	O	M	Insert length: 1212 Std Error: 0.00	
C	O	M	Seq primer: -40MP from Gibco	
C	O	M	High quality sequence stop: 459.	
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F	E	A	1. .616	
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F	E	A	/tissue_type="pooled germ cell tumors"	
F	E	A	/lab_host="DH10B"	
F	E	A	/note="Vector: pRT3D-Pac (Pharmacia) with a modified	
F	E	A	polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA	
F	E	A	from the normalized library NCI_CGAP_Gc4 was prepared, and	
F	E	A	ss circles were made in vitro. Following HMP purification,	
F	E	A	this DNA was used as tracer in a subtractive hybridization	
F	E	A	reaction. The driver was PCR-amplified cDNAs from a pool	
F	E	A	of 5,000 clones made from the same library (clonesIDs	
F	E	A	1257096-1258631, 1469064-1470983, and 1475592-1476743).	
F	E	A	Subtraction by Bento Soares and M. Fatima Bonaldo."	
B	A	S	BASE COUNT	
B	A	S	120 a 182 c 147 g 167 t	
O	R	I	Query Match	
O	R	I	96.2%, Score 601.2; DB 9; Length 616;	

Best Local Similarity 99.5%: Pred. No. 7.4e-99;
Matches 603; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTTCAGAGAGACTGGCCGCGGAGCGAAGACAGAGGCGCTGCACAAAGCG 60
Db 607 AGTTCCTCTTCAGAGAGACTGGCCGCGGAGCGAAGACAGAGGCGCTGCACAAAGCG 548
QY 61 GGGCGCTCGGTGGTGGAGTCCGATGACGGCGCTTCGTGCTGGTGGCGTGTG 120
Db 547 GGGCGCTCGGTGGTGGAGTCCGATGACGGCGCTTCGTGCTGGTGGCGTGTG 488
QY 121 CAGGACAGGCGGAGACAGACACCTGACAGAACACCCGCGAACTGTGCGAGAGAC 180
Db 487 CAGGACAGGCGGAGACAGACACCTGACAGAACACCCGCGAACTGTGCGAGAGAC 428
QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAACGTCTCCGAGAGGGGAG 240
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QY 241 GAGGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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QY 301 CATGATCTCTCCGATTCGTGTTGGGATCCAGCATACGCGCAATGTACACATACAGCCC 360
Db 307 CATGATCTCTCCGATTCGTGTTGGGATCCAGCATACGCGCAATGTACACATACAGCCC 248
QY 361 TGGCAGACAGCAGCAGAGGAGGAGAGACAGAAAGAAACACAGCATGAGAACAGAC 420
Db 247 TGGCAGACAGCAGCAGAGGAGGAGAGACAGAAAGAAACACAGCATGAGAACAGAC 188
QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTTCTGTCTGCTTACTGCGCAGAAAT 480
Db 187 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTTCTGTCTGCTTACTGCGCAGAAAT 128
QY 481 GGTACCAATTTTACGTTTGGATGACCTTCTTTTCCACAAGCAAGAGAAATTT 540
Db 127 GGTACCAATTTTACGTTTGGATGACCTTCTTTTCCACAAGCAAGAGAAATTT 68
QY 541 AACACTGTTTCAAAACCCGGGAGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 67 AACACTGTTTCAAAACCCGGGAGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 8
QY 601 ACAAGTG 606
Db 7 ACAAGTG 2

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RESULT 6
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LOCUS hg51612.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2949166 3'
DEFINITION similar to SW:GP39, HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GP39.1; mRNA sequence.
ACCESSION AM590950
VERSION AM590950.1 GI:7278094
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 649)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonafide, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNUL at:
image.llnl.gov/image/html/resources.shtml

Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 457.
Location/Qualifiers

FEATURES

source

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/issue_type="pooled germ cell tumors"
/lab_host="DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP-GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonafide."

BASE COUNT

132 a 189 c 155 g 173 t

Query Match

Best Local Similarity 96.2%: Score 601.2; DB 10; Length 649;
Matches 603; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTTCAGAGAGACTGGCCGCGGAGCGAAGACAGAGGCGCTGCACAAAGCG 60
Db 607 AGTTCCTCTTCAGAGAGACTGGCCGCGGAGCGAAGACAGAGGCGCTGCACAAAGCG 548
QY 61 GGGCGCTCGGTGGTGGAGTCCGATGACGGCGCTTCGTGCTGGTGGCGTGTG 120
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QY 121 CAGGACAGGCGGAGACAGACACCTGACAGAACACCCGCGAACTGTGCGAGAGAC 180
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Db 367 GAGGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 308
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Db 307 CATGATCTCTCCGATTCGTGTTGGGATCCAGCATACGCGCAATGTACACATACAGCCC 248
QY 361 TGGGACAGACAGCAGAGGAGGAGAGACAGAAAGAAACACAGCATGAGAACAGAC 420
Db 247 TGGGACAGACAGCAGAGGAGGAGAGACAGAAAGAAACACAGCATGAGAACAGAC 188
QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTTCTGTCTGCTTACTGCGCAGAAAT 480
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QY 481 GGTACCAATTTTACGTTTGGATGACCTTCTTTTCCACAAGCAAGAGAAATTT 540
Db 127 GGTACCAATTTTACGTTTGGATGACCTTCTTTTCCACAAGCAAGAGAAATTT 68
QY 541 AACACTGTTTCAAAACCCGGGAGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 67 AACACTGTTTCAAAACCCGGGAGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 8
QY 601 ACAAGTG 606

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Db	7	ACAGTC	2
RESULT 7			
LOCUS	Bf439382/c		
DEFINITION	Bf439382	696 bp	mRNA linear EST 30-MAR-2001
ACCESSION	U00001		
VERSION	U00001		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 696)		
JOURNAL	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: c9apbs-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Seq primer: -400P from Glbco		
	High quality sequence stop: 459.		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3272627"		
	/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT7A3D-Pac (Pharmacia) with		
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Equal amounts of plasmid DNA from five normalized		
	libraries were mixed, and ss circles were made in vitro.		
	Following HAP purification, this DNA was used as tracer in		
	a subtractive hybridization reaction. The driver was		
	PCR amplified cDNAs from pools of 5,000 clones made from		
	the same 5 libraries. The pools consisted of the following		
	libraries and clones: Soares NBHSF pool 1:		
	305984-310919, 323208-325895 Soares NB2HP pool 1:		
	1459382-147935, 147720-148103, 148872-149255, 15002 -		
	150407, 151176-152327 Soares NB2HF8-9W pool 1:		
	758280-760583, 772104-774407 Soares NBHPA pool 1:		
	304776-306311, 320136-322823, 326280-326653 Soares NBHOT		
	pool 1: 723720-726407, 739080-740999 Subtraction by Benc		
	Soares and M. Fatima Bonaldo."		
BASE COUNT	138 a 202 c 164 g 192 t		
ORIGIN			
Query Match	96.1%;	Score 600.8;	DB 12; Length 696;
Best Local Similarity	99.5%;	Pred. No. 8.3e-99;	
Matches 602; Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
8	CTTGAGAGAGATGGCGCGCGGAGACGAGACGAGGCGCTGCAACAAGCGGGCGCTG	67	
605	CCTGCAGAGAGATGGCGCGCGGAGACGAGACGAGGCGCTGCAACAAGCGGGCGCTG	546	
68	TCGGTGTGGATGGCGATGTACGGCGAGAGCGCTTCTCGTGGTGGCGGTGTGACGCG	127	
545	TCGGTGTGGATGGCGATGTACGGCGAGAGCGCTTCTCGTGGTGGCGGTGTGACGCG	486	
128	AGGCGGCGAGACGACGACCTGCGACGAGACACCGCGCAAACTGCTGCGAGACACCTGTAC	187	
485	AGGCGGCGAGACGACGACCTGCGACGAGACACCGCGCAAACTGCTGCGAGACACCTGTAC	426	
188	AGGACGGGGTTATGACCGAGCTGAGGTGAGAAAACGTCCTCGAAGAAGGGAGAGGATC	247	
425	AGGACGGGGTTATGACCGAGCTGAGGTGAGAAAACGTCCTCGAAGAAGGGAGAGGATC	366	

OY	248	ATGTACGGCCGGAATTAGAGACTCTGTCCAGACGTCGTCTTGGTTGGCGCAGACCATTGTC	307
Dd	365	ATGTACGCCGCCGAATTAGAGACTCTGTCCAGACGTCGTCTTGGTTGGCGCAGACCATTGTC	306
OY	308	CTTCCAAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGGCCCTGGGCAG	367
Dd	305	CTTCCAAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGGCCCTGGGCAG	246
OY	368	ACACGACGACGAGGAGACGACGACGAAAAAAGAAAACACAGCATGTGAACACAGTAATAAGA	427
Dd	245	ACACGACGACGAGGAGACGACGACGAAAAAAGAAAACACAGCATGTGAACACAGTAATAAPA	186
OY	428	ATTAACCACTAAATATTTTAGAGCCCTCTGTCTTGCTTACTAGCCACAGAAATGTTACCA	487
Dd	165	ATTAACCACTAAATATTTTAGAGCCCTCTGTCTTGCTTACTAGCCACAGAAATGTTACCA	126
OY	488	ATTTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAAGCAGAGAAATTTAACACTG	547
Dd	125	ATTTTTTCAGTGTGGACCTTGACAGCTTCTTTTGCCACAAGCAGAGAAATTTAACACTG	66
OY	548	TTTCAAACCCCGGGGAGTTGGCTGTGTTTAAGAAAGACCATTAAATGCTTTTAGACAGTGN	607
Dd	65	TTTCAAACCCCGGGGAGTTGGCTGTGTTTAAGAAAGACCATTAAATGCTTTTAGACAGTGT	6
OY	608	AAAAA 612	
Dd	5	AAAAA 1	

RESULT 8
AW149665/C
LOCUS

```

DEFINITION      xfl04h05.x1 NCI CGAP Brn50 Homo sapiens cDNA clone IMAGE:2620569 3'
                  similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
                  GPB39.; mRNA sequence.
ACCESSION       AW149665
VERSION         AW149665.1 GI:6197561
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 690)
AUTHORS        NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute / National Institute of Neurological
                Disorders and Stroke, Brain Tumor Genome Anatomy Project
                (CGAP/BTGA), Tumor Gene Index
JOURNAL COMMENT Unpublished (1998)
CONTACT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/btbp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Glbbo
High quality sequence stop: 402.
Location/Qualifiers
    1..690
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_image="IMAGE:2620569"
    /clone_id="NCI.CGAP.Brn50"
    /tissue_type="medulloblastoma"
    /lab_host="DH10B (phage resistant)"
    /note="Organ: brain; Vector: pTZ19-Dac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
medulloblastoma tumor tissue, and was then primed with a

```

FEATURES

source

[illegible]

Db	491	GCTGACGGACAGGGCGGACAGACACACCTGGACGAACACCGCGGAATGCTGCGAGG	432
OY	177	ACACCGGTACAGGAGCGGGTTGATGACCCAGACTAGGTAGAAAAAGCTCTCCGAGAAG	236
Db	431	ACACCGGTACAGGAGCGGGTTGATGACCCAGACTAGGTAGAAAAAGCTCTCCGAGAAG	372
OY	237	GGAGAGAGATCATGATGACCGCGGAGTATGAGAACCTGCTCAGTCGCTGGGTTTGGCGG	296
Db	371	GGAGAGAGATCATGATGACCGCGGAGTATGAGAACCTGCTCAGTCGCTGGGTTTGGCGG	312
OY	297	CAGCATGATATCCCTCGAATCTGTTGGGCATCCAGCATACGGCCAAATGTCAACAAATCA	356
Db	311	CAGCATGATATCCCTCGAATCTGTTGGGCATCCAGCATACGGCCAAATGTCAACAAATCA	252
OY	357	GCCCTGGGACAGACAGACAGAGGAGAGACAGAGAAAAAGAAAAACACACCATGAGAAC	416
Db	251	GCCCTGGGACAGACAGACAGAGGAGAGACAGAGAAAAAGAAAAACACACCATGAGAAC	192
OY	417	ACAGTAATGATATAAACCATTAAATATTTAGACCCCTCTGTTCTGTCTGTTACTGGCCAGG	476
Db	191	ACAGTAATGATATAAACCATTAAATATTTAGACCCCTCTGTTCTGTCTGTTACTGGCCAGG	132
OY	477	AAATGTTACCAATTTTTCAGTGTGGACTGTGACACTTCTTTTGGCCACACAGACAGAGA	536
Db	131	AAATGTTACCAATTTTTCAGTGTGGACTGTGACACTTCTTTTGGCCACACAGACAGAGA	72
OY	537	ATTTAAACACTGTTTCAAAACCGGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCT	596
Db	71	ATTTAAACACTGTTTCAAAACCGGGGAGTGTGGCTGTGTTAAAGAAAGACATTAATGCT	12
OY	597	TTAGACAGTG 606	
Db	11	TTAGACAGTG 2	

RESULT 11

BP939693/C

LOCUS

DEFINITION

BP939693

540 bp mRNA linear EST 22-JAN-2001

nae80b12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3440591 3'

similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR

GP39. ; mRNA sequence.

BP939693

ACCESSION

BP939693.1 GI:12357104

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 540)

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGM), Tumor Gene Index

Unpublished (1998)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-rt@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LMUL, send email to:

info@image.lmnl.gov

Seq primer: -400p from GIBCO

High quality sequence stop: 467.

Location/Qualifiers

1..540

FEATURES

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3440591"

DB 57 TCAACCCGGGAGTGTGCTGTTAAAGAAACCATTAATGCTTAGACAGTG 1

RESULT 13
LOCUS BM667957/c
DEFINITION 538 bp mRNA linear EST 27-FEB-2002
UI-E-DW0-aggm-j-01-0-UI s1 UI-E-DW0 Homo sapiens cDNA clone
BM667957
ACCESSION BM667957.1 GI:18975788
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 538)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA-Tes.

FEATURES
source
1..538
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-DW0-aggm-j-01-0-UI"
/clone_lib="UI-E-DW0"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DW0 is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (gt)18 tail. The
sequence tag for this library is CGATTAGCGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_Lib=UI-E-DW0
TAG_TISSUE=human lens
TAG_SEQ=CGATTAGCGA"

BASE COUNT 104 a 144 c 122 g 167 t 1 others

ORIGIN

Query Match 85.2%; Score 532.8; DB 13; Length 538;
Best Local Similarity 99.3%; Pred. No. 1.6e-86;
Matches 534; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 88 TAGCGCAGAGCGCTTCTGCTGGTGGCGTGCAGCGACGAGCGCGACGACGACCTG 147
|||||
DB 538 TAGCGCAGAGCGCTTCTGCTGGTGGCGTGCAGCGACGAGCGCGACGACGACCTG 479

QY 148 CAGGACACCCCGCGGAAGTGTGCGAGGACACCGGTACAGAGCGGGTTGATGCCGA 207
|||||
DB 478 CAGGACACCCCGCGGAAGTGTGCGAGGACACCGGTACAGAGCGGGTTGATGCCGA 419

QY 208 GCTGAGGTAGAAAAACGTCTCCGAGAAAGGAGAGATCATGTACGCCGGAAGTAGGA 267
DB 418 GCTGAGGTAGAAAAACGTCTCCGAGAAAGGAGAGATCATGTACGCCGGAAGTAGGA 359

QY 268 CCTGCTCCAGTGTGCTGTGGGTTTGGCCGAGCATGATCCTCCGAATCTGTTGGGCAT 327
DB 358 CCTGCTCCAGTGTGCTGTGGGTTTGGCCGAGCATGATCCTCCGAATCTGTTGGGCAT 299

QY 328 CCAGCATAGCGCCCAATGTACAAACATCAGCCCTGGGACAGACGAGAGAGAGAGA 387
DB 298 CCAGCATAGCGCCCAATGTACAAACATCAGCCCTGGGACAGACGAGAGAGAGAGA 239

QY 388 CAGAGAAAAAGAAAAACAGCATGAGACACAGTAATGAATAAACATTAATAATTGA 447
DB 238 CAGAGAAAAAGAAAAACAGCATGAGACACAGTAATGAATAAACATTAATAATTGA 179

QY 448 GCCCTCTGTCTGTGCTTACGTGCGCAGAGAAATGCAATTTTACGTGTGACTTG 507
DB 178 GCCCTCTGTCTGTGCTTACGTGCGCAGAGAAATGCAATTTTACGTGTGACTTG 119

QY 508 ACAGCTTTCTTTGCGCAAGCAAGAGAGAAATTTACACTGTTTCAACCCGGGGAGTTG 567
DB 118 ACAGCTTTCTTTGCGCAAGCAAGAGAGAAATTTACACTGTTTCAACCCGGGGAGTTG 59

QY 568 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGNAAAAA 625
DB 58 GCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTGNAAAAA 1

RESULT 14
LOCUS A1018769/c 537 bp mRNA linear EST 27-AUG-1998
DEFINITION ov32e04.x1 Soares_testis_NHR Homo sapiens cDNA clone IMAGE:1639038
3' similar to SW:NTRL_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;
mRNA sequence.
ACCESSION A1018769 GI:3232567
VERSION A1018769.1
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 537)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbirp/image/image.html
Insert length: 1394 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 452.

FEATURES
source
1..537
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1639038"
/clone_lib="Soares_testis_NHR"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker: Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAATGGAGCGCCGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 105 a 147 c 126 g 159 t
ORIGIN

Query Match 85.0% Score 531.2; DB 9; Length 537;
Best Local Similarity 99.3% Pred. No. 3.1e-86;
Matches 533; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 84 CATATACGGCGAGCGCTTCCTCGTGGTGGCTGTGACGACGACGCGCGACACGCA 143
DB 537 CATATACGGCGAGCGCTTCCTCGTGGTGGCTGTGACGACGACGCGCGACACGCA 478
QY 144 CCTGACAGAACACCCCGCGAATCTGCTCGAGACACCGGTACAGAGAGCGGTTGATGA 203
DB 477 CTTGACAGAACACCCCGCGAATCTGCTCGAGACACCGGTACAGAGAGCGGTTGATGA 418
QY 204 CCGAGCTGAGGTACAAAAGCTCTCCGAAAGGAGAGAGATCATGTACGCCCGGAAGT 263
DB 417 CCGAGCTGAGGTACAAAAGCTCTCCGAAAGGAGAGAGATCATGTACGCCCGGAAGT 358
QY 264 AGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
DB 357 AGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298
QY 324 GCATCAGCATACGCGCAATGTCAACAATCAGCCCTGGGAGACAGACGAGAGAGGA 383
DB 297 GCATCAGCATACGCGCAATGTCAACAATCAGCCCTGGGAGACAGACGAGAGAGGA 238
QY 384 GAGACAGAGAAAAGAAAAGACAGCATGAGAGACAGTAATGAATTAATTAATTAATTA 443
DB 237 GAGACAGAGAAAAGAAAAGACAGCATGAGAGACAGTAATGAATTAATTAATTAATTA 178
QY 444 TTAAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
DB 177 TTAAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 118
QY 504 CTTGACAGCTTCTTTTCCACAGACAGAGAAATTAATTAATTAATTAATTAATTAAT 563
DB 117 CTTGACAGCTTCTTTTCCACAGACAGAGAAATTAATTAATTAATTAATTAATTAAT 58
QY 564 GTTGGCTGTGTTAAAGAACCAATTAATGCTTTAGACAGTGNAAAAA 620
DB 57 GTTGGCTGTGTTAAAGAACCAATTAATGCTTTAGACAGTGNAAAAA 1

RESULT 15
AM150789/c 561 bp mRNA linear EST 03-NOV-1999
LOCUS
DEFINITION
x939602.x1 NCI-CGAP-Ut1 Homo sapiens cDNA clone IMAGE:262922 3'
similar to SW:GP39, HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39. ; mRNA sequence.

ACCESSION AM150789
VERSION AM150789
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 561)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILM at:
www-bio.1nl.gov/bdrrp/image/image.html

Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Glibco
High quality sequence stop: 414.
Location/Qualifiers
1. 561

FEATURES
source

BASE COUNT 117 a 160 c 124 g 158 t 2 others
ORIGIN
Query Match 84.1% Score 525.8; DB 10; Length 561;
Best Local Similarity 98.0% Pred. No. 2.9e-85;
Matches 541; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 58 GCGGCGCTGCGGTGGTGGAGTGGCATGACGAGCGGCTTCTGCTGGTGGCTG 117
DB 561 GTGGCTGCTGTTGGTGGTGGAGTGGCATGACGAGCGGCTTCTGCTGGTGGCTG 502
QY 118 CTGACAGACAGGCGGAGACACAGCACCCTGCACGAACACCCCGGAACTCTCGAGGA 177
DB 501 CTGACAGACAGGCGGAGACACAGCACCCTGCACGAACACCCCGGAACTCTCGAGGA 442
QY 178 CACCGTGTACAGAGCGGCTTGTATGACCGCTAGAGTAAAGAAAGCTCTCCGAGAGG 237
DB 441 CACCGTGTACAGAGCGGCTTGTATGACCGCTAGAGTAAAGAAAGCTCTCCGAGAGG 382
QY 238 GAGGAGATGATGACGCGCGGAGTGGAGCTCTGACAGTGTGGCTTGGCTTGGCCGC 297
DB 381 GAGGAGATGATGACGCGCGGAGTGGAGCTCTGACAGTGTGGCTTGGCTTGGCCGC 322
QY 298 AGCCATGATCCTCGAATCTGTTGGCATTCAGCATACGCGCAATGTCACAAATCAG 357
DB 321 AGCCATGATCCTCGAATCTGTTGGCATTCAGCATACGCGCAATGTCACAAATCAG 262
QY 358 CCTGGGAGACAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
DB 261 CCTGGGAGACAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
QY 418 CAGTAAT-CAATAAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 476
DB 201 CAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 142
QY 477 AAATGTACCAATTTTCACTGTTGACTGACAGCTTCTTTTCCACAGAGAGAGAG 536
DB 141 AAATGTACCAATTTTCACTGTTGACTGACAGCTTCTTTTCCACAGAGAGAGAG 82
QY 537 ATTTAACACTGTTTCAAAACCCGGGGAGGTTGGCTGTGTTAAAGAAAGCAATTAATCT 596
DB 81 ATTTAACACTGTTTCAAAACCCGGGGAGGTTGGCTGTGTTAAAGAAAGCAATTAATCT 22
QY 597 TTAGACAGTGA 608
DB 21 TTAGACAGTGA 10

Fri Nov 8 18:56:56 2002

us-09-970-966-210.std.rst

Page 12

Search completed: November 7, 2002, 15:02:36
Job time : 843.306 secs

942

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 418.22 Seconds

(without alignments)
11441.218 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttcgcgactgt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2108461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl : *

1: gb_ba : *

2: gb_hlg : *

3: gb_in : *

4: gb_om : *

5: gb_ov : *

6: gb_pat : *

7: gb_ph : *

8: gb_pl : *

9: gb_pr : *

10: gb_ro : *

11: gb_sts : *

12: gb_sy : *

13: gb_un : *

14: gb_vl : *

15: em_ba : *

16: em_fun : *

17: em_hum : *

18: em_in : *

19: em_mu : *

20: em_om : *

21: em_or : *

22: em_ov : *

23: em_pat : *

24: em_ph : *

25: em_pl : *

26: em_ro : *

27: em_sts : *

28: em_un : *

29: em_vl : *

30: em_hlg_hum : *

31: em_hlg_inv : *

32: em_hlg_other : *

33: em_hlg_mus : *

34: em_hlg_pin : *

35: em_hlg_rod : *

36: em_hlg_mam : *

37: em_hlg_vrt : *

38: em_sy : *

39: em_hgo_hum : *

40: em_hgo_mus : *

41: em_hgo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1427	88.1	1832	9	AK094501
2	1310	80.9	129676	9	AC079773
3	1264	78.1	1524	6	AX358762
4	1264	78.1	1524	6	AX362255
5	1149	71.0	2528	6	AX319944
6	1014	62.6	1890	6	AX136281
7	648	40.0	946	6	BC017318
8	541	33.4	826	6	BC011449
9	386	23.8	1362	6	AX319942
10	386	23.8	1362	9	AF034633
11	364	22.6	587	6	AX136698
12	364	22.5	444	6	AX150120
13	315	19.5	369	6	AX093381
14	310	19.1	396	6	AX093191
15	250	15.4	591	6	AX136556
16	142	8.8	14731	9	AC010974
17	47	2.9	209885	2	AC124493
18	38	2.3	1797	10	AB041649
19	30	1.9	125703	2	AC123338
20	27	1.7	487	9	AF150733
21	27	1.7	1086	8	AF082874
22	27	1.7	1114	3	AY118558
23	27	1.7	1368	6	AX285020
24	27	1.7	1614	9	AK026521
25	27	1.7	2625	9	BC028978
26	27	1.7	3155	3	AY094780
27	27	1.7	48206	10	AL645986
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29	27	1.7	127524	2	AL807806
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31	27	1.7	151602	2	AC126321
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ALIGNMENTS

RESULT 1

LOCUS AK094501 1832 bp mRNA PRI 15-JUL-2002

DEFINITION Homo sapiens CDNA FLJ37182 f1s, clone BRAL22001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (RGS20) mRNA.

ACCESSION AK094501

VERSION AK094501.1 GI:21753575

KEYWORDS OLIGO capping; f1s (full insert sequence).

SOURCE Homo sapiens alzheimer cortex CDNA to mRNA, clone lib:BRAL22

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Matsushima, M., Murakawa, K., Kanehori, K., Takahashi, Fujii, A.,
Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuko, Y., Nagai, K.,
and Isogai, T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1832)

AUTHORS Isogai, T. and Yamamoto, J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FUJ Project(HRI Team); 2-6-7
Kazusa-Kamatairi, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DB 295 GTGTGAAGATTCAGAGCTGCAAGACGACGTCCTCCCGAGTTTCATTTGTAATGAC 354
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAATGAGCAAAAGTCCGGGATCATGTA 180
DB 355 GGTGAACGTTCAAGACATGTGTCAAGAAAGTGAATGAGCAAAAGTCCGGGATCATGTA 414
QY 181 CGGCAAGTCCTGTGATCATTCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 240
DB 415 CGGCAAGTCCTGTGATCATTCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 474
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DB 475 CTGTCTCCAGGGAATCACTCACTGTTGATCGATCGCTGCAACACCCCTCTTGTAA 534
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DB 595 CACCATCTCTTCTCAATTAATAGCCCTCTTCTCGGACACCTGCTGAAGTGAAGGATG 654

QY 421 CACCCCTCTCCGATTTGTTCTTCCAGCCCTCGCCCAACCCCACTCCCTGATGA 480
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QY 481 GTTCTCTGAGGTGCTCTTTATTTCTGAGGAGCGGAGTCTGCTCTTTGTT 540
DB 715 GTTCTCTGAGGTGCTCTTTATTTCTGAGGAGCGGAGTCTGCTCTTTGTT 774
QY 541 CTTGTCAATATATGAAAGAGCTCGGTAAGACATTTCTGAATTAATTCAGCTGATGAT 600
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DB 1195 CCCTGGAAGATGCTTAAAGAAATCTTCTCAGTTCTCTTCCAGAGACTGAGCGCGGG 1254
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QY 1081 CGGCGAGGCGCTTCTGCTGAGGCTGGTGCAGCGACAGCGGCGACAGACCTTGC 1140
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 DB 1734 CAGCTTCTTTGCCAAGACAGAGAAATTAACTGTTTCAAAACCCGGGAGATTGC 1793
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 OY 1561 CTGTGTTAAAGAACACCATTAATGCTTTAGACAGTCT 1599
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RESULT 2

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 LOCUS AC079773
 DEFINITION Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.
 AC079773
 VERSION AC079773.8 GI:15145561
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 129676)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074

REFERENCE 2 (bases 1 to 129676)
 AUTHORS Shah, N., Meyer, R., Boyer, E. and Dignan, G.
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 129676)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 6 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 7 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 8 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 9 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 10 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 11 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

REFERENCE 12 (bases 1 to 129676)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2001 this sequence version replaced gi:14483388.

MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://pacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-1122: the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

FEATURES

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Best Local Similarity 99.9% Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1250 GGAAGTAGAGACCTGTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309  
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RESULT 4
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LOCUS Sequence 15 from Patent WO0208288.
DEFINITION AX362255
ACCESSION AX362255.1 GI:18694585
VERSION
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
1 Baker, K.P., Desnoyers, L., Gerltzen, M.E., Goddard, A.,
Godoski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Matanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 15 31-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
1. 1524

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BASE COUNT 321 a 433 c 435 g 335 t

ORIGIN

Query Match 78.1%; Score 1264; DB 6; Length 1524;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGACATTTTGGGATTTGCTTGTCTCCAGGCTTTGCGTCAATCCAGTGTACCA 60
DB 141 GCGACATTTTGGGATTTGCTTGTCTCCAGGCTTTGCGTCAATCCAGTGTACCA 200

QY 61 GTGTGAAGATTTCCAGTGTACCAAGACAGTCTCTCTCCCGAATTCATTGATTCAC 120
DB 201 GTGTGAAGATTTCCAGTGTACCAAGACAGTCTCTCTCCCGAATTCATTGATTCAC 260

QY 121 GTGTGAAGATTTCCAGTGTACCAAGACAGTGTACCAAGACAGTGTACATGTA 180
DB 261 GTGTGAAGATTTCCAGTGTACCAAGACAGTGTACCAAGACAGTGTACATGTA 320

QY 181 CGCGAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTGTGCGGATACAGTCTT 240
DB 321 CGCGAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTGTGCGGATACAGTCTT 380

QY 241 CTGCTCCCGAGGAAATGAACTGATTTGATCAGTGTGCAACACCCCTTTGTAA 300
DB 381 CTGCTCCCGAGGAAATGAACTGATTTGATCAGTGTGCAACACCCCTTTGTAA 440

QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCTGCGGCTGTGCGGATACAGTCTT 360
DB 441 CGGCGCAAGGCGCCAAAGAAAGGGAAGTTCTGCGGCTGTGCGGATACAGTCTT 500

QY 361 CACCATCTGTTCTCAAAATTAAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGATG 420
DB 501 CACCATCTGTTCTCAAAATTAAGCCCTCTTCTGCGCACTGCTGAAGCTGAAGAGATG 560

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QY 601 TTTCAATATGTACTGAAAGAGAGGTGAGTGAAGATTACCCCAATGTCTGTAAAC 660

DB 741 TTTCAATATGTACTGAAAGAGAGGTGAGTGAAGATTACCCCAATGTCTGTAAAC 800
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QY 901 CTGAGTGGGCTCTAGTCACTGAGACTCAATGACTGAGCTTGAAGTGGGCTCGGCT 960
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DB 1340 CTGAGGTAGAAAAACGCTCTCGAAGAGGAGGAGGATCTGTACGCGCGAAGTATGAG 1399

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QY 1321 CACGATACGCGCAATGTACACAAATCAGCCCTGCGACAGCAGAGCAGAGGAGAGAC 1380
DB 1460 CACGATACGCGCAATGTACACAAATCAGCCCTGCGGACAGCAGAGCAGAGGAGAGAC 1519

QY 1381 AGAGA 1385
DB 1520 AGAGA 1524

RESULT 5
AX319944/c 2528 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 3 from Patent WO0181634.
DEFINITION AX319944
ACCESSION AX319944
VERSION AX319944.1 GI:17901491
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
1 Galvin, K.A. and Rudolph-Owen, L.A.
Methods and compositions for the diagnosis and treatment of
cardiovascular and tumorigenic disease using 4941
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